-Mon Eeb

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GenCore version 4.5
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OM protein - protein search, using sw model

January 29, 2002, 11:00:40 ; Search time 34.94 Seconds (without alignments) 47.963 Million cell updates/sec Run on:

US-09-763-397A-25

108 1 MKFLVNVALVFMVVYISYIYAD 22 Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

219241 seqs, 76174552 residues Searched:

219241 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR\_68:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
1: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Si	Description	melittin, major, p	inant pr	hypothetical prote			core antigen - her	NADH dehydrogenase	sapecin B precurso	NADH dehydrogenase	preprotein translo	. preprotein translo	conserved hypothet	hypothetical prote				calcium receptor (	calcium/polyvalent	Ca(2+)-sensing rec	calcium receptor (	conserved hypothet	sapC protein homol	hypothetical prote	hypothetical prote			membrane transport	hypothetical prote	membrane protein M
SUMMARIES	ID	MPHB1	140841	H69453	H86742	D70105	NKVLHH	S44136	S66287	S62703	VXECSE	E86089	669513	T26259	T28208	T15959	T23576	A56715	159362	S40476	B56715	B69934	C64134	T16529	T23523	T28725	T41407	T40296	T19005	T10253
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	Score	102	. 52	51	50.5	49	49	48	48	48	47	47	47	45	45	45	45	45	45		45	44	44	44	44	44	43.5	43.5	43	43
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D82242 T19816 T39616	C82985 B71083 F71839	H64678 E86843 E82954	S54478 T15639 H71352	C40204 T28410 H84852 T32639
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39.8	9.66 8.66 8.66 8.66	8.8.8. 8.8.6.6.	8, 4, 4, 4	38.9 38.9 38.9 38.9
4 4 4 6 6 6	4 4 4 8 8 8 8	444	43 42.5 42.5	4 2 2 4 2 4 2 5 4 4 2 4 2 4 2 4 2 4 2 4
30 31		37 38 38	0 4 4 4 0 1 0 1 0	4 4 4 4 5 4 3 4

## ALIGNMENTS

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S	1
F-1	0

RESULT 1
MPHB1
melittin, major, precursor [validated] - honeybee
N;Contains: melittin F
C;Species: Apis melifera (honeybee)
C;Species: Api

A; Accession: A91640 A; Molecule type: protein A; Residues: 44 + 69 < HAB> R; Gauldie, J; Hanson, J.M.; Shipolini, R.A.; Vernon, C.A. Eur. J. Blochem. 83, 405 + 410, 1978 A; Title: The Structures of some peptides from bec venom. A; Reference number: A91253; MUID: 78126868

A;Accession: B61285
A;Aolecule type: protein
A;Molecule type: protein
A;Residues: 51-69 <GAU>
R;Ramalingam, K.; Bello, J.
Biochem. J. 284, 663-665, 1992
A;Title: Effect of permethylation on the haemolytic activity of melittin.
A;Reference number: \$23131; MUID:92321983

A. Accession: 523131
A. Scatus: preliminary
A. Status: preliminary
B. Schroeder, E.; Luebke, K.; Lehmann, M.; Beetz, I.
B. Schroeder, E.; Luebke, K.; Lehmann, M.; Beetz, I.
A. Title: Haemolytic activity and action on the surface tension of aqueous solutions of A. Reference number: A91266; MUID:72098668
A. Ariontents: annotation; synthesis
A. Note: the structure of melittin was confirmed by synthesis of a period with.full h
B. Kreil, G.; Kreil-Kiss, G.
Blochen: Blophys. Res. Commun. 27, 275-280, 1967
A. Title: The isolation of N-formylglycine from a polypeptide present in bee venom.
A. Reference number: A90165; MUID:6748282
A. Contents: annotation

A;Note: about 10% of melittin is formylated at the amino end R;Luebke, K.; Matthes, S; Kloss, G. Experientia 27, 157-767, 1971 Experientia 27, 157-767, 1971 e. A;Title: Isolation and Structure of N(alpha)-formyl melittin.

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2 KFLVNVALVFMVV---YISYIYA 21
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Best Local Similarity 42.9
Matches 9; Conservative
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H86742
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A; Reference number: A91267; MUID:72098669
A; Contents: annotation; synthesis
A; Note: N-formyl-melittin major was isolated from the venom and its structure was confil
A; Note: N-formyl-melittin major was isolated from the venom and its structure was confil
B; Mollay, C; Vilas, U; Krail, G
Proc. Natl. Acad. Sci. U.S.A. 79, 2260-2263, 1982
A; Pitle: Cleavage of honophoe prepromelittin by an endoprotease from rat liver microsome A; Title: Cleavage of honophoe prepromelitin by an endoprotease from rat liver microsome A; Teathers of Catibskov, M: Terwilliger T.C.
R; Eisenberg, D.; Gribskov, M: Terwilliger T.C.
Submitted to the Brookhaven Protein Data Bank, October 1990
A; Contents: annotation; X-ray crystallography, 2.0 angstroms, residues 44-69
A; Contents: annotation; X-ray crystallography, 2.0 angstroms is refinement.
A; Terwilliger T. C.; Eisenberg, D.
J; Biol. Chem. 257, 6010-6015, 1982
A; Terwilliger T. C.; Eisenberg, D.
A; Terwilliger T. C.; Eisenbe
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R. Mahan, S. M.; McGuire, T.C.; Semu, S.M.; Bowie, M.V.; Jongejan, F.; Rurangirwa, F.R.; R. Mahan, S.M.; McCobiology 140, 2135-2142, 1994
Microbiology 140, 2135-2142, 1994
A; Title: Molecular cloning of a gene encoding the immunogenic 21kDa protein of Cowdria A; Reference number: 140841; MUID:95005467
A; Accession: 140841; Asterial A; Accession: Idonary; translated from GB/EMBL/DDBJ
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H99433
Hypothetical protein AF1633 - Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 22-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   immunodominant protein - heartwater rickettsia
L:Species: Cowdria ruminantium (heartwater rickettsia)
C:Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 29-Sep-1999
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A;Residues: 1-209 cRES>
A;Cross-references: GB:L07385; NID:9289922; PIDN:AAA50280.1; PID:9289923
C;Superfamily: immunodominant protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94.4%; Score 102; DB 1; Length 70;
1larity 100.0%; Pred. No. 4e-08;
Conservative 0; Mismatches 0; Indels
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GB:AE000783; NID:g2687921; PIDN:AAC66442.1; PID:g268
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C; Accession: H69453
R; Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Do R; Klenk, H.P.; Clayton, R.A.; Tomb, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, J. F.; File Schmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L. Shuture 390, 364-370, 1997
A; Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, Smith, H.O.; Wosse, C.R.; Venter, J.C.
A; Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing arch A; Reference number: A69250; MuID:98049343
A; Status: preliminary; nucleic acid sequence not shown; translation not shown A; Rescieues: 1.227 K.E.
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R; Bolordin, A; Wincker, P; Mauger, S; Jaillon, O; Malarme, K; Weissenbach, R; Biblordin, A; Wincker, P; Mauger, S; Jaillon, O; Malarme, K; Weissenbach, A; Wittle: The complete genome sequence of the lactic acid bacterium.
A; Reference number: A86625
A; Accession: H86742
A; Accession: H86742
A; A; Calliniary
A; Molecule type: DNA
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A; Cross-references: GB:AE005176; NID:g12723881; PIDN:AAK05042.1; GSPDB:GN00146
A; Experimental source: strain IL1403
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C;Species: Borrelia burgdorferi (Lyme disease spirochete)
C;Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 28-Jul-2000
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pred. No. 4.2;
6; Mismatches
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Pred. No. 2.5;
6; Mismatches
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C;Accession: $62703
K;Kessler, U.; Zetsche, K.
Plant Mol. Biol. 29, 1081-1086, 1995
A;Title: Physical map and gene organization of the mitochondrial genome from the unic
A;Reference number: $62702; MUID:96145517
A;Status: nucleic acid sequence not shown; translation not shown
               C;Accession: S66287; S32323; JU0224
R;Lee, S.R.; Kurata, S.; Natori, S.
FEBS Lett. 368, 485-487, 1995
A;Title: Molecular cloning of cDNA for sapecin B, an antibacterial protein of Sarcoph A;Reference number: S66287; MUID:95361929
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Genome: mitochondrion
C;Superfamily: NADH dehydrogenase (ubiquinone) chain 3
C;Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylatio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 3 - Platymonas subcordiformis mito
C;Species: mitochondrion Platymonas subcordiformis
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 11-Jun-1999
                                                                                                                                                                                                                                                                                                 two novel sapecin homol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: EMBL:247795; NID:9633584; PIDN:CAA87750.1; PID:9633586
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, January 1995
C;Genetics:
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C;Species: Escherichia coli
C;Dacte: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 16-Jul-1999
C;Accession: A35139; A32873; H65204
R;Downing, W.L.; Sullivan, S.L.; Gottesman, M.E.; Dennis, P.P.
  C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 16-Jul-1999
                                                                                                                                                                    A; Wolecule type: mRNA
A; Residues: 1-88 (LEE>
A; Cross-references: GB.580571; NID:g1245698; PIDN:AAB35004.1; PID:g1245699
R; Yamada, K.; Natori, S.
Biochem J. 291, 275-279, 1993
A; Title: Purification, sequence and antibacterial activity of two novel sala, A; Reference number: S32323; MUID:93228618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                          A,Accession: $32323
A,Molecule type: protein
A,Residues: 55-88 < VAM>
C,Superfamily: sapecin precursor
C,Superfamily: sapecin precursor
C;Keywords: antibacterial; disulfide bond
F;1-24/Domain: signal sequence #status predicted <SIG>F;25-54/Domain: propeptide #status predicted <PRO>F;55-88/Product: sapecin B #status experimental <MAT>F;57-78,64-84,68-86/Disulfide bonds: #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3;
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Pred. No. 3.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        44.4%; Score 48; DB 2; 47.4%; Pred. No. 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9; Mismatches
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Best Local Similarity 30.0.
Rest Local 7; Conservative
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Matches 9; Conserve
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A; Residues: 1-117 <KES>
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C;Species: mitochondrion Candida parapsilosis
C,Date: 06-Feb-1995 #sequence_revision 26-Jul-1996 #text_change 07-Dec-1999
C;Accession: S44136
R;Nosek, J.
                                                                                                                                                                                                                                                                                                                                                               C;Species: heron hepatitis virus, HHBV

A;Note: host Ardea cinerea (gray heron)
C;Accession: C30082
C;Accession: C30082
C;Accession: C30082
J; Sprengel, R; Kaleta, E.F.; Will, H.
J; Virol. 62, 3832-3839, 1988
A;Title: Isolation and characterization of a hepatitis B virus endemic in herons.
A;Reference number: A93037; MUID:88333160
A;Accession: C30082
A;Accession: C30082
A;Accession: C30082
A;Residues: 1-305 <SPR>
A;Residues: 1-305 <SPR>
A;Residues: 1-305 <SPR>
A;Cross-references: GB:M22056; NID:325452; PIDN:AAA45737.1; PID:g325453
C;Superfamily: hepatitis B virus core antigen
C;Keywords: core protein
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A;Reference number: $44135
A;Accession: $44136
A;Accession: $44136
A;Molecule type: DNA
A;Residues: 1-40 <NOS>
A;Residues: 1-40 <NOS>
C;Genetics:
                                                                                                                           Gaps
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C;Superfamily: Borrelia burgdorferi hypothetical protein BB0044
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C;Species: Sarcophaga peregrina
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Pred. No. 6.1;
2; Mismatches
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44.4%; Score 48; DB
Best Local Similarity 35.0%; Pred. No. 1.6;
Matches 7; Conservative 7; Mismatches
                                                                          DB
                                                                                                                        6; Mismatches
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A;Geneme: mitochondrion
A;Genetic code: SGC3
C;Keywords: mitochondrion; NAD; oxidoreductase
                                                                       Score 49;
Pred. No.
                                                                                                                                                                                                                                                                                                                                             - heron hepatitis virus
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                                                                       45.48;
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                                                                     Query Match
Best Local Similarity 47.49
Matches 9; Conservative
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Matches 11; Conservative
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ilarity 41.2%;
Conservative
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Best Local Similarity
Matches 11; Conserv
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Best Local S:
Matches 7
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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-127 <STO>
A;Residues: 1-127 <STO>
A;Coss-references: GB:AE005174; NID:g12518903; PIDN:AAG59177.1; GSPDB:GN00145; UWGP:Z55
A;Experimental source: strain 0157:H7, substrain EDL933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R; Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew R; Perna, N.T.; Plunkett III, G.; Burland, V.; Jim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, Iller, L.; Grootbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, M.Title: Genome sequence of enterohemorrhagic Escherichia coli 0157:H7.

A; Reference number: A85480; MUID:21074935; PMID:11206551
                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-127 <SCH>
B; Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; CC
B; Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; CC
B; Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; CC
A; Rose, D.J.; Mau, B.; Shao, Y.
A; Rose, D.J.; Mau, B.; Mau
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: GB:AE000472; GB:U00096; NID:g2367333; PIDN:AAC76955.1; PID:g1790413; A;Experimental source: strain K-12, substrain MG1655
C;Comment: This integral inner membrane protein is an essential component of the protein C;Genetics:
J. Bacteriol. 172, 1621-1627, 1990
Affilte. Sequence and transcriptional pattern of the essential Escherichia coli secE-nus
A;Reference number: A35139; MUD:90170882
A;Accession: A35139
                                                                                                                                                                                                           A;Cross-references: GB:M30610; NID:9147798; PIDN:AAA24621.1; PID:9147800
R;Schatz, P.J.; Riggs, P.D.; Jacq, A.; Fath, M.J.; Beckwith, J.
Robers Dev. 3, 1035-1044, 1989
A;Title: The secE gene encodes an integral membrane protein required for protein export
A;Reference number: A32873; MUID:89378734
A;Accession: A32873
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A;Molecule type: DNA
A;Residues: 1-127 <BLAT>
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C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 31-Mar-2001
C;Accession: E86089
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5.7;
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40.9%; Pred. No. 5.7;
tive 7; Mismatches
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Pred. No.
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C, Superfamily: protein-export protein secE
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C.Superfamily: protein-export protein secE
C.Keywords: inner membrane; protein export
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Best Local Similarity 40.5%
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9, Conservative
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Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 1-127 <DOW>
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conserved hypothetical protein AF2111 - Archaeoglobus fulgidus conserved hypothetical protein AF2111 - Archaeoglobus fulgidus cispecies: Archaeoglobus fulgidus fulgidus archaeoglobus fulgidus 
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A; Residues: 1-213 <KLE>
A; Residues: 1-213 <KLE>
A; Cross-references: GB: AEO00958; GB: AEO10782; NID: 92689281; PIDN: AAB89138.1; PID: 9264
C; Superfamily: conserved hypothetical protein MJ1677
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A;Aolecule type: DNA
A;Rolecule (1.90 (MIL>
A;Residues: 1.320 (MIL>
A;Cross-references: EMBL:Z82075; PIDN:CAB04930.1; GSPDB:GN00023; CESP:W07A8.1
A;Experimental source: clone W07A8
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A;Title: The genome of Melanoplus sanguinipes entomopoxvirus.
A;Reference number: Z20484; MUID:99102612
A;Accession: T28208
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hypothetical caenorhabditis elegans
c;Species: Caenorhabditis elegans
c;Species: Caenorhabditis elegans
c;Species: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 20-Jun-2000
c;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 20-Jun-2000
c;Accession: T26259
A;Reference number: 220184
A;Reference number: 220184
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A;Introns: 83/1; 141/3; 256/3
C;Superfamily: Caenorhabditis elegans hypothetical protein W07A8.
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Pred. No. 24;
6; Mismatches
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pred. No. 8.8;
6; Mismatches '
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us-09-763-397a-25.rpr

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Submitted to the EMBL Data Library, April 1996
A; Description: The sequence of C. elegans cosmid F02EB.
A; Reference number: 218436
A; Accession: T15959
A; Status: preliminary: translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1-425 AMIL>
A; Residues: 1-425 AMIL>
A; Residues: 1-425 AMIL>
A; Residues: 1-625 AMIL>
A; Residues: 29/3: 69/2: 102/3; 153/1; 214/3; 273/1; 338/1; 379/1
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-331 <AFO>
A;Cross-references: EMBL:AF063866; NID:g4049647; PIDN:AAC97829.1; PID:g4049869
A;Cross-reference: isolate Tuscon
C;Genetics:
A;Note: MSV047
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C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 18-Feb-2000
C;Accession: T15959
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41.7%; Score 45; DB 2; Length 331;
Best Local Similarity 31.6%; Pred. No. 25;
Matches 6; Conservative 8; Mismatches 5; Indels
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Pred. No. 31;
2; Mismatches 7; Indels
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Best Local Similarity 50.0%;
Matches 9; Conservative 7
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homo sapien

Title: Perfect score:

Sequence:

OM protein

Run on:

Scoring table:

Searched:

Minimum DB Maximum DB

Database :

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PRT; 70 AA.

POLSO1; POLSO3;
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
21-JUL-1986 (Rel. 01, Last sequence update)
21-JUL-1986 (Rel. 01, Last annotation update)
MELITYIN PRECURSOR (ALLERGEN API M 3) (API M III).
Apis mellifera (Honeybee), and Apis cerana (Indian honeybee).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Prerygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
NCBI_TaxID=7460, 7461;
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MEDLINE=72098668; PubMed=5139482;
Schroeder E., Luebke K., Lehmann M., Beetz I.;
"Haemolytic activity and action on the surface tension of aqueous solutions of synthetic melittins and their derivatives.";
Experientia 27:764-765(1971).
006799 : 016136 : P12983 · P12983 · P12983 · P12983 · P1759 III D25871 F P41852 : P41852 : P41852 : P037371 : P03737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-83287387; PubMed-6309516;
Vlasak R., Unger-Ullmann C., Kreil G., Frischauf A.-M.;
"Nucleotide sequence of cloned cDNA coding for honeybee
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MEDLINE-72098665; PubMed=5139483;
Luebke K., Matthes S., Kloss G.;
Isolation and structure of N 1-formyl melittin.";
Experientia 27:765-767(1971).
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                                                                                                                                                                                                                                          ALIGNMENTS
                 DEF1_STOCA
ATP2_VIBAL
                                                   NSG2_MOUSE
NU6M_PROWI
                                                                                                                                   COX3_MAGGR
CORA_HPBDU
                                                                                    OLPA_TOBAC
GSPN_AERHY
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MEDLINE-68327913; PubMed-5592400;
 69
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CASR_RAT
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Y044_BORBU
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                                                                                    protein search, using
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2218
2271
2271
2271
2271
2271
2271
228
233
337
401
230
230
330
346
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Match Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1079
1079
1085
                                                                                                                  January 29,
                                 Copyright
                                                                                                                                                                                                                                                         BLOSUM62
```

Score

Result 8 SPECIES=A.mellifera; MEDLINE=82189959; PubMed=7076662; Terwilliger T.C., Elsenberg D.; "The structure of melittin. II. Interpretation of the structure.";

"Structure of melittin isolated from two species of honey bees."; FEBS Lett. 33:241-244(1973).

Kreil G.;

methanococc

mycoplasma

methanococc trichosanth bacillus an

Y027\_METJA Y545\_METJA RIP1\_TRIAN

42 41.5 40.5 40

42.5

haemophilus human herpe

taurus sus scrofa

homo sapien

P56626 P19580 000476 095141 P45082 013009

NPT4\_HUMAN INR2\_BOVIN

CYDD\_HAEIN

CAPB\_BACAN

GUAU\_PIG VGLM\_HSV7J

39.

K-RAY CRYSTALLOGRAPHY.

REVIEW.

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                                                                                                                                                                                                            MEDLINE-9804943; PubMed-9389475;
Rich H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,
Rich H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,
Richardson D.L., Kerlarage A.R., Graham D.E., Kyrpides N.C.,
Richardson D.L., Kerlarage A.R., Graham D.E., Kyrpides N.C.,
Richardson D.L., Relarage A.R., Graham D.E., Kyrpides N.C.,
Rirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,
Rirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,
Peterson S., Reich C.I., McNeill L.K., Badger J.H., Glodek A., Zhou L.,
Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T.,
Sadow P.W., D'Andrea K.P., Bowman C., Fujil C., Garland S.A.,
Wason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                        "The complete genome sequence of the hyperthermophilic, sulphate-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -1 - SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN-ARCS 55210 / B31;
MEDIINE-98065943; PubMed-9403685;
Fraser C.M., Casjens S., Huang W.M., Sutton G.G., Clayton R.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           47.2%; Score 51; DB 1; Length 227;
42.9%; Pred. No. 2;
tive 6; Mismatches 6; Indels
                                                                                                                                 Euryarchaeota; Archaeoglobales; Archaeoglobaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hypothetical protein; Transmembrane; Complete proteome.
TRANSMEM 109 128 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        63DCC7027C15A706 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Borrelia burgdorferi (Lyme disease spirochete).
Bacteria; Spirochaetales; Spirochaetaceae; Borrelia.
NCBL_TaxID=139;
028640;
20-AUG-2001 (Rel. 40, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
HYPOTHETICAL PROTEIN AF1633.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                133 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              archaeon Archaeoglobus fulgidus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         106 MKIMCNVGLVLMMVFAAFYFA 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25313 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MKFLVNVALVFMVVYISYIYA 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20-AUG-2001 (Rel. 40, Last a HYPOTHETICAL PROTEIN BB0044.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nature 390:364-370(1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   128
192
                                                                                                            Archaeoglobus fulgidus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            227 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
es 9; Conserv
                                                                                                                                                                                                      SEQUENCE FROM N.A
                                                                                                                                             Archaeoglobus.
NCBI_TaxID=2234;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Y044_BORBU
O51073;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              reducing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                 Archaea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TRANSMEM
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7044_BORBU
1D 7044_BORBU
1D 70464_B
AC 051073
DT 15-DEC
DT 15-DEC
DT 15-DEC
DT 15-DEC
DT 80044
GN BB0044
GN BB0044
GN BB0014
GN BB0017
GN NCB1_1
RP SEQUE
RR STRAIP
RR STRAIP
RR STRAIP
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Matches
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    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RQQG -> KRQQ (IN MELITIIN 2; POSSIBLY AN ARTEFACT).
                                                                                                                                                                                                                                                                                                                                                                                    MISCELLANEOUS: N-FORMYL-MELITTIN MAJOR HAS 80% OF THE ACTIVITY OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                           SPECIES-A.mellifera; Barnham K.J., Hewish D., Werkmeister J., Curtain C., Kirkpatrick A., Bartone N., Norton R., Rivett D.; Submitted (JUN-1998) to the PDB data bank.
                                                                                                                                                                                                                                                                                                                                                                                                                                          NOTE-Issue 12 of July 2001;
WWW-"http://www.expasy.org/spotlight/articles/sptlt012.html".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (IN MELITIIN 2; POSSIBLY AN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  607F52C091C23BB6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 102; DB 1; 1
Pred. No. 7.6e-08;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            227 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ARTEFACT
                                                                                                                                                                                                                                                                                                                                                                                                                       DATABASE: NAME-Protein Spotlight;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
    Biol. Chem. 257:6016-6022(1982)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94.4%; Scor
100.0%; Pre
ative 0; M
                                                                                                                                                                   MEDLINE-90254148; PubMed-2187536;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MKFLVNVALVFMVVXISXIXA 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MKFLVNVALVEMVVYISYIYA 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           53
54
68
7585 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; X02007; CAA26038.1; -.
                                      STRUCTURE BY NMR OF 44-69.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               43
69
69
69
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Best Local Similarity
Matches 21; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24449
6446
644
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Allergen. SIGNAL

PROPEP

MOD\_RES

VARIANT

HELIX

MOD\_RES

SEQUENCE

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YG33\_ARCFU

YG33\_ARCFU ID YG33\_A

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Gaps

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Indels

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Mismatches

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22

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3 FLVNVALVEMVVYISYIYAD
                                             26 FLVTVPLVCTIVYDSCLYMD
       Conservative
      11;
                                                                                                                    SAPB_SARPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PEPTIDE
DISULFID
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                                                                                          SAPB_SARPE
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      Matches
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                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                           ö
Lathigra R., White O., Ketchum K.A., Dodson R., Hickey B.K., Gwinn M., Dougherty B., Tomb J.-F., Fleischmann R.D., Richardson D., Peterson J., Kerlavage A.R., Quackenbush J., Salzberg S., Hanson M., van Vugt R., Palmer N., Adams M.D., Gocayne J.D., Weidman J., Utterback T., Watthey L., McDonald L., Artlach P., Bowman C., Garland S., Fulji C., Cotton M.D., Horst K., Roberts K., Hatch B., Smith H.O., Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sprengel R., Kaleta E.F., Will H.; "Isolation and characterization of a hepatitis B virus endemic in
                                                                                                                                                                                                                                                                                                                                                           ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Viruses; Retroid viruses; Hepadnaviridae; Avihepadnavirus NCBI_TaxID-28300;
                                                                                                                                                                                                                                                                                                                                  Length 133
                                                                                                                                                                                                                                                                                                                                                           4; Indels
                                                                                                                                                                                                                                                                  Hypothetical protein; Transmembrane; Complete proteome.
                                                                                                                                                                                                                                                                                           133 AA; 16052 MW; A57686EA30F1959B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2B228EF44162CB06 CRC64;
                                                                                                                                                                                                                                                                                                                                 Score 49; DB 1;
Pred. No. 2.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
01-APR-1990 (Rel. 14, Last annotation update)
CORE ANTIGEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        305 AA.
                                                                                                                                                                                                                                                                                                                                                           6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            interPro; IPR002006; Hepatitis_core.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE-88333160; PubMed-3418788;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00906; Hepatitis_core; 1.
                                                                                                                                                                                                                                           EMBL; AE001118; AAC66442.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   305 AA; 34925 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       J. Virol. 62:3832-3839(1988).
                                                                                                                                                                                                                                                                                                                                 45.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; M22056; AAA45737.1; -.
                                                                                                                                                                                                                                                                                                                                                                                 3 FLVNVALVEMVVYISYIYA 21
                                                                                                                                                                                                                                                                                                                                                                                                         12 FLISVFLIFIVSGITYFYS 30
                                                                                                                 Nature 390:580-586(1997).
                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 47.4
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Heron hepatitis b virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                С30082; ИКУЦНН.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Core protein.
SEQUENCE 3(
                                                                                                     burgdorferi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORA_HPBHE
P13845;
                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                 TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORA_HPBHE
     ò
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Length 305;

DB 1; 4.9;

Score 49; Pred. No. 4

45.4%;

Query Match Best Local Similarity

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                           Sarcophaga peregrina (Flesh fly) (Boettcherisca peregrina).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hoxapoda; Insecta;
Pterygota; Meoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Oestroidea; Sarcophagidae; Sarcophaga.
                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE=95361929; PubMed=7635204;
Lee S.-R., Kurata S., Natori S.;
"Molecular cloning of cDNA for sapecin B, an antibacterial protein of Sarcophaga, and its detection in larval brain.";
FEBS Lett. 368:485-487(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Insect immunity; Antibiotic; Cleavage on pair of basic residues;
                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- TISSUE SPECIFICITY: HEMOCYTES AND FAT BODY.
-!- INDUCTION: BY INJURY TO THE LARVAL CELL WALL.
-!- SIMILARITY: BELONGS TO THE ARTHROPOD DEFENSIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9459A0AF3B0EDE3D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF01097; Arthro_defensin; 1.
PROSITE; PS00425; ARTHROPOD_DEFENSINS; FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 48; DB 1;
Pred. No. 2.5;
6; Mismatches
                                          01-JUL-1993 (Rel. 26, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 39, Last annotation update)
SAPECIN B PRECURSOR.
88 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 55-88, AND DISULFIDE BONDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR001542; Arthro_defensin.
  PRT;
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10041 MW;
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  STANDARD;
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Best Local Similarity
9; Conserve
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PIR; JU0224; JU0224
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Schatz P.J., Riggs P.D., Jacq A., Fath M.J., Beckwith J.; 
"The secë gene encodes an integral membrane protein required 
protein export in Escherichia coli."; 
Genes bev. 3:1035-1044(1989).
SEQUENCE FROM N.A.
MEDLINE-89378734; Pubmed-2673920;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Viridiplantae; Chlorophyta; Prasinophyceae; Platymonas.
NCBL_TaxID=3161;
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Plant Mol. Biol. 29:1081-1086(1995).
-!- CATALYTIC ACTIVITY: NADH + UBIQUINONE = NAD(+) + UBIQUINOL.
-!- SIMILARITY: BELONGS TO THE COMPLEX I SUBUNIT 3 FAMILY.
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13668 MW; 11634AEF4742F694 CRC64;
                                                                                                                                                                                   15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
NADH-UBIQUINONE OXIDOREDUCTAŠE CHAIN 3 (EC 1.6.5.3).
                                                                                                                                  117 AA.
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                                                                                                                                  PRT;
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Pfam, PF00507; Oxidored_q4; I. Oxidoreductase; NAD; Ubiquinone; M
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1 MKFLTSLLLLEVVVMVSAV 19
                                                                                                                                                                                                                                                                                                                     Platymonas subcordiformis. Mitochondrion.
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                                                                                                                                  STANDARD;
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P16920;
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Q36518;
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                                                                              RESULT 6
NU3M_PLASU
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SECE_ECOLI
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1- FUNCTION: ESSENTIAL, FOR PROTEIN EXPORT.
-- SUBUNIT: PART OF THE PROXARVOTIC PROTEIN TRANSLOCATION APPARATUS
WHICH COMPRISE SECA, SECB, SECB, SECF, SECF, SECR, THE
TRANSLOCATION CHANNEL SEEMS TO BE COMPSOED OF A SECA HOMODIMER AND
FOUR COPIES OF A SECYEG COMPLEX.
-- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. INNER MEMBRANE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SENDING FROM N.T. RIND 0509952;
MEDLINE-21156231; PUbMed-112588796;
MEDLINE-21156231; PubMed-112588796;
MEDLINE-21156231; PubMed-112588796;
Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K., Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T., Iida T., Takani H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T., Kubara S., Shiba T., Hattori M., Shinagawa H.; Romplete genome sequence of enterchemorrhagic Escherichia coli 0157:H7 and genomic comparison with a laboratory strain K-12.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Schatz P.J., Bieker K.L., Ottemann K.M., Silhavy T.J., Beckwith J.; Anone of three transmembrane stretches is sufficient for the functioning of the SecE protein, a membrane component of the E. coli secretion machinery.
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                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-21074935; PubMed-1120551;
MEDLINE-21074935; PubMed-1120551;
MEDLINE-21074935; PubMed-1120551;
Rose D.J. Mayhew G.F. Evans P.S., Gregor J., Kirkpatrick H.A.,
Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
Rose D.J., Mayhew G.F., Evans P.S., Jenger J., Kirkpatrick H.A.,
Rose D.J., Mayhew G.F., Evans P.S., Jenger J., Kirkpatrick H.A.,
Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
Welch R.A., Blattner F.R.;
"Genome sequence of enteronaemorrhagic Escherichia coli 0157:H7.";
Mature 409:529-533(2001).
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                                                                                                                                                                   Daniels D.L.; Analysis of the Escherichia coli genome. IV. DNA sequence of the ragion from 80.2 to 92.8 minutes."; Nucleic Acids Res. 21:5408-5417(1993).
SEQUENCE FROM N.A.
STRAILNE-112 / MG1655;
MEDLINE-9408932; Pubmed-8265357;
Blattner F.R., Burland V.D., Plunkett G. III, Sofia H.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Evaluating the oligomeric state of SecYEG in preprotein
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EMBO J. 19:852-861(2000).
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MEDLINE-98049343; PubMed-9389475;
MEDLINE-98049343; PubMed-9389475;
MEDLINE-98049343; PubMed-9389475;
MEDLINE-98049343; PubMed-9389475;
MEDLINE-98049343; PubMed-9389475;
METERINAVC-16 / Winn M., Hickey E.K., Peterson J.D.,
Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C.,
Richardson D.L., Merlavage A.R., McKenney K., Adams M.D., Loftus B.,
Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,
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Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T.,
Cotton M.D., Spriggs T., Artiach P., Kaine B.P., Sykes S.M.,
Sadow P.W., D'Andrea K.P., Bowman C., Fujil C., Garland S.A.,
Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "The complete genome sequence of the hyperthermophilic, sulphate-reducing archaeon Archaeoglobus fulgidus.";
Nature 390:364-370(1997).
                                                                                                                                                                                                                             Pfam, PF00584; SecE; 1.
PROSITE; PS01067; SECE_SEC61G; 1.
Protein transport; Translocation; Transmembrane; Inner membrane;
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                                                                                                                                                                                                                                                                                                                                                                                                       Score 47; DB 1; Length 127; Pred. No. 4.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Archaea; Euryarchaeota; Archaeoglobales; Archaeoglobaceae;
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 -!- SIMILARITY: BELONGS TO THE SECE/SEC61-GAMMA FAMILY.
                                                                                                                                                                                                                                                                                                                                                     PERIPLASMIC (PROBABLE).
94D37280522875CE CRC64;
                                                                                                                                                                                                                                                                            CYTOPLASMIC (PROBABLE). PROBABLE.
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                                                                                                                                                                                                                                                                                                                             CYTOPLASMIC (PROBABLE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           213 AA
                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
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EMBL; AF005629; AAG59177.1; --
EMBL; AF002567; BAB38327.1; --
PIR; A35139; VXECSE
PIR; S16341; S16341.
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                                                                                                                                                                                                                                                                                                                                                                   MM;
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                                                                                                                     EMBL; M30610; AAA24621.1; -. EMBL; U00006; AAC43079.1; -.
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37 44
45 63
64 92
93 111
112 127
127 AA; 13643 M
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InterPro; IPR001901; SecE.
Pfam; PF00584; SecE; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Archaeoglobus fulgidus.
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Best Local Similarity
Matches 9; Conserv
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                                                                                                                                                                                                                                                                    Complete proteome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YL11_ARCFU
028169;
                                                                                                                                                                                                                                                                                            TRANSMEM
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-94229358; pubMed-8174787;
Woder B.K., Mao J., Erdos G.W., West C.M., Blumberg D.D.;
Yoder B.K., Mao J., Erdos G.W., West C.M., Blumberg D.D.;
Identification of a new spore coat protein gene in the cellular
slime mold DictyOstellum discoideum.";
Dev. Biol. 163:49-65(1994).
-!- FUNCTION: MAY CONTRIBUTE TO THE STRUCTURE OF THE COAT AT THE
INTERFACE BETWEEN THE MIDDLE, CELLULOSIC LAYER AND THE OUTER,
ELECTRON-DENSE, PROTEINACEOUS LAYER.
-!- SUBCELLULAR LOCATION: ACCUMULATES SPECIFICALLY IN REGULATED
SECRETORY VESICLES OF PRESPORE CELLS (PRESPORE VESICLES). THE
PROTEIN LATER ACCUMULATES EXTRACELLULARLY IN THE SPORE COAT.
-!- INDUCTION: BY C-AMP.
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
-!- SIMILARITY: BELONGS TO THE UPF0056 (MARC) FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Transmembrane; Complete proteome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5B193379E5BC7278 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Dictyostelium discoideum (Slime mold).
Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
SPORE COAT PROTEIN SP87 PRECURSOR (PL3 PROTEIN).
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-!- SIMILARITY: CONTAINS 12 PRESPORE MOTIFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MKFLV--NVALVFMVVYISYIYA 21
                                                                                                                                                                                                                                                                                                                                               EMBL; AE000958; AAB89138.1; -.
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75
118 1
142 1
181 2
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P54643;
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SEQUENCE FROM N.A.
Pearce S.H.S., 'Jhakker R.V.;
Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                       SEQUENCE FROM N.A.
                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                   C.E.;
                                                                                                                                                                  Raue F
 ö
                                                     SPORE COAT PROTEIN SP87.
PRESPORE MOTIF 1.
PRESPORE MOTIF 2.
PRESPORE MOTIF 4.
PRESPORE MOTIF 5.
PRESPORE MOTIF 5.
PRESPORE MOTIF 6.
PRESPORE MOTIF 6.
PRESPORE MOTIF 7.
PRESPORE MOTIF 9.
PRESPORE MOTIF 10.
PRESPORE MOTIF 11.
PRESPORE MOTIF 11.
PRESPORE MOTIF 12.
S X 9 AA REPEATS OF G-G-S-S-G-G-T-S.
                                                                                                                                                                                                                                                                                                                                                                                                             CASR_HUMAN STANDARD; PRT; 1078 AA.

CASR_HUMAN STANDARD; 016108; 016109; 016110;
01-FBB-1995 (Rel. 31, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last sequence update)
EXTRACELLULAR CALCIUM-SENSING RECEPTOR PRECURSOR (CASR) (PARATHYROID CELL CALCIUM-SENSING RECEPTOR).
CASR ON GPRC2A OR PCAR1.
HOMO saplens (Human).
Relazion: Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                             LINKED (GLCNAC. . .) (POTENTIAL).
EF6E29CFF57E78D5 CRC64;
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2-2.
2-3.
8 x 26 AA APPROXIMATE REPEATS.
                                                                                                                                                                      1-4 (APPROXIMATE),
1-5 (APPROXIMATE),
3 x 40 AA APPROXIMATE REPEATS.
                                                                                                                                                                                                                                                                                                                                       DB 1; Length 677;
24;
                                                                                                                                                                                                                                                                                                                                                     8; Indels
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GLY/SER/THR-RICH.
GLY/SER/THR-RICH.
                                                                                                                                                                                                                                                                                                                                       Score 46; DB ]
Pred, No. 24;
4; Mismatches
                                          Sporulation; Signal.
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                                                                                                                                                                                               1 MKFLVNVALVFMVVXISYIYA 21
                                                                                                                                                                                                                                                                                                                                       42.6%;
ilarity 42.9%;
Conservative
                  Dictybb, DD02054; pspb.
InterPro; IPR003645; Foln.
SMART; SM00274; FOLN.
Glycoprotein; Repeat; Spor
       EMBL; U25144; AAA73515.1;
HSSP; P06620; 1INA.
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Best Local Similarity
Matches 9; Conserva:
                                                                                                                                                                                                                                                                                                                  677 AA;
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2568
2568
2568
3308
3348
331
419
                                        Glycoprotein;
SIGNAL
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CARBOHYD
SEQUENCE
                                                       CHAIN
REPEAT
REPEAT
REPEAT
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REPEAT
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REPEAT
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CASR_HUMAN
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A motations in the human Ca(2+)-sensing-receptor gene that cause familial hypocalciuric hypercalcemia.";

Am. J. Hum. Genet. 56:1075-1079(1995).

(9)

SEQUENCE OF 1-61 FROW N.A., AND VARIANT FHH ALA-39.

MEDLINE-95403641; Pubmed-7673400;

A Aida K., Koishi S., Inoue M., Nakazato M., Tawata M., Onaya T.;

Thuman Ca(2+)-sensing receptor gene.";

Thuman Ca(2+)-sensing receptor gene.";

L J. Clin. Endocrinol. Metab. 80:2534-2598(1995).

MEDLINE-9629293; Pubmed-8675635;

X MEDLINE-9629293; Pubmed-8675635;

A Pearce S.H.S., Trump D., Wooding C., Besser G.M., Chew S.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VARIANT ADH ALA-127.
MEDLINE-95179179; PubMed-7874174;
POLIAK M.R., Brown E.M., Estep H.L., McLaine P.N., Kifor O., Park J., Hebert S.C., Seidman C.E., Seidman J.G.;
"Autosomal dominant hypocalcaemia caused by a Ca(2+)-sensing receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ESI
SEQUENCE OF 643-908 FROW N.A.
MEDLINE-96193893; PubMed-8613532;
Bikke D.D., Ratnam A., Mauro T., Harris J., Pillai S.;
Bikke D.D., Ratnam responsiveness and handling during keratinocyte
"Changes in calcium responsiveness and handling during keratinocyte
differentiation. Potential role of the calcium receptor.";
J. Clin. Invest. 97:1085-1093(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VARIANTS FHH GLM-185, LYS-297 AND TRP-795.

MEDLINE-94094324; Pubbed=7916660;

Pollak M.R., Brown E.M., Chou Y.-H.W., Hebert S.C., Marx S.J.,

Stelnmann B., Levi T., Seidman C.E., Seidman J.G.;

"Mutations in the human Ca(2+)-sensing receptor gene cause familial

"Mutations in the human Ca(2+)-sensing receptor gene cause familial
TISSUE-Parathyroid;
MEDLINE-95279439; PubMed-7759551;
Garrett J.E., Capuano I.V., Hammerland L.G., Hung B.C., Brown E.M.,
Hebert S.C., Nemeth E.F., Fuller F.;
"Molecular cloning and functional expression of human parathyroid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE-96343808; Pubmed-8756555;
Freichel M., Zink-Lorenz A., Holloschi A., Hafner M., Flockerzi V.,
                                                                                                                                                                                                                                                                                                                                                TISSUE-Kidney;

#EDILINE-95408281; PubMed-7677761;

Aida K., Kolabi S., Tawata M., Onaya T.;

"Molecular cloning of a putative Ca(2+)-sensing receptor CDNA from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                [8]
VARIANTS FHH MET-62; CYS-66; MET-138; GLU-143 AND GLN-227.
MEDLINE-9524322; Pubbed-7726161;
Chou Y.-H.W., Pollak M.R., Brandi M.L., Toss G., Arnqvist H.,
Atkinson A.B., Papapoulos S.E., Marx S., Brown E.M., Seidman J.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Expression of a calcium-sensing receptor in a human medullary thyroid carcinoma cell line and its contribution to calcitonin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Biochem. Biophys. Res. Commun. 214:524-529(1995).
                                                                                                                                                                                                calcium receptor cDNAs.";
J. Biol. Chem. 270:12919-12925(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                secretion.";
Endocrinology 137:3842-3848(1996).
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Nat. Genet. 8:303-307(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hyperparathyroidism.";
Cell 75:1297-1303(1993).
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EXTRACELLULAR CALCIUM-SENSING RECEPTOR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IV (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
VII (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
II (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC...) (POTENTIAL).
N-LINKED (GLCNAC...) (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                   Alternative splicing; Polymorphism.
                                                                                                                                    Pfam; PF00003; 7tm_3; 1.
Pfam; PF01004; 7tm_3; 1.
Pfam; PF01094; ANF_receptor; 1.
PRINTS; PR00148; GCRMGR.
PRINTS; PR00592; CASENSINGR.
PROSITE; PS00979; G_PROTEIN_RECEP_F3_1; 1.
PROSITE; PS00981; G_PROTEIN_RECEP_F3_2; 1.
PROSITE; PS00981; G_PROTEIN_RECEP_F3_3; 1.
PROSITE; PS500981; G_PROTEIN_RECEP_F3_4; 1.
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N-LINKED
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N-LINKED
N-LINKED
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                                                                                                 InterPro; IPR001828; ANF_receptor
InterPro; IPR000337; GPCR_Mgr.
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090Y96; 008968; 088519; 090Y95
20-AUG-2001 (Rel. 40, Created)
20-AUG-2001 (Rel. 40, Last sequents)
20-AUG-2001 (Rel. 40, Last sequents)
                                                                                                                    GPCR_Mgr.
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45.0%;
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078
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                              G-protein coupled
Disease mutation;
           GCR 2697:
                                 MIM; 601199; -. MIM; 145980; -. MIM; 601198; -.
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TRANSMEM
DOMAIN
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ALTERNATIVE PRODUCTS: 2 ISOFORMS SEEM TO BE PRODUCED BY
ALTERNATIVE PRODUCTS: 2 ISOFORMS SEEM TO BE PRODUCED BY
ALTERNATIVE PRODUCTS: 2 ISOFORMS SEEM TO BE PRODUCED BY
ALTERNATIVE SPECIFICITY: FOUND IN KIDNEY, BUT NOT IN BRAIN, LUNG,
LIVER, HEART, SKELETAL MUSCLE, OR PLACENTA.

HYPERCALCEMIA (FHI) AND NEONDATAL SEVERE HYPERPARATHYROIDISM
(NSHPT), TWO INHERITED CONDITIONS CHARACTERIZED BY ALTERED CALCIUM
(NSHPT), TWO INHERITED CONDITIONS REDUCE THE ACTIVITY OF THE RECEPTOR.

CHARACTERIZED INDIVIDUALS EXHIBIT MILD OR MODEST HYPERCALCEMIA,
CONTRAST, NSHPT IS A RARE AUTOSOMAL RECESSIVE LIFE-THREATENING
CONTRAST, NSHPT IS A RARE AUTOSOMAL RECESSIVE LIFE-THREATENING
CONTRAST, NSHPT IS A RARE AUTOSOMAL RECESSIVE LIFE-THREATENING
CONTRASTAL DEMANNERALIZATION, AND PARATHYROID HYPERPLASTA. IN SOME
INSTANCES NSHPT HAS BEEN DEMONSTRATED TO BE THE HOMOZYGOUS FORM OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         between the Swiss Institute of Bloinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DISEASE: DEFECTS IN PCARI ARE ALSO THE CAUSE OF AUTOSOMAL DOMINANT HYPOPARATHYROIDISM (ADHP). ADHP IS CHARACTERIZED BY HYPOCALCEMIA AND HYPERPHOSPHATEMIA DUE TO INADEQUATE SECRETION OF PARATHYROID HORMONE. SYMPTOMS ARE SEIZURES, TETANY AND CRAMPS. SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DISEASE: DEFECTS IN CASR ARE ALSO THE CAUSE OF AUTOSOMAL DOMINANT HYPOCALCEMIA (ADH) IN WHICH THE RECEPTOR IS ACTIVATED AT SUBNORMAL
                                                 'Calcium-sensing receptor mutations in familial benign hypercalcemia
                                                                                                                                                                                                                                                                                                                                                                      Ward B.K., Stuckey B.G.A., Gutteridge D.H., Laing N.G., Pullan P.T.,
Ratajczak T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CALCIUM IONS. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY A G-PROTEIN THAT ACTIVATES A PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER SYSTEM.
                                                                                                                                                                                                                                                                                                                                                                                                                 "A novel mutation (L174R) in the Ca2+-sensing receptor gene associated with familial hypocalciuric hypercalcemia."; Hum. Mutat. 10:233-235(1997).
Grant D.B., Heath D.A., Hughes I.A., Paterson C.R., Whyte M.P.,
Thakker R.V.;
                                                                                                                                         VARÍANTS ADHP THR-116; HIS-681 AND SER-806, AND VARIANT SER-851
                                                                                                                                                            MEDLINE-96311554; PubMed-8733126;
Baron J., Winer K.K., Yanovski J.A., Cunningham A.W., Laue L., Elimerman D., Cutler G.B. Jr.,
"Mutations in the Ca(2+)-sensing receptor gene cause autosomal dominant and sportait hypoparathyroidism.";
Hum. Mol. Genet. 5:601-606(1996).
                                                                         d neonatal hyperparathyroidism.";
Clin. Invest. 96:2683-2692(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB29413.2; ALT_SEQ.
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MEDLINE-97442275; Pubmed-9298824;
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S83176; AAB46873.1;
S79217; AAB35262.2;
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S81755; AAD14370.1;
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20-AUG-2001 (Rel. 40, Last annotation update)
EXTRACELLULAR CALCIUM-SENSING RECEPTOR PRECURSOR (CASR) (PARATHYROID CELL CALCIUM-SENSING RECEPTOR).
CASR OR GPRC2A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "The calcium sensing receptor and its alternatively spliced form in murine epidermal differentiation.";
                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A., ALTERNATIVE SPLICING, AND TISSUE SPECIFICITY.
STRAIN-C57BL/6; TISSUE-Kidney;
MEDLINE-20092890; Pubmed-10625662;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oda Y., Tu C.-L., Chang W., Crumrine D., Koemueves L., Mauro T., Elias P.M., Bikle D.D.;
. . .) (POTENTIAL)
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                                                                Length 1078
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Q9QY95; Q9QZU8; Q9R1D6; Q9R1Y2;
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9
                                                                DB 1;
                                                                                               5; Mismatches
                                                                Score 45;
Pred. No.
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GCR\_2013; GCR\_2696;

GCRDb; GCRDb;

GCRDb;

GCR\_1337, GCR\_1874; GCR\_2012

GCRDb;

EMBL; EMBL;

EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; GCRDb EXTRACELLULAR CALCIUM-SENSING RECEPTOR. EXTRACELLULAR (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

II (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

III (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

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Best Local Similarity
Matches 9; Conserv
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SEQUENCE FROM N.A.
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PER SEQUENCE OF 646-799 FROM N.A., AND TISSUE SPECIFICITY.

MEDLINE-97231187; PubMed-9076582;

A quarties L.D., Hartle J.E. II, Siddhanti S.R., Guo R., Hinson T.K.;

A distinct cation-sensing mechanism in M373-El osteoblasts

I a bone Miner. Res. 12:393-407(1997).

C. I bone Miner. Res. 12:393-407(1997).

C. I BONE MINER. RES. CHANGES IN THE EXTRACLULAR CONCENTRATION OF CALCIUM IONS. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY A G-PROTEIN THAT ACTIVATES A PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESERNGER SYSTEM.

C. I SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.

C. I ALTERNATIVE PRODUCTS: 2 ISOFORMS; A (SHOWN HERE) AND B; ARE PRODUCED BY ALTERNATIVE SPLICING.

PRODUCED BY ALTERNATIVE SPLICING.

C. I SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.

C. I SIMILARITY: BELONGS TO FAMILY 3.
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RE BRIBL, AF110179; AAD28371.1; - .

RE BRIBL, AF128442; AAD28371.1; - .

RE BRIBL, AF12842; AAD40638.1; - .

RE BRIBL, AF068900; AAC19388.1; - .

RE BRIBL, AF062746; BAA77688.1; - .

RE BRIBL, AF062746; BAA77688.1; - .

RE MAGI, AF159565; AAF00193.1; - .

RE MAGI, AF1351315; GPTC2A.

RICHERPOO, IPRO00183; GPTCR.Mgr.

RE FROM PRONO183; GPTCR.Mgr.

RE FROM PRONO184; ANF_RECEPLOT; 1.

RE PRONO185; PRO0049; GPTCREAMERCEP_F3.1; 1.

RE RESTER PRO0099; GPROTEIN_RECEP_F3.2; 1.

RE ROSITE; PS009981; GPROTEIN_RECEP_F3.3; 1.

RE ROSITE; PS00981; GPROTEIN_RECEP_F3.3; 1.
                                                                                                                                                                                                                                             TISSUB-Epiphyseal cartilage;
MEDLINE=20043955; PubMed=10579354;
Chang W., Tu C., Chen T.-H., Komuves L., Oda Y., Pratt S.A.,
Miller S., Shoback D.;
"Expression and signal transduction of calcium-sensing receptors is cartilage and bone.";
Endocrinology 140:5883-5893(1999).
                                                                                                                                                                                                                                SEQUENCE OF 256-600 FROM N.A. (ISOFORM A), AND TISSUE SPECIFICITY
                                 SEQUENCE FROM N.A. (ISOFORM A), AND TISSUE SPECIFICITY.
STRAIN—BLACK SWISS X 129/SWJ; TISSUE—Kidney;
PLOSTO: Pubmed=10652312;
Pi M. Garner S.C., Flannery P., Spurney R.F., Quarles L.D.;
"Sensing of extracellular cations in CasR-deficient osteoblasts.
Evidence for a novel cation-sensing mechanism.";
J. Biol. Chem. 275:3256-3263(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-NWRI; TISSUE-Brain;
Hildenbrand J., Ammon H.P.T., Wahl M.A.;
Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE-Kidney;
Moawad T.I., Riccardi D.;
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
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Biol. Chem. 275:1183-1190(2000)
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CYTOLASMIC (POTENTIAL).

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IV (POTENTIAL).
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V (POTENTIAL).
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01-FEB-1996 (Rel. 33, Last sequence update)
20-AGG-2010 (Rel. 40, Last annotation update)
2XTRACELULAR CALCIUM-SENSING RECEPTOR PRECURSOR (CASR) (PARATHYROID CELL CALCIUM-SENSING RECEPTOR).
CASR OR GPRC2A OR PCAR1.
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Sukaryota: Metazoa: Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              41.7%; Score 45; DB 1; Length 1079;
45.0%; Pred. No. 47;
tive 5; Mismatches 6; Indels
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L -> P (IN REF. 3).
G -> D (IN REF. 3).
V -> A (IN REF. 2).
Y -> H (IN REF. 2).
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                                                                 Ruat M., Snowman A.M., Snyder S.H.; "Calcium sensing receptor: molecular cloning in rat and localization to nerve terminals.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EXTRACELLULAR CALCIUM-SENSING RECEPTOR.
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                            -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
-!- SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                        Proc. Natl. Acad. Sci. U.S.A. 92:3161-3165(1995).
-!- FUNCTION: SENSE CHANGES IN THE EXTRACELLULAR CONCENTRATION OF
CALCIUM IONS. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY A
G-PROTEIN THAT ACTIVATES A PHOSPHATIDYLINOSITOL-CALCIUM SECOND
MESSENGER SYSTEM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PSO0979; G_PROTEIN_RECEP_F3_1; 1.
PROSITE; PSO0980; G_PROTEIN_RECEP_F3_2; 1.
PROSITE; PSO0981; G_PROTEIN_RECEP_F3_3; 1.
PROSITE; PSSO259; G_PROTEIN_RECEP_F3_4; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein; Signal.
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II (POTENTIAL).
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Proc. Natl. Acad. Sci. U.S.A. 92:131-135(1995).
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InterPro; IPR001828; ANF_receptor.
InterPro; IPR00037; GPCR_Mgr.
Pfam, PF00003; 7tm_3; 1.
Pfam; PF01094; ANF_receptor; 1.
PRINTS; PR00248; GPCRMGR.
PRINTS; PR00592; CASENSINGR.
                                                  MEDLINE-95241465; PubMed-7724534;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1079 AA; 120867
                                                                                                                                                                                                                                                                                                                                   EMBL; U10354; AAC52149.1; -
                                                                                                                                                                                                                                                                                                                                                 EMBL; U20289; AAC52195.1; -
                          SEQUENCE OF 1-294 FROM N.A.
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287
386
446
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488
                                       STRAIN-WISTAR;
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                                                                                                                                                                                                                                       TISSUE-Parathyroid:
MEDLINE-94077182; PubMed-8255296;
MEDLINE-94077182; PubMed-8255296;
Brown E.M., Gamba G., Riccardi D., Lombardi M., Butters R., Kifor O., Sun A., Hediger M.A., Lytton J., Hebert S.C.;
"Cloning and characterization of an extracellular Ca(2+)-sensing receptor from bovine parathyroid.";
Nature 366:575-580(1993).
-: FUNCTION: SENSE CHANGES IN THE EXTRACELLULAR CONCENTRATION OF
                              01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
01-JUN-1994 (Rel. 40, Last annotation update)
EXTRACELLULAR CALCIUM-SENSING RECEPTOR PRECURSOR (CASR) (PARATHYROID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R EMBL; S67307; AAB29171.1; -.

R PIR; S40476.

R GCRDb; GCR_0900; -.

R InterPro; IPR001828; ANF_receptor.

R InterPro; IPR001828; ANF_receptor.

R InterPro; IPR001828; ANF_receptor.

R Pfam; PF01094; ANF_receptor; 1.

R Pfam; PF01094; ANF_receptor; 1.

R PRINTS; PR00592; CASENSINGR.

R PROSITE; PS00999; G_PROTEIN_RECEP_F3_1; 1.

R PROSITE; PS00981; G_PROTEIN_RECEP_F3_2; 1.

R PROSITE; PS00981; G_PROTEIN_RECEP_F3_2; 1.

R PROSITE; PS00981; G_PROTEIN_RECEP_F3_3; 1.

R PROSITE; PS00981; G_PROTEIN_RECEP_F3_4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EXTRACELLULAR CALCIUM-SENSING RECEPTOR. EXTRACELLULAR (POTENTIAL). (COTENTIAL). CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                         -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
-1- SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                          CALCIUM IONS. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY A G-PROTEIN THAT ACTIVATES A PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER SYSTEM.
                                                                                                                            Bos taurus (Bovine).
Sukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoldea;
Bovidae; Bovinee; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   III (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
IV (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
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VI (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
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EXTRACELLULAR (POTENTIAL)
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CYTOPLASMIC (PC
PRT; 1085 AA
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                                                                                              CELL CALCIUM-SENSING RECEPTOR). CASR OR GPRC2A OR PCAR1.
   STANDARD;
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613
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                                                                                                                                                                                            NCBI_TaxID=9913;
CASR_BOVIN P35384;
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Gaps

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Indels

Score 45; DB 1; Length 1079;

Pred. No. 47; 5; Mismatches

41.78; 45.08;

Conservative

Query Match Best Local Similarity Matches 9; Conserv

37 FFLGVVLVFPIMFIQYV 53

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Sequence analysis of the Bacillus subtilis chromosome region between "Sequence and kdg loci cloned in a yeast artificial chromosome."; Microbiology 142:2005-2016(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                     Gaps
         N-LINKED (GLCNAC...) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN-168 / MARBURG;
STRAINE-96349105; Pubmed-8760912;
SOZOKIN A.V., Azevedo V., Zumstein E., Galleron N., Ehrlich S.D.,
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0
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01-0CT-1996 (Rel. 34, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
HYPOTHETICAL 24.7 KDA PROTEIN IN RECQ-CMK INTERGENIC REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 44; DB 1; Length 218;
Pred. No. 18;
5; Mismatches 5; Indels
                                                                                                                                                                         DB 1; Length 1085; 47;
                                                                                                                                                                                                     6; Indels
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                                                                                                                                     5D66DE8C9CD13E47 CRC64;
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88556D50863E14BC CRC64;
(POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Firmicutes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Bacillus.
NCBL_TaxID=1423;
                                                                                                                                                                                                          Mismatches
 CYTOPLASMIC
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Subtilist; BG11438; ypdC.
Hypothetical protein; Transme
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                                                                                                                                           121170
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Best Local Similarity 41.2
Matches 7; Conservative
                                                                                                                                                                                                          Conservative
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447
469
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542
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218 AA;
  Best Local Similarity
Matches 9; Conserv
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299116;
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P50738;
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                                                                                                                                                                                                                              MEDLINE-98196666; PubMed-9537320; Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L., Graham D.E., Overbeek R., Snead M.A., Keller M., Aujay M., Huber R., Fridman R.A., Short J.M., Olson G.J., Swanson R.V.; Fridman R.A., Short J.M., Olson G.J., Swanson R.V.; aeolicus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                       Nature 392:353-358(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hypothetical protein; Transmembrane; Plasmid; Complete proteome. TRANSMEM 30 50 POTENTIAL. TRANSMEM 189 209 POTENTIAL. TRANSMEM 218 238 POTENTIAL. SEQUENCE 271 AA; 31365 MW; 6CE96A93A61953DF CRC64;
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                                                                          (Rel. 39, Last sequence update)
(Rel. 40, Last annotation update)
                                                                                                                                                                  Bacteria; Aquificales; Aquificaceae; Aquifex.
NCBI_TaxID=63363;
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                           271 AA
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                             PRT;
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                                                              30-MAY-2000 (Rel. 39, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 40.73
Best Local Similarity 27.33
Matches 6; Conservative
                                                                                                            HYPOTHETICAL PROTEIN AA23
                               STANDARD;
                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                               Aquifex aeolicus.
                                                                                                                                                                Plasmid ecel
                                                                               30-MAY-2000
                                                                                                  20-AUG-2001
                               YZ23_AQUAE
066414;
RESULT 15
YZ23_AQUAE
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; Search time 66.28 Seconds
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24.587 Million cell updates/sec
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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108
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Perfect score:
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length: 0 length: 2000000000 sed Minimum DB Maximum DB

Total number of hits satisfying chosen parameters:

Maximum Match 100% Listing first 45 summaries Post-processing: Minimum Match 0%

A\_Geneseq\_1101:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

/SIDS8/gcgdata/geneseq/geneseqp/AA2001.DAT:\*

Glutathione-S<sup>\*</sup>tran Infectious salmon Melittin signal pe Human GIL-19/AE289 Cytomegalovirus US Honey bee melittin Honey bee melittin Human VEGF-X prote Human VEGF-X prote Honey bee melittin Recombinant vaccin Description SUMMARIES AAB10640 AAB10641 AAW47008 AAB72437 AAB72437 AAB72433 AAY97249 AAW87499 AAY70278 AAY70301 П 23 23 23 24 25 25 25 27 27 DB Query Match Length 100.0 100.0 100.0 100.0 96.3 94.4 94.4 94.4 89.8 Score 108 108 108 108 102 102 102 97 Result õ

pMelBac secretion Targeting molecule	Secretion signal a	Ehrlichia canis ma	Ehrlichia canis MA		chaffe		Major antigenic pr	Cowdria ruminatium	B. burgdorferi ant	Heron hepatitis B	Human O-fucosyltra	H. pylori flagella	Human secreted pro	Human CaR transmem	G protein-coupled	Human calcium sens	Human calcium sens	Human calcium sens	Dogfish shark kidn	Amino acid sequenc	Chicken calcium-se	Parathyroid calciu	Human parathyroid	Human parathyroid	Human calcium rece	Human parathyroid	Human parathyroid	Human calclum rece	Human wild type ca	Cynomolgous monkey	Protein encoded by	Rat kidney calcium
AAW64613 AAW61590	AAW85766	AAW51098	AAB36192	AAU04202	AAW51099	AAB36193	AAU04203	AAB36194	AAY19802	AAY29763	AAW80573	AAW20456	AAY02715	AAY49110	AAU03853	AAY45001	AAY45000	AAY44999	AAW32059	AAW25762	AAU00508	AAW11889	AAW54846	AAW38274	AAY28840	AAY41780	AAW89565	AAY51827	AAY70325	AAU02195	AAB74391	AAW54847
19 19	20	19	21	22	19	21	22	21	50	20	19	18	20	50	22	21	21	21	18	18	22	17	19	19	20	20	20	21	21	22	22	13
26 26	26	205	202	202	202	205	202	202	133	302	397	206	40	250	425	901	974	1001	1026	1058	1059	1078	1078	1078	1078	1078	1078	1078	1078	1078	1078	1079
96.6		50.9				50.0	0	48.1	45.4	45.4		43.5	41.7	41.7	41.7	41.7	41.7	41.7	41.7	41.7	41.7	41.7	41.7	41.7	41.7	41.7	41.7	41.7	41.7	41.7	41.7	41.7
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13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

AAY70301 standard; peptide; 22 AA. AAY70301; AAY70301 RESULT

ALIGNMENTS

. . . .

Honey bee melittin signal peptide. (first entry) 06-JUN-2000

Recombinant protein; CDC/NIIMALVAC-1; multivalent; malaria; vaccine; T-cell epitope; tetanus toxoid; antigenic epitope; treatment; circumsporozoite protein; CSP; sporozoite surface protein-1; SSP-2; liver stage antigen-1; LSA-1; merozoite surface protein-1; MSP-1; MSP-2; apical membrane antigen-1; AMA-1; erythrocyte binding antigen-175; EBA-175; rhoptry associated protein-1; RAP-1; gamete specific antigen; Pfg27; antiparasitic; prevention; anti-CDC/NIIMALVAC-1 antibody; melittin; honey bee. 

WO200011179-A1. 02-MAR-2000. 99WO-US18869 19-AUG-1999; (NAIM-) NAT INST IMMUNOLOGY. (USSH ) US DEPT HEALTH & HUMAN SERVICES.

Shi YP, Hasnain SE, Lal AA,

Apis sp.

98US-0097703. 21-AUG-1998;

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Line present asymetre is the metatrian sected by signar protection of prombinant protein cocynimates and in the construction of recombinant protein cocynimates. The recombinant protein comprises, melitian signal peptide, vaccine. The recombinant protein comprises, melitian signal peptide, vaccine. The recombinant protein comprises, melitian signal peptide, filss) tag, r-call epitope from teanus toxoid and 21 antigenic epitopes from circumsporozoite protein (CSP), sporozoite surface protein 1 (SSP-2), liver stage antigen-1 (LSA-1), merozoite surface protein 1 (MSP-1), MSP-2, apical membrane antigen-1 (AMA-1), erythrocyte binding antigen-175 (EBA-175), rhoptry associated protein-1 (RAP-1) and gamete specific antigen, Pfg27. These epitopes were obtained at different stages of the life cycle of P. falciparum. CDC/NIIMALVAC-1 vaccine has antiparasitic activity and can used for treatment and prevention of malarial infections. Anti-CDC/NIIMALVAC-1 antibodies can be used for detecting P. falciparum in biological samples.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Recombinant protein; CDC/NIIMALVAC-1; multivalent; malaria; vaccine; r-cell epitope; tetanus toxoid; antigenic epitope; treatment; SSP-2; circumsporozoite protein; CSP; sporozoite surface protein-1; SSP-2; liver stage antigen-1; LSA-1; merozoite surface protein-1; MSP-1; MSP-2; apical membrane antigen-1; AMA-1; erythrocyte binding antigen-175; EBA-175; rhoptry associated protein-1; RAP-1; gamete specific antigen; Pfg27; antiparasitic; prevention; anti-CDC/NIIMALVAC-1 antibody;
                             Novel recombinant protein as vaccine for treating malarial infection comprises antigenic peptides obtained from different stages of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "Recombinant multivalent malarial vaccine"
                                                                                                                                         The present sequence is the melittin secretory signal peptide from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 108; DB 21;
100.0%; Pred. No. 1.6e-10;
ive 0; Mismatches 0;
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/label= Melittin_signal_peptide
/note= "Derived from Honey bee"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23..350
/label= Mature_CDC/NIIMALVAC-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Recombinant vaccine CDC/NIIMALVAC-1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           - Plasmodium falciparum.
                                                     comprises antigenic peptides obta
plasmodium falciparum life cycle
                                                                                                             Claim 2; Page 16; 52pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 mkflvnvalvfmvyisyiyad 22
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Chimeric - Clostridium tetani
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 22; Conserv
WPI; 2000-237654/20
                                                                                                                                                                                                                                                                                                                                                                                                                                         22 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         honey bee
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY70278;
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY70278
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The present sequence is that of recombinant protein CDC/NIMALVAC-1, which is a multivalent, multistage malarial vaccine. The recombinant compress, melittin signal peptide, (His)6 tag, T-cell epitope protein comprises, melittin signal peptide, (His)6 tag, T-cell epitope from tetanus toxoid and 21 antiquin-2 (SSP-2), liver stage contigen-1 (CSP), sporozoite surface protein-2 (SSP-2), liver stage contigen-1 (LSA-1), merozoite surface protein-1 (MSP-1), MSP-2, apical compirance antiquen-1 (MAN-1), erythrocyte binding antiqen-175 (Banigan-175), repetry associated protein-1 (RAP-1) and gamete specific antigen, Pfg27. These epitopes were obtained at different stages of the life cycle of plasmodium falciparum. CDC/NIIMALVAC-1 vaccine has antiparasitic activity and can used for treatment and prevention of malarial infections. Anti-CDC/NIIMALVAC-1 antibodies can be used for detecting contined the contined that the contined that the contined that the continuation of malarial continuation in biological samples.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VEGF-X; vascular endothelial growth factor; human; vulnerary; cytostatic; anticheumatic; antiarthritic; antipsoriatic; antidiabetic; treatment; angiogenesis regulator; vascularization regulator; cancer; psoriasis; rheumaticid arthritis; diabetic retinopathy; blood vessel; organ repair; tissue regeneration; tissue repair; wound; dermal ulcer; pressure sore; venous sore; diabetic ulcer; burns; skin graft growth.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human VEGF-X protein for expression in Baculovirus/insect cell systems.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                       Novel recombinant protein as vaccine for treating malarial infection comprises antigenic peptides obtained from different stages of plasmodium falciparum life cycle
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100.0%; Pred. No. 2.8e-09;
ive 0; Mismatches 0;
                         US DEPT HEALTH & HUMAN SERVICES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AA.
                                                                                                                                                                                                                 Claim 3; Page 43-44; 52pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB10640 standard; Protein; 354
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99US-0124967.
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                                                           Hasnain SE;
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       (NAIM-) NAT INST IMMUNOLOGY.
(USSH ) US DEPT HEALTH & HUN
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Best Local Similarity 100
Matches 22; Conservative
                                                                                            WPI; 2000-237654/20.
N-PSDB; AAZ51336.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       350 AA;
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                                                               Shi YP,
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18-MAR-1999;
08-NOV-1999;
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                                                                  Lal AA,
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Dhanaraj SN, Xu J;
                          2000-442669/38
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                                                                                                                                                                                                                                                                                                                                                     of the invention.
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06-MAY-1997;
09-MAY-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This invention describes a novel vascular endothelial growth factor-X (VEGF-X) protein (Ia) and its encoding polynucleotide (IIa) which has vulnerary, cytostatic, antirheumatic, antiantitic, antiporiatic and antidiabetic activity and acts as an anglogenesis and vascularization regulator. An antisense molecule of the invention is useful for treating or preventing cancer, rheumatoid arthritis, psoriasis and diabetic retinopathy by inhibiting anglogenic activity or inappropriate vascularization including formation and proliferation of new blood vessels, growth and development of tissues, tissue regeneration and organ and tissue repair in a subject. The products of the invention are useful for preparing medicaments for treating wounds such as dermal ulcers, pressure sores, venous sores, diabetic ulcers and burns and to promote skin graft growth, tissue repair, proliferation of new blood vessels, tissue regeneration and organ repair, proliferation of new blood vessels, tissue regeneration. This sequence represents a human vegf-x protein which can be expressed in Baculovirus/insect cell systems and which is
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VEGF-X; vascular endothelial growth factor; human; vulnerary; cytostatic; antirheumatic; antiarthritic; antipsoriatic; antidiabetic; treatment; andiogenesis regulator; vascularization regulator; cancer; psoriasis; rheumatoid arthritis; diabetic retinopathy; blood vessel; organ repair; tissue regeneration; tissue repair; wound; dermal ulcer; pressure sore; venous sore; diabetic ulcer; burns; skin graft growth.
                                                            New vascular endothelial growth factor protein, useful for treating or preventing diseases associated with inappropriate angiogenesis activity such as cancer, rheumatoid arthritis, psoriasis and wounds -
                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                 Length 354;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human VEGF-X protein for expression in E. coli systems.
                                                                                                                                                                                                                                                                                                                                                                                                                 DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 108; DB 21;
100.0%; Pred. No. 2.9e-09;
ive 0; Mismatches 0;
                                                                                                                 Disclosure; Fig 20; 127pp; English.
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                      WPI; 2000-442669/38.
Dhanaraj SN, Xu J;
                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 22; Conserv
                                                                                                                                                                                                                                                                                                                                                                             354 AA;
                                    N-PSDB; AAA71984
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This invention describes a novel vascular endothelial growth factor-X
(VEGF-X) protein (Ia) and its encoding polynucleotide (IIa) which has
vulnerary, cytostatic, antirheumatic, antiparthritic, antiparolatic and
antidiabetic activity and acts as an anglogenesis and vascularization
cegulator. An antisense molecule of the invention is useful for treating
creptulator. An antisense molecule of the invention is useful for treating
creptulator. An inhibiting angiogenic activity or inappropriate
cretinopathy by inhibiting angiogenic activity or inappropriate
vascularization including formation and proliferation of new blood
vessels, growth and development of tissues, tissue regeneration and organ
of tissue repair in a subject. The products of the invention are useful
for preparing medicaments for treating wounds such as dermal ulcers,
pressure sores, venous sores, diabetic ulcers and burns and to promote
skin graft growth, tissue repair, proliferation of new blood vessels,
tissue regeneration and organ repair, proliferation of new blood vessels,
tissue regeneration. This sequence represents a human vEGF-X protein which
can be expressed in E. coli systems and which is described in the method
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New vascular endothelial growth factor protein, useful for treating or preventing diseases associated with inappropriate angiogenesis activity such as cancer, rheumatoid arthritis, psoriasis and wounds -
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prògnosis; cell proliferation; cancer; ageing; ribonucleoprotein.
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/note= "enterokinase cleavage site"
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100.0%; Pred. No. 2.9e-09;
ive 0; Mismatches 0;
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                                                                                                                                                    Disclosure; Fig 21; 127pp; English
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970S-0844419.
970S-0846017.
970S-0851843.
970S-0854050.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 100.
Best Local Similarity 100.
Matches 22; Conservative
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The present invention relates to vaccine for prevention and/or prophylaxis of infectious salmon anaemia in fish. The invention prophylaxis of infectious salmon anaemia in fish. The invention provides for nucleic acid sequence encoding viral proteins of infectious salmon anaemia virus (ISAV) as well as the isolated protein. Nucleic acids encoding viral protein is useful for the manufacture of a DNA vaccine for diagnosis, treatment and/or prophylaxis of infectious salmon anaemia in fish, and viral protein can be used for the manufacture of antibodies that are specific for ISAV. The present equence is infectious salmon anaemia virus 92.M fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       UGGT; UDP-glucose:glycoprotein glucosyltransferase; enzyme; honeybee; melittin signal peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel vaccine for treatment and/or prevention of infectious salmon anemia in fish – \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 104; DB 22; Length 38 Pred. No. 1.3e-08; 1; Mismatches 0; Indels
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   /note= "Mature ISAV 92-M protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 7; Page 39-41; 43pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB72437 standard; Peptide; 21 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (CANA ) NAT RES COUNCIL CANADA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     96.3%;
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                                                                                                                                                                         03-JAN-2001; 2001WO-EP00046.
                                                                                                                                                                                                                              07-JAN-2000; 2000EP-0200054.
29-FEB-2000; 2000EP-0200700.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 95.59
Matches 21; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Melittin signal peptide
                                                                                                                                                                                                                                                                                                                                                                        Biering E, Krossoy B;
                                                                                                                                                                                                                                                                                                                   (ALKU ) AKZO NOBEL NV.
                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-441845/47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-218358/22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    386 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; AAD09875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200112845-A1.
                                                           W0200149712-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18-AUG-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tessier DC,
                                                                                                                12-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB72437;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB72437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence represents a fusion protein from an example of the present invention which describes human telomerase reverse transcriptase (hTRT). The present invention also describes the transcriptase (hTRT). The present invention also describes the following methods: (A) determining whether a test compound is a modulator of hTRT, by detecting the change in hTRT recombinant protein or polynuclectide, on administration of the compound; protein or polynuclectide, on administration of the compound; proparation of recombinant telomerase by contacting a protein of the hTRT RNA or protein in a sample by binding a relevant of the hTRT RNA or protein in a sample by binding a relevant of the hTRT RNA or protein in a sample by binding a relevant of the hTRT RNA or protein in a sample by binding a relevant of the the sample and detecting the complex formed or in the case of RNA detection, amplifying the product with presence of hTRT in the sample; and (D) increasing the proliferation of a vertebrate cell proliferation for exerte a medicament that inhibits ageing. A protein preparation of hTRT and the polynuclectide encoding hTRT can be used in the manufacture of medicaments for inhibiting the effect of ageing or cancer. Inhibitors of telomerase activity can be used to treat conditions that are associated with high telomerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                             Pure and recombinant human Telomerase Reverse Transcriptase and its variants - are useful in the diagnosis, prognosis and treatment of cell proliferation conditions especially cancer and ageing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
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                                                                                                                                                                         Lingner J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1..21
/label= Mellitin_signal_peptide
22..26
/label= Linker_peptide
27..386
                                                                                                                                                                         Harley C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Infectious salmon anaemia virus. Unidentified.
                                                                                                                                                                                                                                                                                                                                                                                                                       Example 6; Page 234-235; 387pp; English.
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                                                                                                                                                                         Chapman KB,
Harley CB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 mkflvnvalvfmvvyisyiyad 22
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                                                                                 (GERO-) GERON CORP.
(UYTE-) UNIV TECHNOLOGY CORP.
97US-0911312.
97US-0912951.
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Best Local Similarity 100.0
Matches 22; Conservative
                                                                                                                                                                   , Cech TR,
Nakamura T,
                                                                                                                                                                                                                                                       WPI; 1998-171633/16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1189 AA;
14-AUG-1997;
14-AUG-1997;
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Chimeric -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Infectious
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                                                                                                                                                                                                  Morin GB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
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Length 386;

us-09-763-397a-25.rag

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interleukin-10 (IL-10) and is assumed to be a cytokine. It can be used in the regulation of cell proliferation and differentiation, haematopoiesis, immune stimulation or suppression, tissue growth and tumour inhibition. In addition, it also has uses in the treatment of inflammation and in nutrition.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cytomegalovirus US2t-DL6 fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chimeric - Human cytomegalovirus.
Chimeric - Apis sp.
Chimeric - Homo sapiens.
Chimeric - Synthetic.
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                                                                                                                                                                                                                                                                                                                   1 MKFLVNVALVFMVVYISYIYA
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                                                                                                                                                                                                              Query Match
Best Local Similarity 100.
Matches 21; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2000-506069/45.
                                                                                                                                               49 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10-AUG-2000
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                                                                                                                                                                                                      The present invention relates to a method for determining the effect of a test sample on UD-glucose:glycoprotein glucosyltransferase (UGGT) activity. The method comprises exposing an acceptor substrate for UGGT to a labelled donor in the presence of the test sample and UGGT. The method is useful for determining UGGT activity. In particular, the method is useful in glucosyltransferase assay and kinetics measurement for reticulum which catalyses the addition of a glucose residue onto asparagine. Linked oligosaccharides, which are present on incorrectly folded glycoproteins. The present sequence is the honeybee melittin signal peptide. This sequence was used in the construction of an expression vector for rat UGGT (see AAF60732 and AAB72436).
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                                     Determining the effect of a test sample on UDP-glucose.glycoprotein glucosyltransferase (UGGT), useful for measuring UGGT activity, comprises exposing an acceptor substrate for UGGT to a labeled donor the presence of UGGT -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (interleukin)-10, useful in upregulation of humoral immune responses, as an antiinflammatory agent and as a modulator of immune responses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human GIL-19 protein that shows a high degree of homology to IL
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cell proliferation; immune stimulation; immune suppression;
haematopolesis regulation; tissue growth; inflammation; cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 21;
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Pred. No. 1.3e-09;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Spaulding V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB36293 standard; Protein; 49 AA.
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100.08; Fix
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                                                                                                                                                              Example 1; Fig 8; 95pp; English.
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Matches 21; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fouser L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2000-687325/67.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21 AA;
N-PSDB; AAF60733.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic.
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Query Match

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human cytomegalovirus (hCMV) US2 protein, which has previously been shown to block the major histocompatibility complex (MHC) class I antigen presentation pathway. The US2 protein does not have to be mutated to cause inhibition of the MHC class II pathway. The US2 protein pathway. The binding domain recognizes MHC I heavy chains, MHC II alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ဌ
                                                                                                                                                                                                                                        US2; hCMV; major histocompatibility complex; MHC; class I; class II; antigen presentation; inhibition; CD8-positive; CD4-positive; T cell; transplant; gene therapy; immunosuppressive; fusion; DL6.
                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Inhibiting recognition of cellular tissue by {\rm CD8+} and {\rm CD4+} T cells, treat or prevent autoimmune diseases, and to improve gene therapy, comprises introducing human cytomegalovirus US2 protein into cells
                         ö
Length 49;
                         Indels
                                                                                                                                                                                                                                                                                                                                                                      1..21
/label= Bee_mellitin_signal_peptide
94.4%; Score 102; DB 21; 100.0%; Pred. No. 3.2e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "Single glycine spacer"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hegde NR;
                                                                                                                                                                                                                                                                                                                                                                                                          /label Soluble_US2_protein
                         Mismatches
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The present sequence is the honey bee (Apis melifica) melittin excretion peptide. It may be used in the Aedes aegypti Densonucleosis virus (AeDNV) based vectors of the invention to aid vector propagation, isolation and subcloning. AeDNV based vectors, esp. confg. the p61, p0.5 and p7 promoters are useful for targeting heterologous proteins to the
chains, and optionally DW-alpha chains. US2 has a double inhibitory effect on the MHC class II pathway, inhibiting recognition of callular tissue by CD8-positive and CD4-positive T cells. US2 or its soluble wariants, can be used to reduce inappropriate immune responses. The US2 protein can be used to improve the persistence of a virus. Vectors encoding soluble US2 protein (residues 281-143) can be used to treat autoimmune disease, especially where it is mediated by MHC II molecules. The vector can also be used to improve gene therapy, and preferably also contains a sequence encoding a therapeutic product. The protein is exagenously supplied or expressed from a recombinant cell, and may also be used to inhibit CD4-positive mediated immune responses, transplant immune responses and gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    expression system; promoter; p61; p0.5; p7; heterologous protein; production; vector; cassette.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Aedes aegypti Densonucleosis Virus expression system - useful
gene expression system in insect cells
                                                                                                                                                                                                                                                                                     94.4%; Score 102; DB 21; Length 177; 100.0%; Pred. No. 1.2e-08; Live 0; Mismatches 0; Indels C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Carlson JO, Higgins DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (RESE ) RESEARCH CORP TECHNOLOGIES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Honey bee melittin excretion peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 13; 62pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAR99533 standard; peptide; 21
                                                                                                                                                                                                                                                                                                                                                                1 MKFLVNVALVFMVVYISYIYA 21
                                                                                                                                                                                                                                                                                                                                                                                   1 mkflvnvalvfmvvyisyiya 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              94US-0334669.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              95WO-US14170.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-NOV-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Afanasiev BN, Beaty B,
                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.
Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1996-251772/25.
                                                                                                                                                                                                                                                  177 AA;
                                                                                                                                                                                                                      immune responses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Apis melifica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  W09614423-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                04-NOV-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17-MAY-1996.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR99533;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nucleus
                                                                                                                                                                                                                                                     Sequence
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                       SSSSSSSSSSSS
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The invention relates to the use of a Aedes aegypti densonucleosis virus (AeDNV) as a heterologous gene expression system. A recombinant protein using the vectors of the invention can be produced by a method that comprises (1) transfecting an insect cell that stably expresses AeDNV comprises (1) transfecting an insect cell that stably expresses AeDNV structural proteins vpl and VP2 with an expression vector comprising the comprising an AeDNV promoter linked to a sequence coding for the protein and with an expression vector comprising the AeDNV nonstructural proteins NS1 and NS2 encoding genes; (2) obtaining infectious viritons from the transfected cell; (3) infecting a second insect cell with the virions; culturing the second cell under conditions such that the protein is expressed, and (4) recovering the protein from the second cell under conditions from the second cell under conditions from the second cell under conditions when the second cell and the protein is albopictus Cévês cells can be transfected with AeDNV vectors without allowed the second cell and the protein from the second cell. Aedes albebraths of forth that the protein is albopictus Cévês cells can be transfected with AeDNV vectors without allowed the conditions that the protein is albebraths of forth that the conditions are the transfected with AeDNV vectors without allowed the conditions that the conditions that the conditions are the transfected with AeDNV vectors without allowed the conditions that the conditions that the conditions that the conditions are the conditions that the conditions are the conditions that the conditions are the conditions that the conditions that the conditions are the conditions that the conditions the conditions that the conditions that the conditions that th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cytopathic effects. The present sequence represents a honey bee cytopathic effects. This signal peptide can be used in the AeDNV mellitin excretion peptide. This signal peptide can be used in the AeDNV expression vectors for secretion or nuclear localisation.
                                                                                                                                                                                                                                                                                                                                                                    AeDNV; Aedes DNV; densonucleosis virus; gene expression; recombinant; structural protein; VP1; VP2; promoter; nonstructural protein; NS1; NS2; virion; transfection; cytopathic; honey bee; excretion peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Recombinant protein production in mosquito cells - using Aedes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 97; DB 20; Length 21
Pred. No. 7.9e-09;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Higgins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (RESE ) RESEARCH CORP TECHNOLOGIES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Afanasiev BN, Beaty BJ, Carlson JO,
Thibault KJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        densonucleosis virus expression system
                                                                                                                                                                                                                                                                                                                                Honey bee melittin excretion peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Column 6; 23pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1;
                                                                                                                                                                            AAW87499 standard; peptide; 21 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MKFLVNVALVFMVVYISYIYA 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                89.8%;
95.2%;
95US-0485341.
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94US-0334669.
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                                                                                                                                                                                                                                                                                    22-FEB-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best_Local Similarity
Matches 20; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1999-069725/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             04-NOV-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US5849523-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-DEC-1998
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                                                                                                                                                                                                                                      AAW87499;
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Gaps

0;

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21

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Thibault KJ;

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RESULT

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Gaps

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Length 21; Indels

89.8%; Score 97; DB 17; L4 95.2%; Pred. No. 7.9e-09; iive 1; Mismatches 0;

Conservative

Query Match Best Local Similarity Matches 20; Conserv

21 AA;

Sequence

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colitis; pneumonia; cystic fibrosis.
                                                                                                                                                        Hein MB,
                                                                                                                                                                           WPI; 1998-399067/34.
N-PSDB; AAV45274.
                                                                                                                                                                                                                                                                                                                                                                                                                  26 AA;
                                            W09830592-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO9920310-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20-OCT-1998;
                                                                                        09-JAN-1998;
                                                                                                             10-JAN-1997;
                                                                                                                                                        Fitchen JH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29-APR-1999.
                                                                  16-JUL-1998
                       Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW85766;
                                                                                                                                                                                                                                                                                                                                                                                               fibrosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW85766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   qq
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ï
                                                                                                                                                                                                                                                                                                                                                                                        This sequence represents a secretion signal from the plasmid pMelBac which is used in a method involving the construction of a target molecule from human J chain protein fragments. This construct is used in a method to target imaging agents to epithelial surfaces at which they may remain or undergo transeptthelial transport via transcytosis. At least one imaging agent is linked to the targeting molecule comprising a polypeptide that (a) forms a closed covalent loop, (b) contains at least J preferably 4, peptide domains having beta-sheet character separated by domains lacking beta-sheet character and (c) is not full length dimeric 19A. The imaging agents are useful in the diagnosis of disease. The target molecule is also capable of specifically binding to a basolateral factor associated with an epithelial surface to cause internalisation of a biological agent linked to the target molecule.
                                                                                                 Target; imaging agent; epithelium; transepithelial transport; diagnosis;
transcytosis; disease; basolateral; internalisation; J chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  J chain; targeting molecule; epithelial; beta-sheet; asthma; cancer; inflammatory disorder; autoimmune disorder; celiac disease;
                                                                                                                                                                                                                                                                                                                        New epithelial tissue targeting agent - used to deliver imaging agents to an epithelial surface for internalisation; useful in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Targeting molecule secretion signal and multiple cloning site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 93.5; DB 19;
Pred. No. 3.5e-08;
0; Mismatches 0;
                                                                           pMelBac secretion signal peptide motif.
                                                                                                                                                                                                                                                                                                                                                                     Example 1c; Page 89; 118pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW61590 standard; Protein; 26 AA.
         AAW64613 standard; Protein; 26 AA
                                                                                                                                                                                                                                                                    Hiatt AC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MKFLVNVALVFMVVYISYIYAD 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   86.6%;
95.5%;
                                                                                                                                                                                                 98WO-US00339
                                                                                                                                                                                                                      97US-0782480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                     03-NOV-1998 (first entry)
                                                                                                                                                                                                                                           (EPIC-) EPICYTE PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                 Fitchen JH, Hein MB,
                                                                                                                                                                                                                                                                                       WPI; 1998-399066/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 21; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26 AA;
                                                                                                                                                                                                                                                                                                  N-PSDB; AAV49671
                                                                                                                                                     WO9830591-A1
                                                                                                                                                                                                                      10-JAN-1997;
                                                                                                                                                                                                 39-JAN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27-OCT-1998
                                                                                                                                                                          16-JUL-1998
                                                                                                                                  Synthetic.
                                                                                                                                                                                                                                                                                                                                                diagnosis
                               AAW64613;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW61590;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW61590
AAW64613
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The secretion signal and multiple cloning site are used in the assembly of a targeting molecule (TM). The TMs are used to target biological agents to epithelial surfaces at which they can be internalised. The TMs comprise a polypeptide that: (a) forms a closed covalent loop; (b) contains at least 3, preferably 4, peptide domains having beta-sheet character separated by domains lacking beta-sheet character; and (c) is not full length dimeric IgA. The TMs are useful to prevent and/or treat diseases associated with epithelial surfaces, e.g. asthma, cancer, (myco)bacterial, viral or fungal infection, inflammatory disorders, autoimmune disorders, celiac disease, colitis, pneumonia and cystic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Targeting molecule; J chain; immunoglobulin; IgM; IgA; substrate;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    epithelial cell; cancer; treatment; therapy;
non-small cell lung carcinoma; breast carcinoma; colon carcinoma;
ovarian carcinoma; prostate carcinoma; endometriosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 26;
                                                                                                                                                                                                                                                                                                                                      New epithelial tissue targeting agent - used to deliver biologically active compounds to an epithelial surface for internalisation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     86.6%; Score 93.5; DB 19; 95.5%; Pred. No. 3.5e-08; ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Secretion signal and multiple cloning site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 1; Page 44; 142pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW85766 standard; Peptide; 26 AA.
                                                                                                                                                                                           Hiatt AC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MKFLVNVALVFMVVYISYIYAD 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    viral infection; inflammation
98WO-US00542.
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                                                                                                                          (EPIC-) EPICYTE PHARM INC.
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ï

McGuire TC;

Mahan SM,

Ganta RR,

Burridge MJ,

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MAP2; major antigenic protein 2; rickettsia; DNA vaccine.
                                                                                                                                                                                                                                                                        Ehrlichia canis major antigenic protein 2 (MAP2).
                                                                                                                                                                                                                                              AAW51098 standard; Protein; 205 AA.
                                                                                                                                                                                                             1 MKFLVNVALVFMVVYISYIYAD 22
                                                                                                                                                                                                                   1 mkflvnval-fmvvyisyiyad 21
                                                                                                                                                                                           Ouery Match 86.6' Best Local Similarity 95.5' Matches 21; Conservative
                                                                                                                                                                                                                                                                                             Ehrlichia canis.
                                                                                                                                                                                                                                                                                                      W09816554-A1.
                                                                                                                                                                                                                                                                                                                         17-0CT-1997;
                                                                                                                                                                                                                                                                 14-SEP-1998
                                                                                                                                                                                                                                                                                                               23-APR-1998.
                                                                                                                                                                                                                                                        AAW51098;
                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                           AAW51098
                                                                                                                                                                                                                                       RESULT
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This polypeptide comprises the major antigen protein 2 gene (MAP2) of Ehrlichia canis. It is encoded by the MAP2 gene (see AAV07181). A claimed composition comprises a nucleic acid (see AAV07181) encoding a polypeptide (see AMS1086-99) that elicits a protective immune response against a rickettsial pathogen. The nucleic acid is used, in human or veterinary medicine, in vaccines to protect against Rickettsia, Ehrlichia, Anaplasma and Cowdria species. The nucleic acid dose not replicate in the host but remains episomal nucleic acid dose not replicate in the host but remains episoma Ehrlichia antigenic polypeptide for at least 19 mth. The Ehrlichia antigenic polypeptides can also be used diagnostically to detect antibodies associated with Ehrlichia infection (claimed).
                                                                                                                                                                                  Composition containing nucleic acid encoding rickettsial antigen useful for, e.g. stimulating protective immune response in humans or
                                                                                                                                                                                                                                                                                                                                Claim 3; Fig 3A; 39pp; English.
                       Barbet AF, Burridge MJ
Nyika A, Rurangirwa FR;
                                                                                                               WPI; 1998-251232/22
                                                                                                                                             N-PSDB; AAV07181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                              animals
οy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     qq
                                                                                                                                                                                                                                                                                                                                                                                                                                     A targeting agent for improving the delivery of drugs to target cells, particularly for delivery of enzymes, binding agents.

Cells, particularly for delivery of enzymes, binding agents.

Inhibitors, nucleic acids, carbohydrates and lipids, is new.

Inhibitors, nucleic acids, carbohydrates and lipids, is new.

Comparison and contains at least three peptide domains having covalent loop and contains at least three peptide domains having beta-sheet character. The targeting molecule preferably comprises all or a portion of a native J chain sequence. J chain comprises all or a portion of a native J chain sequence. J chain comprises all or a portion of a native J chain sequence. J chain comprises all or a portion of a native J chain sequence. J chain comprises all or a portion of a native J chain sequence. J chain composition of at least one biological agent which is capable of entering and threat and probarised epithelial cell. The targeting molecule may be linked to the biological agent by a substrate for an intracellular or extracellular enzyme which is associated with or can be used in a pharmaceutical composition for treating a patient can be used in a pharmaceutical composition for treating a patient can be used in a pharmaceutical composition for treating a patient can be used in a disease associated with non-polarised epithelial cell. Breast carcinoma, colon carcinoma, ovarian carcinoma, prestute canson and endometriosis, viral infection or inflammatory carcinoma and endometriosis, viral infection or inflammatory construction of target molecules described.

Construction of target molecules described.
                                                                                                                                                                                                                                                                                           Targeting molecule useful in drug delivery for treating cancer, viral infection or inflammatory disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 93.5; DB 20;
Pred. No. 3.5e-08;
0: Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                    Example 1; Page 43; 102pp; English
                                                                                                                                                 Hiatt AC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     86.68;
                97US-0954211
                                                                                 (EPIC-) EPICYTE PHARM INC.
                                                                                                                                                    Hein MB,
                                                                                                                                                                                                          WPI; 1999-288174/24.
N-PSDB; AAX08824.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26 AA;
                           20-OCT-1997;
                                                                                                                                                       Fitchen JH,
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Gaps
                                   ;
0
50.9%; Score 55; DB 19; Length 205; 40.0%; Pred. No. 0.31; tive 7; Mismatches 5; Indels
                                                                                                                                                                          Search completed: January 29, 2002, 10:59:20 Job time: 2244 sec
                                                                                                    4 ikfilnvcllfaaiflgysy 23
                                                                           1 MKFLVNVALVFMVVYISYIY
                                          Conservative
            Query Match
Best Local Similarity
Matches 8; Conserv
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ij

Gaps

1;

Indels

Mismatches

; 0

96US-0733230.

17-0CT-1996;

(UYFL ) UNIV FLORIDA

(first entry)

; 0

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; Search time 1760.55 Seconds
(without alignments)
55.199 Million cell updates/sec
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1 MKFLVNVALVFMVVXISYIY......DFFGISYYEKVLAKYKDDLE 350
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// cgn2_6/ptodata/2/paa/USO6_COMB.pep: *
// cgn2_6/ptodata/2/paa/USO6_COMB.pep: *
// cgn2_6/ptodata/2/paa/USO8_COMB.pep: *
// cgn2_6/ptodata/2/paa/USO81_COMB.pep: *
// cgn2_6/ptodata/2/paa/USO81_COMB.pep: *
// cgn2_6/ptodata/2/paa/USO81_COMB.pep: *
// cgn2_6/ptodata/2/paa/USO83_COMB.pep: *
// cgn2_6/ptodata/2/paa/USO83_COMB.pep: *
// cgn2_6/ptodata/2/paa/USO86_COMB.pep: *
// cgn2_6/ptodata/2/paa/USO80_COMB.pep: *
// cgn2_6/ptodata/2/paa/USO80_COMB.pep: *
// cgn2_6/ptodata/2/paa/USO80_COMB.pep: *
// cgn2_6/ptodata/2/paa/USO90_COMB.pep: *
// cgn2_6/ptodata/2/paa/USO90_COMB.pep: *
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// cgn2_6/ptodata/2/paa/USO91_COMB.pep: *
// cgn2_6/ptodata/2/paa/USO91_COMB.pep: *
// cgn2_6/ptodata/2/paa/USO92_COMB.pep: *
// cgn2_6/ptodata/2/paa/USO92_COM
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/cgn2_6/ptodata/2/paa/US098_COMB.pep:*
/cgn2_6/ptodata/2/paa/US099_COMB.pep:*
/cgn2_6/ptodata/2/paa/US00_COMB.pep:*
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3148936 seqs, 277657034 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                            January 29, 2002, 10:16:04
                                                                                                                                                                                                         OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pending_Patents_AA_Main:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Minimum DB seq length: 0 Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-763-397A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BLOSUM62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Database :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Searched:
                                                                                                                                                                                                                                                                                                                 Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

			Description	iland C acadamoos	Triddu /7 ochochoc	Sequence 6, Appli	Sequence 6, Appli	Sequence 18, Appl	Sequence 1, Appli	Sequence 2. Appli	Sequence 8. Appli	Sequence 8, Appli	Sequence 8, Appli
SUMMARIES			ID	11S-09-763-397A-2	7	US-07-677-539B-6	US-07-727-636-6	US-08-948-885-18	US-08-932-929A-1	US-07-842-694-2	US-09-125-031-8	US-09-125-031A-8	US-09-134-333-8
			DB	: 5	1	m	٣	13	13	٣	15	15	15
			Length	350		412	412	412	423	424	127	127	127
	æ	Query	re Match Length DB ID	100.0		11.2	11.2	11.2	10.9	10.9	10.9	10.9	10.9
			Score	1923		215.5	215.5	215.5	210.5	210.5	210	210	210
		Result	NO.			7	3	4	'n	9	7	80	6

υ, n	Sequence 31, Appl	m	'n	'n	'n	٦,	1,	1,	16,	Sequence 2, Appli	Sequence 2, Appli	Sequence 2, Appli	Sequence 2, Appli	Sequence 2, Appli	7	7	10,	Sequence 10, Appl		10,	5,	ι,	5,	'n	ω,	1,	11,	ď	12,	10,	2, 7	θ,	2, 4	Sequence 2, Appli
3 US-07-677-539B-5	22 US-09-820-843A-31	US-08-760-7	13 US-08-903-084-3		13 US-08-932-929A-3	11 US-08-760-797-1	13 US-08-903-084-1	13 US-08-932-929-1	19 US-09-500-376-16	3 US-07-867-768A-2	5 US-08-195-705-2		US-09-1		0S-09	15 US-09-134-333-2	US-09-1	15 US-09-125-031A-10	-60-SD	-60-SD	15 US-09-125-031-5	15 US-09-125-031A-5	15 US-09-125-031B-5	-60-SN	15 US-09-125-031B-8	us-09-3	US-09-1	15 US-09-1.75-683B-9	15 US-09-175-683-12	15 US-09-175-683B-10	US-09-311-8	9 US-09-500-37	8	15 US-09-117-415-2
388	396	424	424	424	424	424	424	424	402	394	394	394	92	92	92	95	108	108	108	108	116	116	116	116	127	96	352	355	361	361	376	384	594	294
10.8	10.8			10.8	10.8	10.7	10.7	10.7	10.6	10.4	10.4	10.4	10.3	10.3	10.3	10.3	10.3	10.3	10.3	10.3	10.3	10.3	10.3	10.3	10.3	10.2	•	•	10.2		•	10.2	10.2	10.2
208.5	207.5	207.5	207.5	207.5	207.5	206.5	206.5	206.5	203.5	200.5	200.5	200.5	198.5	198.5	198.5	198.5	198.5	198.5	198.5	198.5	198.5	198.5	198.5	198.5	198.5	196.5	196.5	196.5	196.5	196.5	196.5	196.5	196.5	196.5
10	12	. 13	14	15	16	17	18	19	20	21	22	23	24	25	<b>5</b> 6	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

```
Sequence 2, Application US/09763397A
GENERAL InfoRMATION:
APPLICANT: The Government of the United States of America, as represented by the APPLICANT: The Government of the Department of Health and Human Services, Centers for APPLICANT: Control and Prevention
APPLICANT: Control and Prevention
APPLICANT: Control and Prevention
APPLICANT: Ding Shi, Ya
APPLICANT: Hasain, Seed E.
TILE REFERENCE: 6395-57049
CURRENT APPLICANTON NUMBER: US 60/097,703
FILE REFERENCE: 1996-08-21
PRIOR FILING DATE: 1996-08-21
PRIOR PLILING DATE: 1999-08-19
PRIOR PLILING DATE: 1999-08-19
PRIOR PLILING DATE: 1999-08-19
PRIOR PLILING DATE: 1999-08-19
NUMBER OF SEQ ID NOS: 26
SEQ ID NO 2
LENGTH: 350
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
CORGANISM: Objection 3.1
US-09-763-397A-2

QUETY MATCH SIMILIARITY 100.0%; Score 1923; DB 21; Length 350;
Bast Local Similarity 100.0%; Pred: 0. Indels 0; Gaps 0;
```

```
29 KH-----KKLKQPGDGNPWSPCSVTCG------KPKDELDYENDIEKKICKME 70
                                                                                                                                                                               Sequence 6, Application US/07727636
GENERAL INFORMATION:
APPLICANT: LALTAF A.
APPLICANT: GOLDMAN, IRA F.
TITLE OF INVENTION: CIRCUMSPOROZOITE PROTEIN OF PLASMODIUM
TITLE OF INVENTION: REICHENOWI AND VACCINE FOR HUMAN MALARIA
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHWAN, DARBY & CUSHMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11.2%; Score 215.5; DB 3; Length 412; ilarity 62.2%; Pred. No. 2.8e-10; Conservative 2; Mismatches 7; Indels 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 18, Application US/08948885
GENERAL INFORMATION:
APPLICAMT: Jessell, Thomas M. and Avihu Klar
TITLE OF INVENTION: CLOWING, EXPRESSION AND USES OF A
TITLE OF INVENTION: NOVEL SECRETED PROTEIN, F-SPONDIN
NUMBER OF SEQUENCES: 20
                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
PILING DATE: 19910710
CLASSIFICATION: 424
ATTORNEY /AATONIN: 424
                                                                                                                                                                                                                                                                                   STREET: 1615 L STREET, N.W. CITY: WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5683/91540
KH-----KKLKQPGDGNPWSPCSVTCG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGBMT INFORMATION:
NAME: SCOTT, WATSON T.
REGISTRATION NUMBER: 26,581
REFERENCE/DOCKET NUMBER: 5683,
TELEPHONE: 202-661-367
TELEFRAX: 202-661-367
TELEFRAX: 202-622-0944
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   412 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             , MOLECULE TYPE: peptide US-07-727-636-6
                                                                                    388 KCSSVFNVVNSSIG 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            388 KCSSVFNVVNSSIG 401
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                                                               71 KCSSVFNVVNSNSG 84
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Matches 46; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 4
US-08-948-885-18
                                                                                                                                                  RESULT 3
US-07-727-636-6
                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
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                                                                                                                                                                   61 DIEKKICKMEKCSSVFNVVNSNSGCFRHLDEREECKCLLEDSGSNGKKITCECTKPDSKP 120
                                                                                                     61 DIEKKICKMEKCSSVFNVVNSNSGCFRHLDEREECKCLLEDSGSNGKKITCECTKPDSKP 120
                                                                                                                                                121 IVQYDNENANPNANPNANPDGNCEDIPHVNEFSAIDLGNAEKYDKMDEPQHYGKSLTPLE 180
                                                                                                                                                                                                                 181 ELYKPNDKSLYQYIKANSKFIGITELSNTFINNAGQHGHMHGNEREDERTLTKEYEDIVL 240
                                                                                                                                                                                                                                      241 KEFTYMINFGRGQNYWEHPYQKSDQPKQYEQHLTDYEKIKEGKPLDKFGNIYDYHYEHSS 300
                                                                                                                                                                                                                                                                                                          Gaps
                 1 MKFLVNVALVFMVVISYIYADHHHHHHHKHKKLKQPGDGNPWSPCSVTCGKPKDELDYEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 215.5; DB 3; Length 412; Pred. No. 2.8e-10; 2; Mismatches 7; Indels 19
                                                                                                                                                                                                                                                                                                                                                                         301 PSSTKSSSPSNVKSASLATRLMKKFKAEIRDFFGISYYEKVLAKYKDDLE 350
                                                                                                                                                                                                                                                                                                                                                          301 PSSTKSSSPSNVKSASLATRLMKKFKAEIRDFFGISYYEKVLAKYKDDLE 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY

ZIP: USA
ZIP: 20036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBW PC compatible
OMPETATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 19911205
CLASSIFICATION: 424
ATTORNEY/ABENT INFORMATION:
NAME: SCOTT, WATSON T.
REGISTRATION NUMBER: 26,581
REGISTRATION NUMBER: 5683/91540
TELECPHONE: 202-861367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: CUSHMAN, DARBY & CUSHMAN STREET: N.W.
CTRY: WASHINGTON
STATE: D.C.
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .;
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TELER: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 412 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            412 amino acids
AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 11.2
Best Local Similarity 62.2
Matches 46; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        , MOLECULE TYPE: peptide US-07-677-539B-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN, I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/07/842,694 FILING DATE: 1992027
                                                                                                                                                                                                                                                                                                                                                                                                                                                 10.9%; Score 210.5; DB 1 63.4%; Pred. No. 8.4e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2, Application US/07842694
GENERAL INFORMATION:
APPLICANT: Cohen, Joseph
APPLICANT: De Wilde, Michel
TITLE OF INVENTON: Malaria Vaccine Antigen
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: SmithKline Beecham Corporation
STREET: P.O. Box 1539 / Corporate Patents
CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29 KH----KKLKQPGDGNPWSPCSVTCG-----
                                                                                                                                                                B45015-1FWC2
                                                       APPLICATION NUMBER: 08/663,371
FILING DATE: 13-JUNE-1996
ATTORNEY/AGENT INFORMATION:
NAME: Baumeister, Kirk
REGISTRATION NUMBER: 33,833
REFRENCE/DOCKET NUMBER: B45015-
TELECOMMUNICATION INFORMATION:
TELEFAX: 610-270-5096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COmpatible
OPERATING SYSTEM: PC-DOS/MS-DK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Canter, Carol G
REGISTRATION NUMBER: 31151
REFERENCE/DOCKET NUMBER: B
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31151
  18-SEPT-1997
                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHRAROTERISTICS:
LENGTH: 423 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 424 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 63.4
Matches 45; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                  single
                     CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         182 KCSSVFNVVNS 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  71 KCSSVFNVVNS 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
                                                                                                                                                                                                                                                                                                                                                                   linear
                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ANTI-SENSE: NO US-07-842-694-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: King
STATE: PA
                                                                                                                                                                                                                                                                                                                                                                   ; TOPOLOGY:
US-08-932-929A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 6
US-07-842-694-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 13; Length 412;
                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/948,885
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1. Application US/08932929A

GENERAL INFORMATION:
APPLICANT: De Wilde, Michel
APPLICANT: Cohen, Joseph
TITLE OF INVENTION: Hybrid Protein Between CS
TITLE OF INVENTION: Hybrid Protein Between CS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKilne Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. 2.8e-10;
2; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CUMIA... 52...
CAIP: 19406.
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEO for Windows Version 2.0
                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/313,288
FILING DATE: January 5, 1995
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 40028-A-PCT-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 11.2%; Score 215.5; Best Local Similarity 62.2%; Pred. No. 2.8 Matches 46; Conservative 2; Mismatches
                   ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/932,929A
                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 18: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 412 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: peptide US-08-948-885-18
                                                                                                                                       COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              388 KCSSVFNVVNSSIG 401
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          71 KCSSVFNVVNSNSG 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
                                                                              New York
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                                                                                               USA
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                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ΡA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-932-929A-1
                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE:
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RESULT 9

US-09-134-333-8

US-GO-134-333-8

Sequence 8, Application US/09134333

Sequence 8, Application US/09134333

Sequence 8, Application US/09134333

Sequence 8, Application US/09134333

APPLICANT: LONGACRE-ANDE, SHIRLEY

APPLICANT: NATO, FARIDABAN

TAPLICANT: MENDIS, MAINNEL, JOHN

APPLICANT: MENDIS, KAMINI

TITLE OF INVENTION: RECOMBINANT PROTEIN CONTAINING A C-TERMINAL FRAGMENT OF FLASMODIUM MSP-1

FILE REFERENCE: 0660-0135-0XCIP

CURRENT APPLICATION NUMBER: US/09/134,333

CURRENT APPLICATION NUMBER: PCT/FR97/00290

EARLIER FILING DATE: 1999-04-18

EARLIER FILING DATE: 1999-04-18

EARLIER FILING DATE: 1996-012-14

NUMBER OF SEQ ID NOS: 14

SOFTWARE: PATENTIN VET. 2.1

SEQ ID NO 8

LENGTHARE: PATENTIN VET. 2.1

LENGTHARE: PATENTIN VET. 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 ALFLESFIFFVTKEFNISQHQCVKKQCPBEFN-------ISQHQC 41
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      68 KMEKCSSVENVVNSNSGCFRHLDEREECKCLL------99
                                                                                                                                                                                                                                                                                                                                                                     60; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                    8 ALVEMVVYISYIYADHHHHHHHHHKHKLKQPGDGNPWSPCSVTCGKPKDELDYENDIEKKIC 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 ALLELESFIFFVTKEFNISQHQCVKKQCPEFFN-------ISQHQC 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               68 KMEKCSSVFNVVNSNSGCFRHLDEREECKCLL-----------------99
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                                                                                                                                                                                                                                                                                                                      Length 127;
                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 33.6%; Pred. No. 1.6e-10;
Matches 49; Conservative 14; Mismatches 23;
     PCT/FR97/00290
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100 ----EDSGSNGKKITCECTKPDSKPI 121
PRIOR APPLICATION NUMBER: PCT/FF
PRIOR FILING DATE: 1997-02-14
PRIOR APPLICATION NUMBER: FR96//
PRIOR FILING DATE: 1996-02-14
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PATENTIN VEY: 2.1
SEQ ID NO 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; ORGANISM: Plasmodium falciparum US-09-134-333-8
                                                                                                                                                                                                                      ); ORGANISM: Plasmodium falciparum
US-09-125-031A-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT
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                                                                                                                                                                                                                                                                                                                                                                     Sequence 8, Application US/09125031

Sequence 8, Application US/09125031

GENREAL INFORMATION:
APPLICANT: LONGACRE-ANDRE, SHIRLEY
APPLICANT: MATO, FARIEDARANO
APPLICANT: MATO, FARIEDARANO
APPLICANT: MATO, FARIEDARANO
TITLE 0F INVENTION: PACOMBINANT PROFEIN CONTAINING A C-TERMINAL FRAGMENT OF
TITLE 0F INVENTION: PLASMODIUM MSP-1
FILE REFERENCE: 0660-0139-0XPCT
CURRENT APPLICATION NUMBER: DC9/125,031
CURRENT APPLICATION NUMBER: PC7/FR97/00290
EARLIER FILING DATE: 1997-03-10
EARLIER FILING DATE: 1997-02-14
EARLIER FILING DATE: 1996-02-14
EARLIER FILING DATE: 1966-02-14
SEALIER FILING DATE: 1966-02-14
SEALIER FILING DATE: 1966-02-14
SOFTWARE: PRECENTIN VOICE: 12
SEQUENCE TO NOS: 14
SEQ ID NOS: 14
SEQ ID NOS: 14
SEQ ID NOS: 14
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GUNERAL INCRMATION.
APPLICANT: LONGACRE-ANDRE, SHIRLEY
APPLICANT: BARNELL, OGHN
APPLICANT: BARNELL, OGHN
APPLICANT: MATO. FARINI
APPLICANT: MATO. FARINDANO
TITLE OF INVENTION: RECOMBINANT PROTEIN CONTAINING A C-TERMINAL FRAGMENT OF
TITLE OF INVENTION: PLASMODIUM MP-1
FILE REFERENCE: 0660-0139-0ARCT
CURRENT APPLICANTON NUMBER: US/09/125,031A
CURRENT FILING DATE: 1999-03-10
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                                                                                                                                                                          124 KHIEQYLKKIKN-SISTEMSPCSVTCGNGIQVRIKPGSANKPKDELDYENDIEKKICKME 182
                                                                                                   Gaps
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                                                                                                                                               ----KPKDELDYENDIEKKICKME 70
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 ALLFLFSFIFFVTKEFNISQHQCVKKQCPEEFN~------ISQHQC 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            68 KMEKCSSVFNVVNSNSGCFRHLDEREECKCLL--------------------------99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22 VKKQCP-----ENSGCFRHLDEREECKCLLNYKQEGDKCVENPNPTCNENNGGCDADA 94
                                                                                                   19;
                                                    Length 424;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 10.9%; Score 210; DB 15; Length 127; Best Local Similarity 33.6%; Pred. No. 1.6e-10; Matches 49; Conservative 14; Mismatches 23; Indels 66
                                                 Score 210.5; DB 3; Length 4:
Pred. No. 8.4e-10;
1; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100 ----EDSGSNGKKITCECTKPDSKPI 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       95 KCTEEDSGSNGKKITCECTKPDSYPL 120
                                                                                                                                                 29 KH----KKLKQPGDGNPWSPCSVTCG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 127
TYPE: PRT
ORGANISM: Plasmodium falciparum
US-09-125-031-8
                                                    Query Match
Best Local Similarity 63.4%;
Matches 45; Conservative
                                                                                                                                                                                                                                                                             183 KCSSVFNVVNS 193
                                                                                                                                                                                                                                                  71 KCSSVFNVVNS 81
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US-09-125-031A-8
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APPLICANT: Council of Scientific and Industrial Research
TITLE OF INVENTION: A COMPUTATIONAL METHOD FOR THE IDENTIFICATION OF CANDIDATE PRO
TITLE OF INVENTION: USEFUL AS ANTI-INFECTIVES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----KPKDELDYEND 61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 388;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATIOS SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NATA:
APPLICATION NUMBER: US/07/727,636
FILING DATE: 19910710
CLASSIFICATION 1424
ATTORNEY/AGENT INFORMATION:
REGISTRATION WHABER: 26,581
REFERENCE/DOCKET NUMBER: 5683/91540
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-861-3067
TELEFAX: 202-862-0944
TELEX: 6714627 CUSH
SEQUENCE CHARACTERISTICS:
LINFORMATION FOR SEO ID NO: 5:
SEQUENCE CHARACTERISTICS:
LINFORMATION ACID
TTELES: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 208.5; DB 3;
Pred. No. 1.1e-09;
4; Mismatches 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29 KHKKLKQPGD------GNPWSPCSVTCG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTHER INFORMATION: Circumsporozoite (CS) protein MAME/KBY: misc_feature CTHER INFORMATION: 91|4493889 US-09-820-843A-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ch 10.8%; Score 207.5; DB 2;
11 Similarity 51.8%; Pred. No. 1.4e-09;
43; Conservative 4; Mismatches 9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILE REFERENCE: 063915
CURRENT APPLICATION NUMBER: US/09/820,843A
CURRENT FILING DATE: 2001-03-30
NUMBER OF SEQ ID NOS: 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-820-843A-31; Sequence 31, Application US/09820843A; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62 IEKKICKMEKCSSVFNVVNSNSG 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Plasmodium falciparum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10.8%;
58.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 10.89
Best Local Similarity 58.39
Matches 42; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; MOLECULE TYPE: peptide US-07-727-636-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             366 SSVFNVVNSSIG 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     73 SSVFNVVNSNSG 84
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Matches 43; Conserv
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LENGTH: 396
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13;
                                                                                              APPLICANT: LAL, ALTAF A.
APPLICANT: GOLDMAN, IRA F.
TITLE OF INVENTION: CIRCUMSPOROZOITE PROTEIN OF PLASMODIUM
TITLE OF INVENTION: REICHENOWI AND VACCINE FOR HUMAN MALARIA
NUMBER OF SEQUENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-07-727-636-5
Sequence 5, Application US/07727636
Sequence 5, Application US/07727636
Sequence 5, Application:
APPLICANT: LALA ALTAF A.
APPLICANT: GOLDMAN, IRA F.
TITLE OF INVENTION: CIRCUMSPOROZOITE PROTEIN OF PLASMODIUM
TITLE OF INVENTION: REICHENOWI AND VACCINE FOR HUMAN MALARIA
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN, DARBY & CUSHMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 3; Length 388;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
CONTRACTION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PACENTIN Release #1.0, Version #1.25
CUBRENT APPLICATION DATA:
FLING DATE: 19911205
CLASSIFICATION NUMBER: US/07/677,539B
FLING PRECENT INFORMATION:
NAME: SCOTY, WATSON T.
REFERENCE/OCKET NUMBER: 56,581
REFERENCE/OCKET NUMBER: 56,81
TELEPAN: 202-861-367
TELEFAN: 202-861-367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .1e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 208.5; D
Pred. No. 1.1e-
4; Mismatches
                                                                                                                                                                                     STREET: L615 L STREET, N.W.
CITY: WASHINGTON
STATE: D.C.
COUNTRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: CUSHMAN, DARBY & CUSHMAN STREET: 1615 L STREET, N.W.
                                                                 Sequence 5, Application US/07677539B
GENERAL INFORMATION:
APPLICANT: LAL, ALTAF A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 58.3%;
Matches 42; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           388 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 388 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          366 SSVFNVVNSSIG 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  73 SSVFNVVNSNSG 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: WASHINGTON STATE: D.C.
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20036
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                                           US-07-677-539B-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-07-677-539B-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
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Gaps

13;

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APPLICANT: Slaoui, Moncef
APPLICANT: Mijendale, Frans
TITLE OF INVENTION: VACCINE FORMULATIONS CONTAINING
TITLE OF INVENTION: 3-0-DEACYLATED MONOPHOSPHORYL LIPID A AND A CARRIER
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 13; Length 424;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 3, Application US/08932929

GENERAL INFORMATION:
APPLICANT: De Wilde, Michel
APPLICANT: Cohen, Joseph
TITLE OF INVENTION:
TITLE OF INVENTION: PLASMODIUM AND HBAGG
NUMBER OF SEQUENCES: 4
CORRESPONDENCE BORRESS:
ADDRESSEE: Smithkline Beecham Corp./Corporate
ADDRESSEE: Intellectual Property
STREET: PO. Box 1539 - UW2220

STATE: Pennsylvania
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1.6e-09;
9;
                                                                                                                                                                                                                                                               OPERATING SYSTEM: DOS SOFTWARE: FESTSED FOR WINDOWS VERSION 2.0 SOFTWARE: FESTSED FOR WINDOWS VERSION 2.0 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/903,084
FILING DATE: 17-JUL-1997
CLASSIFFICATION: 424
PRIOR APPLICATION NUMBER: 08/741,575
FILING DATE: 30-OCT-1996
APPLICATION NUMBER: 08/303,542
FILING DATE: 09-SEP-1994
FILING DATE: 09-SEP-1994
ATYORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match
10.8%; Score 207.5;
Best Local Similarity 51.8%; Pred. No. 1.66
Matches 43; Conservative 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29 KHKKLKQPGD------GNPWSPCSVTCG-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Kerekes, Zoltan
REGISTRATION NUMBER: 38,938
REFERENCE/DOCKET NUMBER: B451
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5024
TELEFAX: 610-270-5090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62 IEKKICKMEKCSSVFNVVNSNSG 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS: LENGTH: 424 amino acids
                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : 424 amino acids amino acid
                                                                                                                    STREET: 709 of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-903-084-3
                                                                                                                                                                                U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS:
                                                                                                                                                                                               19046
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                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 15
US-08-932-929-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 424;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                       APPLICANT: De Wilde, Michel
APPLICANT: Chean, Joseph
TITLE OF INVENTION: HYBRID PROTEIN BETWEEN CS FROM
TITLE OF INVENTION: HYBRID PROTEIN BETWEEN CS FROM
TITLE OF INVENTION: PLASMODIUM AND HBSAG
NUMBER OF SEQUENCES:
ADDRESSEE: Intellectual Property
STREET: P.O. Box 1539 - UW2220
CITY: King of Prussia
STATE: USA
                                                                                                                                                                                                                                                                                                                           Score 207.5; DB 11,
Pred. No. 1.6e-09;
4; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ---GNPWSPCSVTCG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 3. Application US/08903084; GENERAL INFORMATION:
APPLICANT: Bruck, Claudine
APPLICANT: Erancotte, Myriam
APPLICANT: Kummert, Suzanne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            170 IEKKICKMEKCSSVFNVVNSSIG 192
     363 IEKKICKMEKCSSVFNVVNSSIG 385
                                                                                       US-08-760-797-3; Sequence 3, Application US/08760797; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62 IEKKICKMEKCSSVFNVVNSNSG 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 10.8%;
Best Local Similarity 51.8%;
Matches 43; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             424 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29 KHKKLKOPGD------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 610 270-5090 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: Si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
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US-08-903-084-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-760-797-3
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                                                                         RESULT
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ZIP: 19406-0939

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/932,929
FILING DATE: 18-SEP-1997
CLASSIFICATION NUMBER: US/08/663,371
FILING DATE: 21-OCT-1994
ATTORNEY/AGENT INVORMATION:
NAME: Baumeister, Kirk
REGISTRATION NUMBER: 33,833
REFERENCE/DOCKET NUMBER: B45015-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610,270-5096
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 424 amino acid
STAPE: Anno acid
STAPE: TELEVEN: Anno acids
TTREE: Anno acids
STAPE: TYPE: Anno acids
STAPE: TYPE: Anno acids
STAPE: TYPE: Anno acids
TYPE: Anno acids
STAPE: TYPE: Anno acids
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Search completed: January 29, 2002, 10:55:58 Job time: 2394 sec

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Query Match 10.8%; Score 207.5; DB 13; Length 424; Best Local Similarity 51.8%; Pred. No. 1.6e-09; Matches 43; Conservative 4; Mismatches 9; Indels 27; Gaps

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Appli Appli Appli Appli Appli Appli Appli

Sequence Seq

Appli Appli Appli Appli

Sequence

us-09-763-397a-25.rai

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APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Lingner, Joachim
APPLICANT: Chapman, Karu
APPLICANT: Chapman, Karu
APPLICANT: Harley, Calvin B.
APPLICANT: Harley, Calvin B.
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBR OF SEQUENCES: 727
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPAtible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor CITY: San Francisco STATE: California COUNTRY: USA ZIP: 94111-3834 COMPUTER READABLE FORM:
US-08-480-751-5
US-08-913-918-5
US-08-13-7181-5
US-08-481-7181-5
US-08-481-55-6
US-08-481-55-6
US-08-913-918-6
US-08-913-918-6
US-08-13-7181-6
US-08-13-7181-6
US-08-13-7181-6
US-08-13-7181-6
US-08-13-7181-6
US-08-67-8181-17
US-08-61-181-17
US-08-113-7508-1
                                                                                                                                                                                                                                                                                                                                                      ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 09-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/974,549A
FILING DATE: 19-NOV-1997
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-0CT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 08/911,312 FILING DATE: 14-AUG-1997 PRIOR APPLICATION DATA: PAPLICATION NUMBER: US 08/912,951
                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 613, Application US/08974549A; Patent No. 6166178; GENERAL INFORMATION:
   411.7
411.7
411.7
411.7
411.7
411.7
38.9
338.9
338.0
337.0
36.1
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US-08-974-549A-613
     Sequence 613, App
Sequence 36, Appl
Sequence 2, Appli
Sequence 2, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Appl
Appli
A
                                                                                                                                         (without alignments)
15.356 Million cell updates/sec
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Sequence 2, A
Sequence 2, A
Sequence 43,
Sequence 24,
Sequence 21,
Sequence 11,
Sequence 11,
Sequence 6, A
                                                                                                                       January 29, 2002, 10:59:58; Search time 32.24 Seconds
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Sequence 7
Sequence 7
Sequence 7
Sequence 7
Sequence 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Description
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/cgn2_6/ptodata/2/laa/6B_COMB.pep:*
/cgn2_6/ptodata/2/laa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/laa/PCTUS_COMB.pep:*
                   GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-974-549A-613

US-08-960-190A-36

US-08-134-669-2

US-08-134-669-2

US-08-134-669-2

US-08-954-211-43

US-08-953-326-24

US-08-953-326-24

US-08-953-326-24

US-08-953-326-24

US-08-953-326-24

US-08-953-326-24

US-08-953-326-24

US-08-941-458-7

US-08-485-588-7

US-08-484-565-7

US-08-481-986-7

US-08-481-986-7

US-08-481-986-7

US-08-481-986-7

US-08-481-986-7

US-08-481-986-7

US-08-481-986-7

US-08-481-565-8

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US-08-353-784-8
US-08-484-719B-8
US-08-485-588-5
US-08-484-565-5
                                                                                                                                                                                                                                                                                                                212252 seqs, 22503292 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                        OM protein - protein search, using sw model
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1 MKFLVNVALVFMVVYISYIYAD
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Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                          US-09-763-397A-25
                                                                                                                                                                                                                                                                                                                                                                                   Minimum DB seq length: 0
Maximum DB seq length: 200000000
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211
211
212
265
205
305
305
397
1058
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Perfect score:
                                                                                                                                                                                                                                                               Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Database :
                                                                                                                                                                                                                                                                                                                Searched:
                                                                                                                                                                                                                                Sequence:
                                                                                                                       Run on:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Thibault, Kelly J.
APPLICANT: Thibault, Kelly J.
APPLICANT: Arnasiev, Boris N.
APPLICANT: Arnasiev, Boris N.
APPLICANT: Beaty, Boris N.
APPLICANT: Beaty, Barry
TITLE OF INVENTION: SYSTEM
TITLE OF INVENTION: SYSTEM
TORRESPONDENCES: 2
CORRESPONDENCES: 2
ADDRESSE: Soully, Scott, Murphy & Presser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: New to.n.

COUNTRY: United States

ZIP: IN30
COMPUTER READABLE FORM
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATIOS SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/34,669
FILING DATE: 04-NOV-1994
STELESFICATION: 435
ATORNEY/AGRYI INFORMATION:
NAME: DiGiglio, Frank S.
REFERENCE/POCKET NUMBER: 9485
TELEPHONE: (516) 742-4343
TELEPHONE: (516) 742-4343
TELEPHONE: (516) 742-4343
TELEPHONE: (516) 742-4366
TELERA: 230 901 SANS UR
INFORMATION FOR SEO ID NO: 2:
SEQUENCE CHARACTERISTICS:
FENGTH: 21 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Scully, Scott, Murphy & Presser STREET: 400 Garden City Plaza CITY: Garden City
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: COL]ess, Peter F
REGISTRATION NUMBER: 33,860
REFRENCE/DOCKET NUMBER: 48002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 2, Application US/08334669
; Patent No. 5627048
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                                                                                                                                                                                                                                                                                                                                                                                      36:
                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New York
United States
                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-960-190A-36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: peptide US-08-334-669-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
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100.0%; Score 108; DB 4; Length 1189;
Best Local Similarity 100.0%; Pred. No. 8.3e-09;
Matches 22; Conservative 0; Mismatches 0; Indels 0.
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CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 36, Application US/08960190A
Sequence 36, Application US/08960190A
September No. 6232445
September No. 632445
September No. 632446
September No. 63
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APPLICATION NUMBER: US/08/960,190A FILING DATE: 29-OCT-1997 CLASSIFICATION. 536 PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                             APPLICATION AND ATA:
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
PRIOR APPLICATION DATA: WO PCT/US97/17885
PRIOR APPLICATION DATA: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT: NPORMATION:
REFERENCE/DOCETT NUMBER: 36,429
REGISTRATION NUMBER: 36,429
REFERENCE/DOCETT NUM
                                                                                        UMBER: US 08/915,503
14-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MKFLVNVALVFMVVYISYIYAD 22
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MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Win
         FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION:
; OTHER INFORMATION:
US-08-974-549A-613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: Protein
LOCATION: 1..1189
OTHER INFORMATION:
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US-08-960-190A-36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     qq
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Length 26;
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Patent No. 6251392
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Hiatt, Andrew C.
APPLICANT: Fitchen, John H.
TITLE OF INVENTION: NOVEL EPITHELIAL CELL TARGETING AGENT NUMBER OF SEQUENCES: 89
CORRESPONDENCE ADDRESS:
             APPLICANT: Fitchen, John H.
TITLE OF INVENTION: NOVEL EPITHELIAL TISSUE IMAGING AGENT
NUMBER OF SEQUENCES: 93
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
CITY: Seattle
COUNTRY: USA
ZIP: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/782,480
FILING DATE: 10-JAN-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFRENCE/DOCKET NUMBER: 310098.402
TELEPHONE: (206) 622-4900
TELEPHONE: (206) 622-4900
TELEPHONE: (206) 622-4900
TELEFAXION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/954,211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AUDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CIY: Seattle
STATE: Mashington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 93.5; DB 3;
Pred. No. 2.6e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MKFLVNVALVFMVVYISYIYAD 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MKFLVNVAL-FMVVYISYIYAD 21
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95.5%;
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CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 86.6'
Best Local Similarity 95.5'
Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26 amino acids
Hein, Mich B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein
                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
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: USA
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US-08-954-211-43
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                                       Length 21;
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Pred. No. 6e-09;
                                                                               Indels
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SOFTWARE PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,341A
FILING DATE: June 7, 1995
CLASSIPTCATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: D1619110, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 94852-I
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION SANS UR
TELESAS. (516)742-4346
TELESAS. (516)742-4366
TELESAS. (516)742-4366
TELESESSECIED NO: 2:
                                                                                                                                                                                                                                                                                                                              APPLICANT: Afanasiev, Boris N.
APPLICANT: Carlson, Jonathan O.
APPLICANT: Beaty, Barry J.
APPLICANT: Highins, David R.
APPLICANT: Thibault, Kelly J.
TITLE OF INVENTION: AEDES AEGYPTI DENSOVIRUS TITLE OF INVENTION: EXPRESSION SYSTEM NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                     Score 97; DB 1;
Pred. No. 6e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Scully, Scott, Murphy & Presser STREET: 400 Garden City Plaza CITY: Garden City STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                           1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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GENERAL INFORMATION:
APPLICANT: Hiatt, Andrew C.
                                                                                                                                                                                                                                                                       Sequence 2, Application US/08485341A Patent No. 5849523 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MKFLVNVALVFMVVYISYIYA 21
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ilarity 95.2%;
Conservative 1
                                   Query Match
Best Local Similarity 95.2%;
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                         1 MKFLVNVALVFMVYISYIYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
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Best Local Similarity
Matches 20; Conserv
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APPLICANT: Mahan, Suman M.

TITLE OF INVENTION: Nucleic Acid Vaccines Against Rickettsial Diseases of
TITLE OF INVENTION: Animals and Humans
TITLE OF INVENTION: Animals and Humans
FILE REFERENCE: UF-16701
CURRENT APPLICATION NUMBER: US/08/953,326
CURRENT FILIAG DATE: 1997-10-17
EARLIER APPLICATION NUMBER: 08/953,326
EARLIER APLICATION NUMBER: 08/953,326
EARLIER FILING DATE: 1996-10-17
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PATENTING DATE: 1996-10-17
NUMBER OF SEQ ID NOS: 24
LENGTH: 205
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      45.4%; Score 49; DB 4; Length 305; 55.0%; Pred. No. 2.3; 7; Indels tive 2; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 10
US-08-978-741-6
Sequence 6, Application US/08978741
Patent No. 61000706
GENERAL INFORMATION:
TITLE OF INVENTION: O-FUCOSYLTANSferase
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
STREET: 1 DNA WAY
CITY: South San Francisco
STATE: Callfornia
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 11, Application US/09248588; Patent No. 6231864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: PRT
; ORGANISM: Ehrlichia chaffeensis
US-08-953-326-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 FLVNVALVFMVVYISYIYAD 22
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Best Local Similarity 55.0%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT ORGANISM: Hepatitis B virus US-09-248-588-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 9
US-09-248-588-11
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US-08-953-326-23

Sequence 23, Application US/08953326

Patent No. 6251872

GENERAL INFORMATION:

APPLICANT: Barbet, Anthony F.

APPLICANT: Garta, Roman R.

APPLICANT: Buridge, Michael J.

APPLICANT: Buridge, Michael J.

APPLICANT: Warangirwa, Fred R.

APPLICANT: Wahan, Suman M.

TITLE OF INVENTION: Nucleic Acid Vaccines Against Rickettsial Diseases of TITLE OF INVENTION: Nucleic Acid Vaccines Applicant: APPLICANT: Nucleic Acid Vaccines Against Rickettsial Diseases of TITLE OF INVENTION: Nucleic Acid Vaccines Against Rickettsial Diseases of TITLE OF INVENTION: Nucleic Acid Vaccines Against Rickettsial Diseases of TITLE OF INVENTION: Nucleic Acid Vaccines Against Rickettsial Diseases of TITLE OF INVENTION: Nucleic Acid Vaccines Against Rickettsial Diseases of TITLE OF INVENTION NUMBER: US/08/953,326

EARLIER PELLING DATE: 1997-10-17

EARLIER PLILING DATE: 1997-10-17

NUMBER OF SEQ ID NOS: 24

SEQ ID NO 23

LENGTH: 205

HAVEN: 100

HAVEN: 100

SEQ ID NO 23

HAVEN: 100

HAVEN: 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  86.6%; Score 93.5; DB 4; Length 26; 95.5%; Pred. No. 2.6e-08; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match

Sol. 9%; Score 55; DB 4; Length 205; Best Local Similarity 40.0%; Pred. No. 0.18;

Matches 8; Conservative 7; Mismatches 5; Indels
                                            REFERENCE/DOCKET NUMBER: 310098.403
TELECHONE (206) 622-4900
TELEPHONE: (206) 622-4900
TELEPAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 anino acids
TYPE: amino acid
TYPE: amino acid
TYPE: Jenear
HOLGORY: linear
US-08-954-211-43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESGLT 8
US-08-953-326-24
; Sequence 24, Application US/08953326
; Patent No. 6251872
; GENERAL INFORMATION:
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              REGISTRATION NUMBER: 31,392
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APPLICANT: Burridge, Michael J.
APPLICANT: Nyika, Aceme
APPLICANT: Rurangirwa, Fred R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MKFLVNVALVEMVVXISYIY 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 86.6
Best Local Similarity 95.5
Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TYPE: PRT
; ORGANISM: Ehrlichia canis
US-08-953-326-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 δ
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Gaps
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                                         Krapcho, Karen J.
Hammerland, Lance G.
VENTION: CHIMERIC RECEPTORS AND METHODS FOR VENTION: DENTIFYING COMPOUNDS ACTIVE AT VENTION: METABOTROPIC GLUTAMATE RECEPTORS AND VENTION: THE USE OF SUCH COMPOUNDS IN THE VENTION: TREATMENT OF NEUROLOGICAL DISORDERS VENTION: AND DISEASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       41.7%; Score 45; DB 2;
45.0%; Pred. No. 35;
Live 5; Mismatches
              APPLICANT: Krapcho, Karen J.
APPLICANT: Krapcho, Karen J.
APPLICANT: Hammerland, Lance G.
TITLE OF INVENTION: CHIMERIC RECEPTORS F
TITLE OF INVENTION: IDENTIFYING COMPOUNT
TITLE OF INVENTION: THE USE OF SUCH COMP
TITLE OF INVENTION: A SUCH COMP
TITLE OF INVENTION: A SOFT OF SUCH COMP
TITLE OF INVENTION: THE USE OF SUCH COMP
TITLE OF INVENTION DATA: APPLICATION NUMBER: US/08/687, 289A
FILING DATE: JULY 25, 1996
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: 60/001,526
FILING DATE: JULY 26, 1995
ATTORNEY APPLICATION: THEORYMATION:
ANALE CASALLING SECTION: THEORYMATION:
ANALE CASALLING SECTION:
ANALE CASALLING 
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ADDRESSEE: Vinson & Elkins L.L.P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 220/004
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              785 KFITFSMLIFFIVWISFIPA 804
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 1058 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match
Best Local Similarity 45.v.
Best Local 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (213) 955-044
TELEX: 67-3510
INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear MOLECULE TYPE: Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: sin
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-687-289A-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   45.4%; Score 49; DB 3; Length 397; 50.0%; Pred. No. 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: Plasmid insert encoded protein US-09-333-729A-7
                                         MEDIUM TYPE: 3.5 Inch, 1.44 Mb floppy disk COMPUTER: 18M PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WinPatin (Genentech) CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/978,741 FILING DATE: 26-No. 6100076-1997 CLASSIFICATION DATA: APPLICATION DATA: ATORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:

APPLICANT: Wang, Yang
APPLICANT: Spellman, Michael W.

TILLE OF INVENTION: O'FUCOSyltransferase;
FILE REFERENCE: P1041P1D1-Substitute
CURRENT APPLICATION WUMBER: US/09/333,729A
CURRENT FILING DATE: 1999-06-15

PRIOR FILING DATE: 1997-11-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 7, Application US/09333729A Patent No. 6270987
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                                                                                                                                                                                                                                                                                                                                                                                           NAME: Svoboda, Craig G.
REGISTRATION NUMBER: 39,044
REFERENCE/DOCKET NUMBER: P10
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 KFLVNVALVFMVVYISYIYA 21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 KFLVNVALVFMVVYISYIYA 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 397 amino acids TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10; Conservative
                       COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS:
SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 11
US-09-333-729A-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-978-741-6
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Query Match
Best Local Similarity 45.0%; Pred. No. 36;
Matches 9; Conservative 5; Mismatches 6; Indels
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Patent No. 576369
GENERAL INFORMATION
APPLICANT: Edward M. Brown
APPLICANT: Steven C. Hebert
APPLICANT: James E. Garrett, Jr.
TITLE OF INVENTION: OALCIUM RECEPTOR-ACTIVE
TITLE OF INVENTION: ALVON
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: SILLE 4700
STREET: SILLE 4700
STREET: SILLE 4700
STREET: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                 PRILIGATION NUMBER: 08/353,/b4

APPLICATION NUMBER: DCT/US/94/12117

FILING DATE: 2 December, 1994

APPLICATION NUMBER: U.S. 08/292,827

FILING DATE: 23 AQUAST, 1994

APPLICATION NUMBER: U.S. 08/141,248

FILING DATE: 22 OCTODER: 1993

APPLICATION NUMBER: U.S. 08/009,389

FILING DATE: 23 FEDIWARY, 1993

APPLICATION NUMBER: U.S. 08/017,127

FILING DATE: 21 FEDIWARY, 1993

APPLICATION NUMBER: U.S. 08/017,127

FILING DATE: 23 AQUAST, 1992

APPLICATION NUMBER: U.S. 07/749,451

FILING DATE: 23 AQUAST, 1992

APPLICATION NUMBER: U.S. 07/749,451

FILING DATE: 23 AQUAST, 1991

ATTORNEY/AGENT INFORMATION:

REGISTRATION NUMBER: 38,179

REFERENCE/DOCKET NUMBER: 3 13/005

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION PROFESSORIES SECURATION:

TELECOMMUNICATION PROFESSORIES SECURATION:

TELECOMMUNICATION PROFESSORIES SECURATION:

SECURATE: 1078 AMIGO ACIGS

WANDER: HEREFIELD ACIDS

SECURATE: 1078 AMIGO ACIGS
PRIOR APPLICATION DATA: described below: APPLICATION NUMBER: 08/353,784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: FASTSEQ
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,565
FILING DATE: 7 June, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    805 KFITFSMLIFFIVWISFIPA 824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 KFLVNVALVFMVVYISYIYA 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein US-08-485-588-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          οp
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                                                                                                                     COUNTRY: U.S.

2IF: 2004-1008

COMPUTER READABLE PORM:
MEDIUM TYPE: FLOSPY disk
COMPUTER: IRW PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATEMIT Release #1.0, Version #1.30
CUBRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/134,513
FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 7, Application US/08485588
Sequence 7, Application US/08485588
Sequence 7, Application US/08485588
Sequence 7, Application GENERAL INFORMATION:
APPLICANT: Steven C. Hebbert
APPLICANT: James E. Garrett, Jr.
TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE
TITLE OF INVENTION: ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: First Interstate World Center:
STREET: Suite 4700
STREET: G33 Mest Fifth Street
CITY: Los Angeles
STATE: California
COMPUTER READABLE FORM:
MEDIUM TYPE: 35" Diskette, 1.44 Mb storage
COMPUTER: IBM PC Compatible
COMPUTER: SASTERE
STATE: CALIFORNIA SYSTEM:
COMPUTER: SASTERE
STATE: G3 TATE: G3 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: FASTSEQ
CURRENT APPLICATION DATA:
APPLICATION NUBER: US/08/485,588
FILING DATE: 7 June, 1995
CLASSIFICATION: 435
PRICOR APPLICATION DATA: including application
             1455 Pennsylvania Avenue, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BRI331/13003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY AGENT INFORMATION:
NAME: SATAC, MICHAEL A.
REGISTRATION NUMBER: 36,912
REFERENCE/DOCKET NUMBER: BR133
TELEPOMUNICATION INFORMATION:
TELEPHONE: (202)639-6604
INFORMATION FOR EMO IN SEQ ID NO: 2:
SEQUENCE CHRRACTERISTICS:
LENGTH: 1059 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SS: not relevant not relevant E: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         804 KFITFSMLIFFIVWISFIPA 823
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 KFLVNVALVFMVVYISYIYA 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: no
                                                    Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: not r
MOLECULE TYPE: pr
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-134-513-2
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US-08-485-588-7
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Query Match 41.7%; Score 45; DB 1; Length 1078; Best Local Similarity 45.0%; Pred. No. 36; Matches 9; Conservative 5; Mismatches 6; Indels
CLASSIFICATION: 435
PRIOR APPLICATION DATA: including application PRIOR APPLICATION DATA: including application PRIOR APPLICATION DATA: including application PRIOR APPLICATION DATA: described below: 9 APPLICATION NUMBER: 08/35,784
FILING DATE: 2 December, 1994
APPLICATION NUMBER: 0.5. 08/29,827
FILING DATE: 23 August, 1994
APPLICATION NUMBER: 0.5. 08/14,248
FILING DATE: 22 August, 1993
APPLICATION NUMBER: 0.5. 08/00,389
FILING DATE: 23 February, 1993
APPLICATION NUMBER: 0.5. 08/01,127
FILING DATE: 12 February, 1992
APPLICATION NUMBER: 0.5. 07/934,161
FILING DATE: 1 February, 1992
APPLICATION NUMBER: 0.5. 07/934,161
FILING DATE: 1 February, 1992
APPLICATION NUMBER: 0.5. 07/49,451
FILING DATE: 1 February, 1992
APPLICATION NUMBER: 0.5. 07/49,451
FILING DATE: 1 February, 1992
APPLICATION NUMBER: 0.5. 07/49,451
FILING DATE: 1 February, 1992
APPLICATION NUMBER: 0.5. 07/49,451
FILING DATE: 1 February, 1992
APPLICATION NUMBER: 23 August, 1991
ATTORNEYAGENT INFORMATION:
NAME: Heber, Sheldon 0.
REGISTRATION NUMBER: 213/006
TELEFAN: 67-3510
INFORMATION FOR SEQ ID NO: 7: SEQUENCE CHARACTERISTICS:
LENGTH 1078 amino acid
TYPE: amino acid
TOPOLOGY: 1 inear
MOLECULE TYPE: protein
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2 KFLVNVALVFMVVYISYIYA 21 ð

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Gaps

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Search completed: January 29, 2002, 10:59:59 Job time: 2145 sec

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January 29, 2002, 10:14:44 ; Search time 310.82 Seconds (without alignments) 83.410 Million cell updates/sec
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1923
1 MKFLVNVALVEWVVXISXIX.......DFFGISYYEKVLAKYKDDLE 350
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2: \SIDSB\gcgdata\geneseq\geneseqp\AA1981.DAT:*

3: \SIDSB\gcgdata\geneseq\geneseqp\AA1981.DAT:*

5: \SIDSB\gcgdata\geneseq\geneseqp\AA1981.DAT:*

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6: \SIDSB\gcgdata\geneseq\geneseqp\AA1985.DAT:*

7: \SIDSB\gcgdata\geneseq\geneseqp\AA1986.DAT:*

8: \SIDSB\gcgdata\geneseq\geneseqp\AA1981.DAT:*

10: \SIDSB\gcgdata\geneseq\geneseqp\AA1981.DAT:*

11: \SIDSB\gcgdata\geneseq\geneseqp\AA1981.DAT:*

12: \SIDSB\gcgdata\geneseq\geneseqp\AA1991.DAT:*

13: \SIDSB\gcgdata\geneseq\geneseqp\AA1991.DAT:*

14: \SIDSB\gcgdata\geneseq\geneseqp\AA1993.DAT:*

15: \SIDSB\gcgdata\geneseq\geneseq\geneseqp\AA1993.DAT:*

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19: \SIDSB\gcgdata\geneseq\geneseq\geneseqp\AA1993.DAT:*

10: \SIDSB\gcgdata\geneseq\geneseq\geneseqp\AA1993.DAT:*

11: \SIDSB\gcgdata\geneseq\geneseq\geneseqp\AA1993.DAT:*

12: \SIDSB\gcgdata\geneseq\geneseq\geneseqp\AA1993.DAT:*

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16: \SIDSB\gcgdata\geneseq\geneseq\geneseqp\AA1993.DAT:*

17: \SIDSB\gcgdata\geneseq\geneseq\geneseqp\AA1993.DAT:*

18: \SIDSB\gcgdata\geneseq\geneseq\geneseqp\AA1999.DAT:*

20: \SIDSB\gcgdata\geneseq\geneseq\geneseq\geneseqp\AA1999.DAT:*

21: \SIDSB\gcgdata\geneseq\geneseq\geneseq\geneseq\geneseq\geneseq\geneseq\geneseq\geneseq\geneseq\geneseq\geneseq\geneseq\geneseq\geneseq\geneseq\geneseq\geneseq\geneseq\geneseq\geneseq\geneseq\geneseq\geneseq\geneseq\geneseq\geneseq\geneseq\geneseq\geneseq\geneseq\geneseq\geneseq\geneseq\geneseq\geneseq\geneseq\geneseq\geneseq\geneseq\geneseq\geneseq\geneseq\geneseq\geneseq\geneseq\geneseq\geneseq\geneseq\geneseq\geneseq\geneseq\geneseq\geneseq\geneseq\
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     522463 seqs, 74073290 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                               OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Title:
Perfect score:
Sequence:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Searched:
                                                                                                                                                                                                                                                                       Run on:
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

		Description	Recombinant vaccin	NS1 81-RLfdelta9.	NS181RLFAuth plasm	NS1 81-RLfAuth, P	NS1 81 (NANP) 4 RL EAU	NS1 81 (NVDP) 4 RLFAU	NS1_81~RLfAuth + (	Merozoite surface	Sequence encoded b	CS protein of mala	Sequence encoded b
		ID	AAY70278	AAR13175	AAR07945	AAR13176	AAR13178	AAR13179	AAR13177	AAB37609	AAP83144	AAP60416	AAP80835
		DB	21	13	11	12	12	12	12	55	σ	۷	σ
		Match Length DB ID	350	309	319	319	335	335	327	108	411	412	412
땅	Ouery	Match	100.0	13.1	12.8	12.8	12.8	12.8	12.6	11.5	11.2	11.2	11.0
		Score	1923	252	247	247	247	247	243	222	215.5	215.5	211.5
	Result	NO.	П	7	m	4	Ŋ	9	7	<b>6</b> 0	6	<i>g</i> <sup>1</sup>	/

WO200011179-A1. 02-MAR-2000.

FX XX X

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	3 6	· .	. 0	424		AAR37797	RTS protein.	Synt
	14	æ.	Ö	116		AAW36103	PfMSP1(p19)A	prote
	15	œ.	0	116		AAW22592	PfMSP1(p19)A	prote
	10 11		o c	127		AAW22593	PfMSP1(p19)S	prot
.,	1 6			177		AAB37608	Merchanite sur	prote
	13		. 0	355		AAY09372	Merozoite su	fac
	20	io i	0.	355		AAY05832	Merozoite su	ာ့
	22	196.5	10.2	361		AAY09373	Merozoite su	surface
	23			1639		AAW54145	P. falciparu	m synt
	24		0	ω,		AAY09374	Modified merozoite	ozoite
	52	· .	0	376		AAY05834	Modified merozoite	ozoite
	26	m .		180		AAR07290	Circumsporozoi	oite a
	280	٠œ		373		AAB83925	A major merozor	zoite he bi
	52	179		ာဇာ		AAP91632	Rhoptry membrane a	rane a
	30	174		622		AAR27532	Plasmodium for	alcipa
	31	17		622		AAR68840	Plasmodium for	alcipa
	32	145.5		354		AAB10640	Human VEGF-X	prote
	 	45.		354		AAB10641	Human VEGF-X	prote
	34	144	٠	4.0		AAB36293	Human GIL-19,	/AE289
	3.6	131		400		AAY70795	Dlasmodium fo	action a
	37	131		5 6		AAR41356	MSP1EGF2A EG	F2-11k
	38	130.5		563		AAR10551	Plasmodium k	nowles
	38	13		390		AAY49255	N19 polyepit	ope ca
	40			99		AAR66442	Plasmodium fa	alcipa
	41	C 1		29		AAG63513	A peptide which ma	1ch ma
	42	$\alpha$		63		AAR14263	gour	branch
	4 4	710		23.5		AAY70282	Plasmodium fa	ium falcipa
	45	126.5		40	16	AAR87213	Circumsporozo P.falciparum	orce (
						ALIGNMENT	TS	
		П,						
AAI	AAY / UZ / E	278				(		
a x	¥		scandard;	1; Frotein	: 11	350 AA.		
AC.	AAY7	170278;						
XX								
DŢ	90	-JUN-2000	) (first	st entry	λ,			
A A	PAC	Recombinant	t vaccino		MITM	CDC /NITMALVAC - 1		
×	,			2				
KW	Rec	combinant	t prote	ein; CDC	/NII	Recombinant protein; CDC/NIIMALVAC~1; multivalent;	ultivalent; malaria; vaccine,	
KW	J-T	sell epitor	tope; t	etanus	toxo	tetanus toxoid; antigenic	treatment	
X	:G	circumsporozoit	Φ.	•	S	P; sporozoit	surface protein-2; SSP-2;	
M 2	1.1	ver stage	e antic		SA-1	, merozoite	-1; MSP-1; M	SP-2;
M S	d d	apical mem	memorane	tigen	€ (	gen-1; AMA-1; erytni	1cigen-1/5;	
X X	Pfc	Pfg27: antibarasit	ioperasi	10:00	even	tion: anti-C	aced processing, war-i; gamete specific antige revention: anti-CDC/NIMALVAC-1 antibody:	
KW	hor	honey bee.		4			( [ ] )	
XX	ī							
SOS	ธิรั	Chimeric ~	Apis	Apis sp.	1			
200	55	meric -	Plasmo	riaium fa Sdium fa	falcipar	cioarum.		
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五日	Ke	Кеу		Location/Qualifier	/Qua	lifiers		
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1 E			`	Tabel-	* Mellttl "Derived	ttin_signal_peptid ved from Honey bee	_peptide	
i F	Prot	otein		23350	7 7 7		ney bee	

AAY.	AAY70278 .
ID	AAY70278 standard; Protein; 350 AA.
×	
AC	AAY70278;
XX	
DŢ	06-JUN-2000 (first entry)
XX	
DE	Recombinant vaccine CDC/NIIMALVAC-1.
XX	
X	Recombinant protein; CDC/NIIMALVAC~1; multivalent; malaria; vaccin
ΚM	T-cell epitope; tetanus toxoid; antigenic epitope; treatment;
Κĸ	circumsporozoite protein; CSP; sporozoite surface protein-2; SSP-2
KW	liver stage antigen-1; LSA-1; merozoite surface protein-1; MSP-1;
X	apical membrane antiqen-1; AMA-1; erythrocyte binding antiqen-1
Κ¥	EBA-175; rhoptry associated protein-1; RAP-1; gamete specific anti
Υ×	Pfg27; antiparasitic; prevention; anti-CDC/NIIMALVAC-1 antibody;
ΚW	honey bee.
×	
SO	Chimeric - Apis sp.
SO	Chimeric - Clostridium tetani.
SO	Chimeric - Plasmodium falciparum.
×	
HН	Key Location/Qualifiers
FT	Peptide 1.,22
ΕŢ	/label- Melittin_siqual_peptide
FT	/note= "Derived from Honey bee"
FJ	Protein 23350
H	/label- Mature CDC/NIIMALVAG-1
FT	/note= "Recombinant multivalent malarial vaccine"
>	

19-AUG-1999;

N-PSDB; AAZ51336

```
The polypeptide is prepd. by genetic engineering of genes encoding the P. falciparum circumsporozoite (CS) protein [Dame et al., Science 225: 593 (1994)], and the influence virus non-structural protein [NSI), [Base et al., Nucleic Acids Research, 8: 5945 (1980)]. The DNA encoding the 1st 91 AAS of the N-terminal of NSI (1980)]. The DNA encoding the 1st 91 AAS of the N-terminal of NSI (NSI_81) is linked via a synthetic sequence to DNA encoding Region turn is fused to DNA encoding Region [1.contg. flanking regionless the 18 AA signal region, which in turn is fused to DNA encoding Region [1.contg. flanking region sess the first nine N-terminal AAS. This CS fusion is designated REIGelias). The Pro residue separating the ASP (at the C-terminal of the linker) from Rifeliate9 is an artifact of a filled in BamHI site. The peptide can be used in a vaccine for protection against
                                                                                                                                                                                                                                                                                                                                                       /label= AAS 297-412 of CS protein
/note= "Rejoon II flanking region minus 9 N-term-
inglon II flanking region minus 9 N-term-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Polypeptide comprising immunogenic determinants from P falciparum - for vaccine against malaria infection in humans.
                                                                                                                                                                           "Influenza virus nonstructural protein 1"
                             Immunogenic determinant; circumsporozoite; CS; vaccine; malaria; hybrid; influenza virus; non-structural protein 1; fusion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13.1%; Score 252; DB 12; Length 309; larity 45.0%; Pred. No. 7.8e-13; Conservative 1; Mismatches 1; Indels 64
                                                                                                                                                                                                                                                                                    /label= AAs 19-123 of CS protein
/note= "Region 1 contg. flanking region less
signal sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             See also AAR12306-R12311 and AAR13176-R13179.
                                                                                                                                                            /label= N-terminal of NS1
                                                                                                                                                                           /note= "Influenza virus n
82..87
/label= synthetic linker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hollingdale MR;
                                                                                                                                                                                                                                           `label= artifact
'note= "see comments"
                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 1; Page 7; 18pp; English.
                                                                          Plasmodium falciparum.
Influenza virus (A/PR/8/34/).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      89US-0447746.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      90EP-0313257.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (SMIK ) SMITHKLINE BEECHÂM.
(USSA ) US SEC OF THE ARMY.
(BIOM-) BIOMEDICAL RES INST.
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                                                                                                                                                                                                                                                                                                                                          194..309
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gordon DM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1991-179771/25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
ses 54; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             309 AA;
NS1_81-RLfdelta9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      08-DEC-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      06-DEC-1990;
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                                                                                                                                                                                                                                                                                                                                                                                                                         EP432965-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gross MS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                            Peptide
                                                                                                                               Key
Region
                                                                                                                                                                                                                              Region
                                                                                                                                                                                                                                                                            Region
                                                                                                                                                                                                                                                                                                                                            Region
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Matches
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 qq
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                                                                                                                                                                                                                                                                                                       ELYKPNDKSLYQYIKANSKFIGITELSNTFINNAGQHGHMHGNEREDERTLTKEYEDIVL 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DIEKKICKMEKCSSVFNVVNSNSGCFRHLDEREECKCLLEDSGSNGKKITCECTKPDSKP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 IVQYDNFNANPNANPNANPDGNCEDIPHVNEFSAIDLGNAEKYDKMDEPQHYGKSLTPLE 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 241 KEFTYMINFGRGONYWEHPYQKSDQPKQYEQHLTDYEKIKEGKPLDKFGNIYDYHYEHSS 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                           Novel recombinant protein as vaccine for treating malarial infection comprises antigenic peptides obtained from different stages of plasmodium falciparum life cycle -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MKFLVNVALVFMVVYISYIYADHHHHHHHKHKKLKQPGDGNPWSPCSVTCGKPKDELDYEN 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels .0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 100.0%; Score 1923; DB 21; Length 350; Best Local Similarity 100.0%; Pred. No. 5.8e-151; Matches 350; Conservative 0; Mismatches 0; Indels .0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PSSTKSSSPSNVKSASLATRLMKKFKAEIRDFFGISYYEKVLAKYKDDLE 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (NAIM-) NAT INST IMMUNOLOGY.
(USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                            Claim 3; Page 43-44; 52pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ŕ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR13175 standard; Protein; 309
                                                                                                                                Lal AA, Shi YP, Hasnain SE;
                99WO-US18869.
                                              98US-0097703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                              WPI; 2000-237654/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         350 AA;
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Sequence

19

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à g 181 181

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2;

Gaps

64;

29-AUG-1991

AAR13175;

AAR13175

301

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301

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AAR13176 standard; Protein; 319 AA.

**AAR13176** 

(first entry)

29-AUG-1991

AAR13176;

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5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          239 eqylkkiknsistewspcsvtcgngiqvrikpgsankpkdeldyendlekkickmekcss 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            239 istewspcsvtcgngiqvr1kpgsankpkdeldyendiekkickmekcssvfnvvnssig 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
42 ----WSPCSVTCG------KPKDELDYENDIEKKICKMEKCSSVFNVVNSNSG 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----KPKDELDYENDIEKKICKMEKCSS 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The product is useful in preparation of vaccines for treatment and prophylaxis of plasmodium sporozite infection. It may be easily produced in large pure quantities(from a transformed E.coli expression system.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New polypeptide used in malaria vaccine - comprises immunogenic determinants from 1st and 2nd flanking regions of plasmodium surface protein and intermediate repeat domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12.8%; Score 247; DB 11; Length 319; 41.5%; Pred. No. 2.Je-12; ative 1; Mismatchés 1; Indels 74
                                                                                                                                                                                                                                                                            89.193
/Jabel- Fragment of circumsporozite protein
204..319
                                                                                                                                                                                                                                                                                                                 /label- Fragment of circumsporozite protein
                                                                                                                                                                                                                                            1..81
/label= NS181 protein fragment
/note= "from plasmid pMG-1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 2; Page 11-12; 24pp; English.
                                                                                                                                                                                                                                Location/Qualifiers
                                                                                AAR07945 standard; protein; 319 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29 KHKKLKQPGDGNP------
                                                                                                                                                       NS181RLFAuth plasmid product.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             42 -------WSPCSVTCG
                                                                                                                                                                                                                                                                                                                                                                                         90EP-0304720
                                                                                                                                                                                                                                                                                                                                                                                                              89US-0346863
                                                                                                                                                                                                                                                                                                                                                                                                                                      (SMIK ) SMITHKLINE BEECHAM
                                                                                                                                22-FEB-1991 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  r matcn
Local Similarity 41.5'
les 54; Copservative
                                                                                                                                                                                                       Plasmodium falciparum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gross MS, Young JF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1990-350299/47.
N-PSDB; AAQ06580.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          319 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VENVVNSNSG 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      expression system.
                                                                                                                                                                                Malaria; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                        01-MAY-1990;
                                                                                                                                                                                                                                                                                                                                                                                                              03-MAY-1989;
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                                                                                                                                                                                                                                                                                                                                        EP398540-A.
                                                                                                        AAR07945;
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Domain
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the P. falciparum circumsporozoite (CS) protein | Dame et al.,

Science 225: 593 (1984), and the influenza virus non-structural

Science 225: 593 (1984), and the influenza virus non-structural

protein 1 (NSI), | Baez et al., Nucleic Acids Research, 8 : 5845

(1980)]. The DNA encoding the 1st 81 AAs of the N-terminal of NSI

(NSI,81) is linked via a synthetic sequence to DNA encoding Region

I contg. flanking regionless the 18 AA signal region. Which in

turn is fused to DNA encoding Region II-contg. flanking region.

C This CS fusion is designated REfAuth. The Pro residue separating

the Asp (at the C-terminal of the linker) from REfAuth is an arti-
fact of a filled in BamHr site; the Gly separating Region I and

C Region II-contg. CS flanking regions is an artifact of a synthetic

FORI/TATHII I linker. The peptide can be used in a vaccine for

protection against malaria.

The complete nucleotide and AA sequences are given in EP-304720,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The polypeptide is prepd. by genetic engineering of genes encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Polypeptide comprising immunogenic determinants from P falciparum - for vaccine against malaria infection in humans.
                                                                                                     Immunogenic determinant; circumsporozoite; CS; vaccine; malaria;
hybrid; influenza virus; non-structural protein 1; fusion.
                                                                                                                                                                                                                                       'note= "Influenza virus nonstructural protein 1"
                                                                                                                                                                                                                                                                                                                                 /note= "Region 1 contg. flanking region less signal sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                    /note="see comments"
|195..39
|/labl= AAs 288-412 of CS protein
|/note= "Region II flanking region"
                                                                                                                                                                                                            1..81
/label= N-terminal of NS1
                                                                                                                                                                                                                                                        82..87
/label= synthetic linker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hollingdale MR;
                                                                                                                                                                                                                                                                                                                "see comments"
                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 2; Page 10; 18pp; English.
                                                                                                                                                                                                                                                                                                  /label= artifact
                                                                                                                                                                                                                                                                                                                                                                                                        /label= artifact
                                                                                                                                            Plasmodium falciparum.
Influenza virus (A/PR/8/34).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         90EP-0313257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     89US-0447746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (SMIK ) SMITHKLINE BEECHAM. (USSA ) US SEC OF THE ARMY. (BIOM-) BIOMEDICAL RES INST.
                                                                                                                                                                                                                                                                                                                             89..193
/label- 4
                                                                                                                                                                                                                                                                                                                  'note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gordon DM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1991-179771/25.
                                                                       NS1_81-RLfAuth.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         06-DEC-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     08-DEC-1989;
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AAR13179;
       Gross MS,
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                                                                                                                                                                                                                                                                                                                                                               RESULT
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                                                              ;;
                                                                                           179 khkikqqqqqqqnknnqqnqqqqqqhnmpndpnrnvdenanannavknnnneepsdkhi 238
                                                                                                                   42 ------WSPCSVTCG------KPKDELDYENDIEKKICKMEKCSS
                                                                                                                                                                                                                                                                                                                           note= "Influenza virus nonstructural protein 1"
                                                                                                                                                                                                                                                         circumsporozoite; CS; vaccine; malaria; non-structural protein 1; fusion.
                                                              74;
                                                                                                                                                                                                                                                                                                                                                                                  /label= artifact
/note= "see comments"
105..209
/label= AAs 19-123 of CS protein
/note= "Region 1 contg. flanking region less signal sequence"
                                               Length 319;
                                                                1; Indels
                                                                                                                                                                                                                                                                                                                                            /label= immunodominant repeat region
/note= "four tetrapeptide repeat units"
                                                                                                                                                                                                                                                                                                                                                                                                                                   /label= artifact
/note="see comments"
/label= AAS 288-412 of CS protein
/note= "Region II flanking region"
                                               Score 247; DB 12;
Pred. No. 2.1e-12;
1; Mismatches 1;
    filed May 1, 1990.
See also AAR12306-R12311 and AAR13175-R13179.
                                                                                                                                                                                                                                                                                                                  1..81
/label= N-terminal of NS1
                                                                                                                                                                                                                                                                                                                                                            98..103
/label= synthetic linker
                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                              AAR13178 standard; Protein; 335 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (SMIK) SMITHKLINE BEECHAM.
(USSA) US SEC OF THE ARMY.
(BIOM.) BIOMEDICAL RES INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                89US-0447746.
                                                  12.8%;
41.5%;
                                                                                                                                                                                                                                                                                  Plasmodium falciparum.
Influenza virus (A/PR/8/34).
                                                                                                                                                                                                                             29-AUG-1991 (first entry)
                                                                                29 KHKKLKQPGDGNP-----
                                                                                                                                                                                                                                                            Immunogenic determinant;
hybrid; influenza virus;
                                                  Query Match 12.8
Best Local Similarity 41.5
Matches 54; Conservative
                                                                                                                                                                                                                                            NS1_81(NANP)4RLfAuth.
                                                                                                                                                    1111111: 1
299 vfnvvnssig 308
                                                                                                                                            75 VFNVVNSNSG 84
                            319 AA;
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                                                                                                                                                                                                               AAR13178;
                              Sequence
                                                                                                                                                                                                                                                                                                                                                              Peptide
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Region
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                                                                                                                                                                                   RESULT
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The polypeptide is prepd. by genetic engineering of genes encoding the P. falciparum circumsporozoite (CS) protein [Dame et al., ct he P. falciparum circumsporozoite (CS) protein [Dame et al., ct he protein in (NS1), [Bagz et al., Nucleic Acids Research, 8 : 5845 ct (1980)]. The DNA encoding the ist 81 AAs of the N-terminal of NS1 (NS1_81) is linked to a synthetic sequence encoding four repeat curies from the immunodominant region, which in turn is linked via a synthetic sequence to DNA encoding Region I contg. flanking region a synthetic sequence to DNA encoding Region II-contg. flanking region is an artifact of a filled-in BamHI crostic. Cs flanking region is an artifact of a filled-in BamHI crostic. Cs flanking region is an artifact of a filled-in BamHI crostic. Site; the Gly separating the Region is an artifact of a filled-in BamHI crostic. Cs flanking region is an artifact of a filled-in BamHI crostic. Site; the Gly separating the Region is an artifact of a filled-in BamHI crostic can be used in a yaccine for protection against malaria. See also AAR12306-R12311 and AAR13175-R13179.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              42 ------WSPCSVTCG------KPKDELDYENDIEKKICKMEKCSS 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "Influenza virus nonstructural protein 1" 82..97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Immunogenic determinant; circumsporozoite; CS; vaccine; malaria;
hybrid; influenza virus; non-structural protein 1; fusion.
                                                                                               Polypeptide comprising immunogenic determinants from P falciparum for vaccine against malaria infection in humans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 335;
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pred. No. 2.3e-12;
1; Mismatches 1;
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/label= N-terminal of NS1
Hollingdale MR;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR13179 standard; Protein; 335 AA.
                                                                                                                                                                                              Example 4; Page 11; 18pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12.8%;
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Influenza virus (A/PR/8/34).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 54; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29 KHKKLKQPGDGNP----
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  Gordon DM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1111111: 1
315 vfnvvnssig 324
                                                      WPI; 1991-179771/25
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 335 AA;
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AAR13177 standard; Protein; 327 AA.
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                            AAR13177;
                                                                                                                                                                                        Peptide
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 AAR13177
                              The polypeptide is prepd. by genetic engineering of genes encoding the P falciparum circumsporozoite (CS) protein [Dame et al., Science 225: 593 (1984)], and the influenza virus non-structural protein 1 (NSI), [Baez et al., Nucleic Acids Research, 8: 5845 (1980)]. The DNA encoding the 1st 81 AAs of the N-terminal of NSI (NSI_al) is linked to a synthetic sequence encoding four repeat units (the variant form) from the immunodominant region, which in turn is linked via a synthetic sequence to DNA encoding Region I contg. flanking region less the 18 AA signal region. This is linked to DNA encoding Region II-contg. flanking region II-contg. Cs. the Region I-contg. CS flanking region is an artifact of a filled-in BamHI site; the Gly separating the Region I and II-contg. CS flanking region is an artifact of a filled-in BamHI site; the Gly separating the Region I in and II-contg. CS flanking region is an artifact of a synthetic Fokl/TthIII I inter. The peptide can be used in a vaccine for protection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            255 eqylkkiknsistewspcsvtcgnglqvrikpgsankpkdeldyendiekkickmekcss 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Polypeptide comprising immunogenic determinants from P falciparum - for vaccine against malaria infection in humans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12.8%; Score 247; DB 12; Length 335;
41.5%; Pred. No. 2.3e-12;
ative 1; Mismatches 1; Indels 74;
              /no.c. 209
/label- AAs 19-123 of CS protein
/note- "Region 1 contg. flanking region less
signal sequence"
                                                                                               /label- AAs 288-412 of CS protein
/note- "Region II flanking region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   See also AAR12306-R12311 and AAR13175-R13178. O
                                                                                                                                                                                                                                                 Gross MS, Gordon DM, Hollingdale MR;
/label= artifact
/note= "see comments"
                                                                        /note="see comments"
211..335
                                                                                                                                                                                                                                                                                                                      Example 5; Page 11; 18pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29 KHKKLKQPGDGNP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (62)
                                                                                                                                                                                                                             (BIOM-) BIOMEDICAL RES INST
                                                                                                                                                                   90EP-0313257
                                                                                                                                                                                       89US-0447746
                                                                                                                                                                                                         SMIK ) SMITHKLINE BEECHAM.
                                                                                                                                                                                                                     USSA ) US SEC OF THE ARMY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       54; Copservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                    WPI; 1991-179771/25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  315 vfnvvnssig 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       335 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        75 VFNVVNSNSG 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linker. The pe
against malaria
                                                                                                                                                                   06-DEC-1990;
                                                                                                                                                                                       08-DEC-1989;
                                                                                                                                               19-JUN-1991
                                                                                                                            EP432965-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                   Region
                                                         Region
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RESULT

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The polypeptide is prepd. by genetic engineering of genes encoding the P. falciparum circumsporozoite (CS) protein [Dame et al., Science 225: 593 (1984)], and the influenza virus non-structural protein 1 (NS1), [Baez et al., Nucleic Acids Research, 8: 5845 (1980)]. The DNA encoding the 1st 81 AAs of the N-terminal of NS1 (NS1_81) is linked via a synthetic sequence to DNA encoding Region I contg. flanking region less the 18 AA signal region. This is linked to a synthetic sequence encoding two repeat units from the immunodominant region, which in turn is fused to DNA encoding Region II-contg. flanking region. The Pro residue separating the Asp (at the C-terminal of the linker) from the Region I-contg. C flanking region is an artifact of a filled-in Bamil site; the Gly separating the repeat units and the Region II-contg. CS flanking region is an artifact of a synthetic FOKI/TthIII I linker. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Polypeptide comprising immunogenic determinants from P falciparum - for vaccine against malaria infection in humans.
                                                                                                                                     Immunogenic determinant; circumsporozoite; CS; vaccine; malaria;
hybrid; influenza virus; non-structural protein 1; fusion.
                                                                                                                                                                                                                                                                                                                                                                                                                                          "Influenza virus nonstructural protein 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "Region 1 contg. flanking region less
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "two tetrapeptide repeat units"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /label= immunodominant repeat region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          203..327
/label- AAs 288-412 of CS protein
/note= "Region II flanking region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           89.193
/label= AAs 19-123 of CS protein
                                                                                                                                                                                                                                                                                                                                                                          1..81
/label- N·terminal of NS1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     signal sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /label= synthetic linker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hollingdale MR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "see comments"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="see comments"
203..327
                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /label= artifact
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /label= artifact
                                                                                                                                                                                                                                 Plasmodium falciparum.
Influenza virus (A/PR/8/34/).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     89US-0447746.
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(USSA ) US SEC OF THE ARMY.
(BIOM-) BIOMEDICAL RES INST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  90EP-0313257
29-AUG-1991 (first entry)
                                                               NS1_81-RLfAuth + (NANP)2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        . 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                 'note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gross MS, Gordon DM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1991-179771/25.
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Length 108;

SSXS

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Query Match
Best Local Similarity
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                                  Matches
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                                                                           δλ
                                                                                                         qq
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention relates to non-natural variants of a C-terminal fragment of a Plasmodium merozoite surface protein-1 (MSP-1). The non-natural variants have reduced affinity for at least 1 antibody capable of blocking a second antibody that inhibits the proteolytic cleavage of plasmodium MSP-1_4_2, and has the same affinity for at least one third antibody that inhibits the proteolytic Cleavage of plasmodium MSP-1_4_2, and has the same affinity for at least MSP-1_4_2, compared to natural MSP-1_1_9. The non-natural variants of the present invention are useful for immunising a mammal against malaria, and can be used to treat malaria. The present sequence is MSP-119 protein.
                                                                                                                                                2
                                                                                                                                          Gaps-f
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                                                                                                                                                                                                                                                                             179 khkkikqpgdgnpdpnanpnanpnknhqgngqghnmpndpnrnvdenanannavknnnn 238
                                                                                                                                                                                    --- 41
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel variants of the C-terminal fragment of Plasmodium merozoite surface protein-1, useful as vaccines for treating or preventing malaria -
   peptide can be used in a vaccine for protection against malaria.
See also AAR12306-R12311 and AAR13175-R13179.
                                                                                                                                                    82;
                                                                                                               Length 327;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Merozoite surface protein; protazoacide; vaccine; malaria.
                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Syed S,
                                                                                                               Score 243; DB 12;
Pred. No. 4.7e-12;
1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Feeney J, Morgan W,
                                                                                                                                                                                                                                                                 ---WSPCSVTCG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 5; Fig 15; 126pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB37609 standard; Protein; 108
                                                                                                                                                       ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Merozoite surface protein-119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99GB-0009072.
99US-0311817.
99CA-2271451.
                                                                                                                   / 12/6%;
39.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20-APR-2000; 2000WO-GB01558.
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                                                                                                                                                                                                                                                                                                                                                                         316
                                                                                                                                                                                                                                                                                                                                       84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27-FEB-2001 (first entry)
                                                                                                                                      Local Similarity 39.1 nes 54; Conservative
                                                                                                                                                                                                                                                                                                                                                            ckmekcssvfnvnssig
                                                                                                                                                                                                                                                                                                                                        67 CKMEKCSSVFNVNSNSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Birdsall B,
                                                                                                                                                                                          KHKKLKQPGDGNP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Plasmodium falciparum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-015762/02.
N-PSDB; AAC68977.
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                                                               327 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200063245-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13-MAY-1999;
25-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Holder A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB37609;
                                                                   Sequence
                                                                                                                       Query Match
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                                                                                                                                            Best Loca
Matches
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Sequence of the CS gene (AAN81108) is from lambda-mPfl. A recombinant DNA molecule is claimed, comprising functional DNA coding sequence fused, in phase, to a portion of the Pre-S2 region of a hepatitis B Virus (HBV) Pre-S3-protein coding sequence. The functional DNA coding sequence comprises the Pre-S2 coding sequence, Pre-S1 coding sequence, pre-S1 coding sequence or entire Plasmodium, or a HIV coding sequence such as an HIV coding sequence such as an HIV envelope gene sequence, e.g. HIV C7 protein coding region, HIV Peptide 121 coding region, or HIV Dreesman peptide coding region.
                         .,
                                                                                                 -- EDSGSNGKKIT 110
                         Gaps
                                                                                                             23.HHHHHHHKHKKLKQPGDGNPWSPCSVTCGKPKDELDYENDIEKKICKMEKCSSVFNVVNSN 82
                                                                   them
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Repeat region, repeat unit = NANPNVDP"
211..286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA encoding hepatitis B virus antigens and hybrids contg. thused for expression in yeast to obtain vaccines and bivalent vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Repeat region, repeat unit = NANP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Repeat region, repeat unit = NANP"
                          Indels
                                                                                                                                                                                                                                                                                                               Sequence encoded by the circumsporozoite (CS) gene from
                                                                                                                                                                                                                                                                                                                                                  antigen; immunogen; probe; hybridisation;
Score 222; DB 22;
Pred. No. 5.4e-11;
8; Mismatches 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example; Fig 3Aa-3Af; 101pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ż
                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                        AAP83144 standard; protein; 411 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                        106..120
/note="Region 1"
147..206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Harford
  11.5%;
35.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     87US-0009325.
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                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ..206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cabezon T, De Wilde M,
                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (SMIK ) SMITH KLINE-RIT
                                                                                                      83 SGCFRHLDEREECKCLL--
                                                                                                                                                                                                                                                                                                                                                                     Immunoassay; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                             Plasmodium falciparum.
                                                                       Plasmodium falciparum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1988-229751/33
                                                                                                                                                      111 CECTKPDSKPI 121
                                                                                                                                                                    N-PSDB; AAN81108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25-JAN-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-JAN-1987;
                                                                                                                                                                                                                                                                                           20-NOV-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17-AUG-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EP278940-A.
                              47;
                                                                                                                                                                                                                                                                     AAP83144;
                                                                                                                                                                                                                                                                                                                                                          Vaccine;
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AAP80835 standard; protein; 412 AA
          71 KCSSVFNVVNSNSG
                                                                                                              18-SEP-1990
                                                                                           AAP80835;
                                                            AAP80835
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                                                   ä,
                                                                                  ıı ||:|
328 khiegylkkikn-sistewspcsvtcgngnqvrikpgsankpkdeldyendiekkickme 386
                                                    Gaps
                                                                      --KPKDELDYENDIEKKICKME 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The Plasmodium CS gene was used to isolate peptides capable of inducing an immune response to the parasite. Peptide antigens may be synthesised in pure form and used to generate an immune response in vaccination against malaria. The featured repeat units are claimed and must be present in popies of 2-1000. Sequence 412 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New immunologically active pure synthetic peptide(s) - used for protection against infection by malaria parasite.
                                                   19:
                               Length 411;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Socre 215.5; DB 7; Length 412
pred. No. 1.2e-09;
2; Mismatches 7; Indels 1
                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Schneider I;
                              Score 215.5; DB 9;
Pred. No. 1.2e-09;
2; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                L
S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dame JB, Williams JL,
                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                     /label- Repeat unit
                                                                                                                                                                                    AAP60416 standard; Protein; 412 AA.
                                                                      29 KH----KKLKQPGDGNPWSPCSVTCG--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Fig 2; 49pp; English.
                                                                                                                                                                                                                                                  CS protein of malaria parasite.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11.2%;
                              11.2%;
62.2%;
                                                                                                                                                                                                                                                                                                                                                                                                 85EP-0107794.
                                                                                                                                                                                                                                                                                                                                                                                                                      84US-0624564
                                                                                                                                                                                                                                                                                                                                                                                                                                        (USDC ) US SEC OF COMMERCE. (USGO ) US GOVERNMENT. (USSA ) US SEC OF THE ARMY.
                                                                                                                                                                                                                             (first entry)
                                      Best Local Similarity 62.2
Matches 46; Conservative
                                                                                                                                                                                                                                                                      Sporozoite; vaccination.
                                                                                                                       387 kcssvfnvvnssig 400
                                                                                                              84
                                                                                                                                                                                                                                                                                          Plasmodium falciparum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1986-008635/02.
                                                                                                             71 KCSSVFNVVNSNSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
411 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; AAN60362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  McCutchan TF,
                                                                                                                                                                                                                                                                                                                                                                                                                      26-JUN-1984;
                                                                                                                                                                                                                                                                                                                                                                                                 24-JUN-1985;
                                                                                                                                                                                                                             13-JUN-1991
                                                                                                                                                                                                                                                                                                                                                                            02-JAN-1986
                                                                                                                                                                                                                                                                                                                                                        EP166410-A.
                                                                                                                                                                                                        AAP60416;
                              Query Match
 Sequence
                                                                                                                                                                                                                                                                                                                          Region
                                                                                                                                                                 RESULT 10
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Plasmid WR201 was obtained from the Walter Reed Army Institute of
Research, and results from insertion of a 2.3 kb EcoRI fragment from
lambda mpfl encoding the complete CS protein gene P. falciparum into
vector pUC8. A recombinant DNA vector is claimed, which comprises a DNA
sequence contg. the coding sequence of the CS P. falciparum into
Inked to an expression control sequence. Prefd. expression control
sequences include the yeast glyceraldehyde-3P-dehydrogenase gene (TDH3)
promoter and the yeast ornithine carbamoyl transferase gene (TDH3)
promoter and the yeast ornithine carbamoyl transferase gene (TDH3)
promoter and the yeast ornithine carbamoyl transferase gene (TDH3)
promoter and the yeast ornithine carbamoyl transferase gene (TDH3)
promoter and the yeast ornithine carbamoyl transferase gene (TDH3)
promoter and the yeast ornithing its first first 50bp. Also claimed is a
transformed host cell, a method of culturing the call to produce CS, the
protein coding sequence, minus its first 50bp. Also claimed is a
transformed host cell, a method of culturing the call to produce CS, the
contain, and a vaccine. The vector comprises a 192 bp Sau3A fragment
coding for 16 tetrapeptide repeats of the P. falciparum CS protein
derived from Sau3A digestion of a 1215 bp StuI-RsaI fragment of WR201
containing the P. falciparum CS protein coding sequence minus
approx. its first 50 bp, or two, three, four or more tandem copies of
such 192 bp Sau3A fragment.
                                                                                                                                                                                                                          Circumsporozoite gene; Plasmodium falciparum; lambda mPfl; vaccine;
                                                                                                                                                                                                                                                                yeast glyceraldehyde-3P-dehydrogenase gene (TDH3) promoter;
yeast ornithine carbamoyl transferase gene (ARG3); repeat region.
                                                                                        Sequence encoded by the circumsporozoite (CS) gene of Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Expression of P. falciparum circumsporozoite protein by yeast using recombinant DNA vector having coding sequence linked to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="repeat region, repeat unit=NANPNVDP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="repeat region, repeat unit=NANP"
212..287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="repeat region, repeat unit=NANP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
124..147
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      87US-0008791.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (SMIK ) SMITH KLINE RIT SA.
(first entry)
                                                                                                                                       falciparum in lambda mPfl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      148..207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gathoye AM;
                                                                                                                                                                                                                                                                                                                                                                                                           Plasmodium falciparum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1988-235171/33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAN81781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-JAN-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-JAN-1987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO8805817-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11-SEP-1988.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  De Wilde M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Region
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412 AA;

Sequence

KH----KKLKQPGDGNPWSPCSVTCG------KPKDELDYENDIEKKICKME 70

Conservative

46;

Matches 29

g

ð

3

19; Gaps

'n

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11-NOV-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-NOV-1991;
27-FEB-1992;
                                                                                                                                                                                                                                                                                                       RTS* protein
                                                                                                                                                                                                                                                                                     27-SEP-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO9310152-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27-MAY-1993
                                                                                                                                                                                                                                                                                                                                        strain 768;
S protein.
                                                                                                                                                                                                                                                                                                                                                                    Synthetic.
                                                                                                                                                                                                                                                                   AAR37797:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cohen J,
                                                                      response.
                                                                                      Sequence
                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                  cloning;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                 Protein
                                                                                                                          Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Region
                                                                                                                                                                                                                                                                                                                                                                                             Region
                                                                                                                                                                                                                                                                                                                                                                                                                Region
                                                                                                                                                                                                                                  RESULT 13
                                                                                                                                                                                                                                                                                                                         RTS;
                                                                                                                                 Matches
                                                                                                                                                                                                                                           AAR37797
                                                                                                                                                                                                                                                                    8×33333333333
                                                                                                                                                                    Dp
                                                                                                                                                                                     δ
                                                                                                                                                                                                       g
                                                                                                                                                    δ
                          ë,
                                                                                                                                                                                                                                                                                                 'note= "Derived from S. cerevisiae TDH3 gene sequence"
                                                      This sequence represents the RTS hybrid protein which is encoded by the RTS expression cassette. This hybrid consists of a methionine residue derived from S. cerevisiae TDH3 gene sequence, three amino acids, Met-Ala-Pro, derived from a nucleotide sequence created by the cloning procedure used to construct the hybrid gene, a stretch of 189 amino acids representing amino acids 210 to 398 of the
                           Gaps
                                                                                                                                                                                                                                                                                                                                   of
                                          29 KH-----KKLKQPGDGNPWSPCSVTCG------KPKDELDYENDIEKKICKME 70
                                                                                                                                                                                                                                                                                                                                                             (adw
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hybrid protein comprising Plasmodium circumsporozoite protein and HBsAg - useful as a vaccine for treating patients susceptible to Plasmodium infections
                                                                                                                                                                                                                                                                                                                                    the CSP
                                                                                                                                                                                                                 RTS; expression cassette; hybrid protein; S. cerevisiae; TDH3; cloning; circumsporozoite protien; CSP; Plasmodium falciparum; strain 7G8; hepatitis B virus; HBV; adw serotype; preS2 protein;
                           19;
                                                                                                                                                                                                                                                                                                                                                          /note= "Carboxy terminal amino acids from HBV serotype) preS2 protein"
        Length 412;
                                                                                                                                                                                                                                                                                                                                    oţ
         Score 211.5; DB 9; Length Pred. No. 2.6e-09; 3; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                        /note= "S protein of HBV (adw serotype)"
                                                                                                                                                                                                                                                                                                                                   /note= "Represents amino acids 210-398
                                                                                                                                                                                                                                                                                                                   'note= "Cloning artefact"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS
                                                                                                                                                                                                                                                                                                                                             P. falciparum"
                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                              AAR37796 standard; Protein; 424 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Fig 5; 59pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              91GB-0024390.
92US-0842694.
                                                                                                                                                                                                                                                                                                                                                                                                                                             92WO-EP02591.
           11.0%;
60.8%;
                                                                                                                                                                                  (first entry)
            Query Match
Best Local Similarity 60.8
Matches 45; Conservative
                                                                                                                                                                                                                                                                                                                                                      194..197
                                                                                                                                                                                                                                                                                                                                                                               198..424
                                                                                          71 KCSSVFNVVNSNSG 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            De Wilde M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1993-182494/22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; AAQ42566.
                                                                                                                                                                                                                                                                                                                                                                                                                                             11-NOV-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-NOV-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27-FEB-1992;
                                                                                                                                                                                                                                                                                                                                                                                                           WO9310152-A.
                                                                                                                                                                                                                                                                                                                                                                                                                             27-MAY-1993
                                                                                                                                                                                 27-SEP-1993
                                                                                                                                                                                                   RTS protein
                                                                                                                                                                                                                                                S protein.
                                                                                                                                                                                                                                                                Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cohen J,
                                                                                                                                                               AAR37796;
                                                                                                                                                                                                                                                                                                                                                                                  Protein
                                                                                                                                                                                                                                                                                                                             Protein
                                                                                                                                                                                                                                                                                                            Region
                                                                                                                                                                                                                                                                                                                                                       Region
                                                                                                                                                                                                                                                                                           Region
                                                                                                                                                                                                                                                                                  Key
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/note= "Derived from S. cerevisiae TDH3 gene sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                          circumsporozoite protien (CSP) of Plasmodium falciparum strain 7GB, an amino acid Arg created by the cloning procedure, four amino acids, pro-val-Thr-Asn, representing the four carboxy terminal residues of hepatitis B virus (HBV), adw serotype, pres2 protein, and a stretch of 226 amino acids specifying the S protein of HBV, adw serotype. This protein, and RTS* (see also AAR37797), may be combined with adjuvant and used in a vaccine for preventing plasmodium infections. The vaccines produce a humoral response and also a cellular immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "Represents amino acids 210-398 of the CSP of
                                                                                                                                                                                                                                                                                                                                                                                                                                29 KH-----KKLKQPGDGNPWSPCSVTCG------KPKDELDYENDIEKKICKME 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "Carboxy terminal amino acids from HBV (adw
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                expression cassette; hybrid protein; S. oerevisiae; TDH3; ing; circumsporozoite protien; CSP; Plasmodium falciparum; in 7G8; hepatitis B virus; HBV; adw serotype; preS2 protein;
                                                                                                                                                                                                                                                                                                                                                                                   19;
                                                                                                                                                                                                                                                                                                                                    14; Length 424;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "S protein of HBV (adw serotype)"
                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                 Score 210.5; DB 14;
Pred. No. 3.3e-09;
1; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                serotype) preS2 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "Cloning artefact"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P. falciparum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAR37797 standard; Protein; 424 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        91GB-0024390.
92US-0842694.
                                                                                                                                                                                                                                                                                                                                    10.9%;
ilarity 63.4%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      92WO-EP02591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             198..424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 194..197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 De Wilde M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1993-182494/22.
N-PSDB; AAQ42567.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      81
                                                                                                                                                                                                                                                                                                                                                                   1 Similarity
45; Conserv
                                                                                                                                                                                                                                                                    424 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               71 KCSSVFNVVNS
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This is the amino acid sequence of a recombinant protein comprising amino acids 1613-1705 of the Plasmodium falciparum merozoite surface protein 1 (MSP1) 19 kD C-terminal fragment (p19), linked to a glycosylphosphatidylinositol membrane anchoring sequence. p19 is the C-terminal fragment of the 42 kD MSP1 from Plasmodium species. The recombinant protein can be used for the production of anti-malarial vaccines, where the p19 fragment provides a high level of protective immunity since it includes epitopes not presented in the p42 fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "amino acids derived from P. falciparum MSP1 p19 fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "glycosylphosphatidylinositol anchoring sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Recombinant protein containing the merozoite surface protein-1 p19 fragment - useful in anti-malarial vaccines, diagnosis and protein purification
                                                                                                                                                                                                                                                                                                                                                                                                                              10.3%; Score 198.5; DB 18; Length 116;
llarity 44.2%; Pred. No. 5.3ez09;
Conservative 5; Mismatches 9; Indels 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Plasmodium vivax; merozoite surface protein; MSP1; p19; Plasmodium falciparum; malaria; vaccine; immunity; epitope.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nato F;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       59 ENDIEKKICKMEKCSSVFNVVNSNSGCFRHLDERECKCLL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ------EDSGSNGKKITCECTKPDSKPI 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mendis K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW22592 standard; Protein; 116 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                        Disclosure; Fig 1B; 85pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Longacre-Andre S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PfMSP1(p19)A protein sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (INSP ) INST PASTEUR.
(UYNY ) UNIV NEW YORK STATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97WO-FR00291.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25-MAR-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Plasmodium falciparum
                                        WPI; 1997-425033/39.
                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 42; Conserv
                                                                                                                                                                                                                                                                                                                                                                             ¥,
                                                         N-PSDB; AAT94550
                                                                                                                                                                                                                                                                                                                                                                             116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO9730159-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Barnwell JW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14-FEB-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14-FEB-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-AUG-1997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic
                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW22592;
     Roth C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Roth C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW22592
     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5
                                                                                                     This sequence represents the RTS* hybrid protein which is encoded by the RTS* expression cassette. This hybrid consists of a methionine created derived from S. cerevisiae TDH3 gene sequence, three amino acids. Met-Ala-Pro, derived from a nucleotide sequence created by the cloning procedure used to construct the hybrid gene, a stretch of 189 amino acids representing amino acids 210 to 398 of the circumsporozoite protien (GSP) of Plasmodium falciparum strain NFS4, an amino acida Arg created by the cloning procedure, four amino acids, on amino acid Arg created by the cloning procedure, four amino acids, or hepatitis B virus (HBV), adw sercype, pres2 protein, and a stretch of 226 amino acids specifying the S protein of HBV, adw sercype. This protein, and RTS (see also AAR37796), may be combined with an adjuvant and used in a vaccine for preventing plasmodium infections. The vaccines produce a humoral response and also a cellular (fmuule).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              96..116
/note= "glycosylphosphatidylinositol anchoring sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note- "amino acids derived from P. falciparum MSP1 p19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hybrid protein comprising Plasmodium circumsporozoite protein and HBsAg – useful as a vaccine for treating patients susceptible to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9; Indels 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14; Length 424;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               epitope.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Longacre-Andre S, Mendis K, Nato F;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Plasmodium vivax; merozoite surface protein; MSP1; Plasmodium falciparum; malaria; vaccine; immunity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 207.5; D
Pred. No. 5.9e-
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---GNPWSPCSVTCG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW36103 standard; Protein; 116 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              fragment"
                                                                          Disclosure; Fig 9; 59pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PfMSP1(p19)A protein sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62 IEKKICKMEKCSSVFNVVNSNSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10.8%;
51.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PASTEUR.
NEW YORK STATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97WO-FR00290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 51.8
Matches 43; Conservative
                                      Plasmodium infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Plasmodium falciparum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29 KHKKLKQPGD---
                                                                                                                                                                                                                                                                                                                                                                                                           424 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (INSP ) INST
(UYNY ) UNIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Barnwell JW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO9730158-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-MAR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14-FEB-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14-FEB-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW36103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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Region
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This is the amino acid sequence of a recombinant protein comprising amino acids 1613-1705 of the Plasmodium falciparum merozoite surface protein 1 (MSP1) 19 kD C-terminal fragment (p19), linked to a glycosylphosphatidylinositol membrane anchoring sequence. p19 is the C-terminal fragment of the 42 kD MSP1 from Plasmodium species. The recombinant protein can be used for the production of anti-malarial vaccines, where the p19 fragment provides a high level of protective immunity since it includes epitopes not presented in the p42 fragment.
                                                                  Recombinant protein containing Plasmodium merozoite surface protein-1 p42 fragment - useful in antimalarial vaccines, also new antibodies for diagnosis and protein purification
                                                                                                                                                             Disclosure; Fig 1B; 85pp; French.
WPI; 1997-425034/39.
P-PSDB; AAW22592.
                                                                                                                                                                                                                                                                                                                                                                                                                        Seguence
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100 ------EDSGSNGKKITCECTKPDSKPI 121 54 nnggcdadakcteedsgsngkkitcectkpdsypl 88 δ

; ;

Gaps

39;

Query Match
Best Local Similarity 44.2%; Pred. No. 5.3e-09;
Matches 42; Conservative 5; Mismatches 9; Indels 39;

59 ENDIEKKICKMEKCSSVFNVVNSNSGCFRHLDEREECKCLL---

q

Search completed: January 29, 2002, 10:21:40 Job time: 416 sec

Sequence 130, App Sequence 7603, Ap Sequence 7603, Ap Sequence 12299, A Sequence 7601, Ap Sequence 7601, Ap Sequence 12297, A Sequence 11070, A Sequence 35195, A Sequence 31198, A Sequence 31188, A Sequence 31818, A

Sequence

30545, A

Sequence Sequence Sequence

Sequence

Title: Perfect score:

Run on:

Sednence:

Scoring table:

Searched:

Database :

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US-09-084-471C-13
US-10-005-368-261
US-09-08-427-30545
US-09-708-427-30545
US-09-708-427-7603
US-09-708-427-7603
US-09-708-427-12299
US-09-708-427-12299
US-09-708-427-12297
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US-09-980-916-44
US-09-708-427-31818
US-09-708-427-31816
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Pred. No. 1.7e-08;
5; Mismatches 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DIEKKICKMEKCSSVFNVVNSNSGCFRHLDEREECKCLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SQUERAL INFORMATION
SQUERAL INFORMATION
APPLICANT: Birdsall, Berry
APPLICANT: Birdsall, Berry
APPLICANT: Birdsall, Berry
APPLICANT: Borgall, Berry
APPLICANT: Morgal, William
APPLICANT: Syed, Shabih
TITLE OF INVENTION: Malaria Vaccine
FILE REFERENCE: 18396/1005
CURRENT PILING DATE: 2001-10-16
PRIOR APPLICATION NUMBER: COT/GB00/01558
PRIOR PILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: 09/311,817
PRIOR PILING DATE: 1999-05-13
PRIOR FILING DATE: 1999-05-25
PRIOR FILING DATE: 1999-05-25
PRIOR FILING DATE: 1999-05-25
PRIOR FILING DATE: 1999-04-20
NUMBER OF SEQ ID NOS: 3
SOFTWARE: PATENTIN VETSION 3.0
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Sequence 2, Application US/09978756
GENERAL INFORMATION:
APPLICANT: Holder, Anthony
APPLICANT: Birdsall, Berry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Plasmodium falciparum
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Best Local Similarity
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US-09-978-756-1
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613, App
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13367, A
14308, A
13366, A
14306, A
14306, A
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1 MKFLVNVALVFMVVXISYIY......DFFGISYYEKVLAKYKDDLE 350
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Sequence 20
Sequence 7,
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/cgn2_6/ptodata/2/paa/NCG6_NEW_COMB.pep:*
/cgn2_6/ptodata/2/paa/USO7_NEW_COMB.pep:*
/cgn2_6/ptodata/2/paa/USO9_NEW_COMB.pep:*
/cgn2_6/ptodata/2/paa/USO9_NEW_COMB.pep:*
/cgn2_6/ptodata/2/paa/USO9_NEW_COMB.pep:*
/cgn2_6/ptodata/2/paa/USO0_NEW_COMB.pep:*
                           GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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S-09-117-415B-18
S-09-117-415B-10
S-09-269-874A-1
S-09-269-874A-3
S-09-269-874A-3
S-09-269-874A-3
S-09-445-096A-70
S-09-718-756-3
S-09-718-758-3
S-09-718-758-3
S-09-718-758-3
S-09-718-77-813-8
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US-09-978-756-2

US-09-117-415B-22

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US-09-269-874A-7

US-09-269-874A-7

US-09-269-874A-5

US-09-269-874A-5

US-09-269-874A-5

US-09-269-874A-7

US-09-708-477-143

US-09-708-427-1336

US-09-708-427-1336

US-09-708-427-1433

US-09-708-427-1433

US-09-708-427-1433

US-09-708-427-143

US-09-708-471-6-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   173191 seqs, 36597120 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUMMARIES
                                                                                                                                                                                   January 29, 2002, 10:16:24
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Maximum Match 100%
Disting first 45 summaries
                                                                                                                                   OM protein - protein search, using sw model
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Maximum DB seq length: 2000000000
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Gaps -- 99 53

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108 108 105.5 5.5

Score

Result ş 1996.5 1996.5 1996.5 1996.5 1996.5 1996.5 1996.5 1996.5 1996.5

Length 96; Indels

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US-09-117-446B-22
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Yang, Shutong
TITLE OF INVENTION: Malaria Vaccine Based Upon the Addition
of a NSAl Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Coleman, COLEMAN SUDOL SAPONE, PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 376;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 196.5; DB 5
Pred. No. 8.7e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/117,415B
FILING DATE: 29-Jul-1998
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        316 GGCDADAKCTEEDSGSNGKKITCECTKPDSYPL 348
                                                                                          CURRENT APPLICATION NUMBER: US/09/978,756
CURRENT FILING DATE: 2001-10-16
PRIOR APPLICATION NUMBER: PCT/GB00/01558
PRIOR FILING DATE: 2000-04-20
PRIOR FILING DATE: 1999-04-20
PRIOR APPLICATION NUMBER: 09/311,817
PRIOR APPLICATION NUMBER: 2,271,451
PRIOR FILING DATE: 1999-05-25
PRIOR PELING DATE: 1999-05-25
PRIOR PELING DATE: 1999-05-25
PRIOR FILING DATE: 1999-05-25
NUMBER OF SEQ ID NOS: 3
SOFTWARE: PatentIn version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: R12-030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WordPad (ASCII)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: Henry D. Coleman,
STREET: 714 Colorado Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Coleman, Henry D. REGISTRATION NUMBER: 32,559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 679-0090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2) Application US/09117415B; Sequence 2) Application US/09117415B; GENERAL INFORMATION:
APPLICANT: Engine chuirond
                                                          TITLE OF INVENTION: Malaria Vaccine FILE REFERENCE: 18396/1005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (212) 679-9121
RMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 594 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Plasmodium falciparum
US-09-978-756-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10.2%;
44.1%;
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Feeney, James
                                      Syed, Shabih
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION
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518 NISQHQCVKKQCP-----QNSGCFRHLDEREECKCLLNYKQEGDKCVENPNPTCNENN 570
                                                                                                                                                                                                                                     :| : | ::| 481 NISQHQCVKKQCP-----QNSGCFRHLDEREECKCLLNYKQEGDKCVENPNPTCNENN 533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Davidson, Eugene
Yang, Shutong
TITLE OF INVENTION: Malaria Vaccine Based Upon the Addition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Coleman, COLEMAN SUDOL SAPONE, PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 613;
                                                                                                                 Length 594;
                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10.2%; Score 196.5; DB 5; 44.1%; Pred. No. 1.6e-07;
                                                                                                                 DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .6e-07;
                                                                                                                 Score 196.5; DB 5 Pred. No. 1.5e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 DIEKKICKMEKCSSVFNVVNSNSGCFRHLDEREECKCLL-
                                                                                                                                                                                                             61 DIEKKICKMEKCSSVFNVVNSNSGCFRHLDEREECKCLL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/09/117,415B
FILING DATE: 29-Jul-1998
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5; Mismatches
                                                                                                                                                                                                                                                                                                                              534 GGCDADAKCTEEDSGSNGKKITCECTKPDSYPL 566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100 ------EDSGSNGKKITCECTKPDSKPI 121
                                                                                                                                                                                                                                                                                                      100 ------EDSGSNGKKITCECTKPDSKPI 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: R12-030 TELECOMMUNICATION : TELEPHONE: (212) 679-0090 TELEFAX: (212) 679-9121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     of a MSA1 Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO:
US-09-117-415B-22
MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO:
US-09-117-415B-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Henry D. Coleman STREET: 714 Colorado Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Coleman, Henry D. REGISTRATION NUMBER: 32,559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 22 Application US/09117415B GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: WordPad (ASCII)
CURRENT APPLICATION DATA:
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LENGTH: 613 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
                                                                                                               10.2%;
44.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 22
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                                                                                                                 Query Match 10.2%
Best Local Similarity 44.1%
Matches 41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Bridgeport
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
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Sequence 16, Application US/09117415B
GENERAL INPORMATION:
APPLICANT: Davidson, Eugene
Yang, Shutong
TITLE OF INVENTION: Malaria Vaccine Based Upon the Addition
NUMBER OF SEQUENCES: 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 39;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10.2%; Score 196.5; DB 5
44.1%; Pred. No. 1.6e-07;
tive 5; Mismatches 8
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPAG (ASCII)
CURRENT APPLICATION DATE:
FILING DATE: 29-Jul-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 DIEKKICKMEKCSSVFNVVNSNSGCFRHLDEREECKCLL
                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/117,415B
FILING DATE: 29-Jul-1998
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  571 GGCDADAKCTEEDSGSNGKKITCECTKPDSYPL 603
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                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Coleman, Henry D.
REGISTRATION NUMBER: 32,559
REFERENCE/DOCKET NUMBER: R12-030
TELECOMMUNICATION INFORMATION:
TELEPAR: (212) 679-0090
TELEFAR: (212) 679-0121
INFORMATION FOR SEQ ID NO: 20:
                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPad (ASCII)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TOPOLOGY: linear; MOLECULE TYPE: protein; SEQUENCE DESCRIPTION: SEQ ID NO: 20: US-09-117-4158-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Henry D. Coleman,
STREET: 714 Colorado Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Coleman, Henry D.
REGISTRATION NUMBER: 32,559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 679-0090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 631 amino acids
TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 16:
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COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match 10.2%
Best Local Similarity 44.1%
Matches 41; Conservative
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536 NISQHQCVKKQCP-----QNSGCFRHLDEREECKCLLNYKQEGDKCVENPNPTCNENN 588
                                                                                                                                   APPLICANT: Davidson, Eugene
Yang, Shutong
TITLE OF INVENTION: Malaria Vaccine Based Upon the Addition
of a MSAl Peptide
CORRESPONDENCES: 24
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                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Henry D. Coleman, COLEMAN SUDOL SAPONE,
STREET: 714 Colorado Avenue
CITY: Bridgeport
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READBALE FORM:
MEDUUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPad (ASCII)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/117,415B
FILING DATE: 29-Jul-1998
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 DIEKKICKMEKCSSVFNVVNSNSGCFRHLDEREECKCLL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: COLOMAN, HOLY D.
REGISTRATION NUMBER: 32,559
REFERENCE/DOCKET NUMBER: R12-030
TELEPHONE: (212) 679-0090
TELEFAX: (212) 679-9121
INFORMATION FOR SEO ID NO: 18:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10.2%; Score 196.5;
44.1%; Pred. No. 1.6e
tive 5; Mismatches
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MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 18:
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ADDRESSEE: Henry D. Coleman,
STREET: 714 Colorado Avenue
RESULT 5
US-09-117-4/5B-18
'Sequence' 18, Application US/09117415B
'FORMATION:
CANDERAL MECRMATION:
CANDER OF THE 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10, Application US/09117415B INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 631 amino acids TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: Connecticut
COUNTRY: USA
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ZIP: 10017
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Best Local Similarity
Matches 41; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-117-415B-18
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36216 SEQUENCE CHARACTERISTICS: LENGTH: 649 amino acids

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QQ
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                                                                                                                                                                                                                                         :| :: | ::| ONSGCFRHLDEREECKGLLNYKQEGDKCVENPNPTCNENN 588
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                                                                                                                                            Length 649;
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APPLICANT: Bulard, Hermann
TITLE OF INVENTION: Recombinant Process for Preparing a TITLE OF INVENTION: Complete Malaria Antigen, GP190/MSP1; FILE REFERENCE: GRUE-003
CURRENT APPLICATION UNDBER: US/09/269,874A; CURRENT FILING DATE: 1999-08-02
PRIOR FILING DATE: 1997-10-02
PRIOR FILING DATE: 1997-10-02
PRIOR FILING DATE: 1996-10-02
NUMBER OF SEQ ID NOS: 8
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 7, Application US/09269874A; GENERAL INFORMATION:
APPLICANT: Bujard, Hermann
TITLE OF INVENTION: Recombinant Process for Preparing a
TITLE OF INVENTION: Complete Malaria Antigen, GP190/MSP1
FILE REFERENCE: GRUE-003
CURRENT APPLICATION NUMBER: US/09/269,874A
CURRENT FILING DATE: 1999-08-02
PRIOR APPLICATION NUMBER: PCT/EP97/05441
PRIOR APPLICATION NUMBER: DE 19640817.2
PRIOR FILING DATE: 1996-10-02
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                                                                                                                                                                                 Indels
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44.1%; Pred. No. 5e-07;
tive 5; Mismatches 8;
                                                                                                                                          Score 196.5; DB 5;
Pred. No. 1.7e-07;
5; Mismatches 8;
                                                                                                                                                                                                                       61 DIEKKICKMEKCSSVFNVNSNSGCFRHLDEREECKCLL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 DIEKKICKMEKCSSVFNVVNSNSGCFRHLDERECKCLL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1560 GGCDADAKCTEEDSGSNGKKITCECTKPDSYPL 1592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100 ------EDSGSNGKKITCECTKPDSKPI 121
                                                                                                                                                                                                                                                                                                ---EDSGSNGKKITCECTKPDSKPI 121
                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 8 SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 7
TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-09-117-4158-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: Plasmodium falciparum US-09-269-874A-7
                                                                                                                                                10.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match
Best Local Similarity 44....
Best Local Similarity 44....
                                                                                                                                                Query Match 10.29
Best Local Similarity 44.19
Matches 41; Conservative
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US-09-269-874A-7
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1526 NISQHQCVKKQCP-----QNSGCFRHLDEREECKCLLNYKQEGDKCVENPNPTCNENN 1578
                                                                                                                                                                                                                                                   1526 NISQHQCVKKQCP-----QNSGCFRHLDEREECKCLLNYKQEGDKCVENPNPTCNENN 1578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 1639;
                                                                                                                               Length 1621;
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                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Bujard, Hermann
TITLE OF INVENTION: Recombinant Process for Preparing a
TITLE OF INVENTION: Complete Malaria Antigen, GP190/MSP1
FILE REFERENCE: GRUE-003
CURRENT APPLICATION NUMBER: US/09/269,874A
CURRENT FILING DATE: 1999-08-02
PRIOR APPLICATION NUMBER: PCT/EP97/05441
PRIOR APPLICATION NUMBER: DE 19640817.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 10.2%; Score 196.5; DB 5; Best Local Similarity 44.1%; Pred. No. 5.2e-07; Matches 41; Conservative 5; Mismatches 8;
                                                                                                                                    DB 5;
                                                                                                                               Score 196.5; DB 5,
Pred. No. 5.1e-07;
5; Mismatches 8;
                                                                                                                                                                                                                           61 DIEKKICKMEKCSSVFNVVNSNSGCFRHLDEREECKCLL--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENUERAL INFORMATION:
GENUERAL INFORMATION:
APPLICANT: Holder, Anthony
APPLICANT: Hidsall, Berry
APPLICANT: Morgan, William
APPLICANT: Speed, Shabih
TITLE OF INVENTION: Malaria Vaccine
FILE REFRENCE: 18396/1005
CURRENT FILING DATE: 2001-10-16
                                                                                                                                                                                                                                                                                                                                               1579 GGCDADAKCTEEDSGSNGKKITCECTKPDSYPL 1611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    --- EDSGSNGKKITCECTKPDSKPI 121
                                                                                                                                                                                                                                                                                                                         100 ------EDSGSNGKKITCECTKPDSKPI 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR FILING DATE: 1996-10-02
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 1639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT FILING DATE: 2001-10-16
PRIOR APPLICATION NUMBER: PCT/GB00/01558
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: 09/311,817
PRIOR FILING DATE: 1999-05-13
PRIOR APPLICATION NUMBER: 2,271,451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-269-874A-3; Sequence 3, Application US/09269874A; GENERAL INFORMATION:
LENGTH: 1621
TYPE: PRT
ORGANISM: Plasmodium falciparum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Plasmodium falciparum
                                                                                                                                       10.28;
44.18;
                                                                                                                                         Query Match 10.2%
Best Local Similarity 44.1%
Matches 41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100 ----
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US-09-978-756-3
                                                                      US-09-269-874A-5
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/note= "fusion protein composed of
                                                                                                                                                                                                                                                                                              Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/09/402,181A
FILING DATE: 29-Sep-1997
CLASSIFICATION: CURROWN>
                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    melittin signal sequence and full length hTRT protein" sequence bescription: SEQ ID NO: 613:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 015389-002620US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-0CT-1996
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
FILING DATE: 06-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/911,312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 14-AUG-1997
PPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Ausenhus, Scott L. REGISTRATION NUMBER: 42,271
                                                                                                                 Sequence 613, Application US/09402181A
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 613:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 1189 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS: <Unknown>TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                            Morin, Gregg B.
Harley, Calvin B
                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
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       577 GVSQDTSTN-
                                                                                              US-09-402-181A-613
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                                                                                                                                                                                                                                                                                                                                                                                                        101 DSGSNGKKITCECTKPDSKPIVQYDNFNANP-----NANPNANPDGNCEDIPHVNEF 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       481 STGFEKPSTSFVGNEEI-GSIIDGKGLNDEVN-NQIEDETVPVSNKEY-----YEY 529
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 530 NYGRPNKQFTKKINASVQKNPAYFGQH------DKFYFNGNYYDLSAKEANKL 576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         192 -- OYIKANSKFIGITELSNTFINNAGQHGHMHGNEREDER--TLTKEYEDIVLKEFTYMI 247
                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                     43;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Wang, Ouijun
APPLICANT: Vang, Yan-Ping
APPLICANT: Vang, Yan-Ping
APPLICANT: Valein, Michel H.
TITLE OF INVENTION: LACTOFERRIN RECEPTOR GENES OF MORAXELLA
FILE REFERENCE: 1038-989 MIS
CURRENT APPLICATION NUMBER: US/09/445,096A
CURRENT APPLICATION NUMBER: 003-22
PRIOR APPLICATION NUMBER: 003-62
PRIOR FILING DATE: 1997-06-03
PRIOR FILING DATE: 1998-06-02
NUMBER OF SEQ ID NOS: 77
SOFTWARE: PALENTIN Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 905;
                                                                                                                                                                                                                                                                                      DB 5; Length 394;
                                                                                                                                                                                                                                                                                                                                  11; Indels
                                                                                                                                                                                                                                                                                                                                                                              50 GKPKDELDYENDIEKKICKMEKCSSVFNVVNSNSGCFRHLDEREECKCLL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     133 ENPNPTCNENNGGCDADATCTEEDSGSSRKKITGECTKPDSYPL 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100 -----TDSGSNGKKITCECTKPDSKPI 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 5;
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                                                                                                                                                                                                                                                                                    Score 187.5; DB Pred. No. 4.5e-07
                                                                                                                                                                                                                                                                                                                             7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1) Score 109.5; ilarity 21.4%; Pred. No. 1.2; Conservative 32; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 70, Application US/09445096A GENERAL INFORMATION:
PRIOR FILING DATE: 1999-05-25
PRIOR APPLICATION UNMBER: 9909072.2
NUMBER OF SEQ ID NOS: 3
SOFTWARE: Patentin version 3.0
SEQ ID NO 3
LENGTH: 394
                                                                                                                                                                                     ; ORGANISM: Plasmodium falciparum US-09-978-756-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Moraxella catarrhalis
                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 41.3%;
Matches 43; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Loosmore, Sheena M. APPLICANT: Du, Run-Pan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 61; Conserv
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                                                                                                                                                                  TYPE: PRT
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Sequence 30543, Application US/09708427
; Sequence 30543, Application US/09708427
; GENERAL INFORMATION:
; GENERAL INFORMATION:
; GENERAL INFORMATION:
; TITLE OF INVENTION: THEREBY
; CURRENT APPLICATION NUMBER: US/09/708,427
; CURRENT FILING DATE: 2000.11-09
; NUMBER OF SEO ID NOS: 83364
; SOFTWARE: PATENTIN version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     72 CS-----SVFNVVNSNSGCFRHLDEREECKCLLEDSGSNGKKITCECTKPDSKPIVQYD 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             63 CHGPDHELSLEN-----GHMTERSCYVCRVSIQGMFYK---CRQCSFEAHPLCTYA 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           126 NFNANP------NANDNANPDGNCEDIPHVNEFSAIDLGNAEKYDKMDEPQHY 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  111 PMHASSPDLLVTKQRSLHGHAGQPSPPHQYGQGIPY------GYPHMGQPEPY 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   173 GKSLTPLEELYKPNDKSLYQYIKANS---KFIGITELSNTFINNAGQHGHMHGNEREDER 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25 HHHHKHKKLKQPGDGNPWSPCSVTCGKPK------DELDYENDIEKKICK---MEK 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                230 TLTKEYEDIVLKEFTYMINFGRGONYWE---HPYQKSDQPKQYEQHLTDYEKIKEGKP 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9 HFTHNHLLTQVNGIG----TYTCDGCKLYGEGRTYRCSDCDYDLHEYCATCPSILLNS
                                                             LOCATION: 1..1189
CTHER INFORMATION: /note= "fusion protein composed of melitrin signal sequence and full length hTRT protein"
SEQUENCE DESCRIPTION: SEQ ID NO: 613:
US-09-721-477-613
                                                                                                                                                                                                                                                                      Score 108; DB 5; Length 1189;
Pred. No. 2.2;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 105.5; D. Pred. No. 0.62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc_feature
LOCATION: 1..286
OTHER INFORMATION: Xaa is any amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ), OTHER INFORMATION: Ceres Seq. ID 1829492
US-09-708-427-30543
                                                                                                                                                                                                                                                                                                                         ;
0
                                                                                                                                                                                                                                                                                                                                                                                              1 MKFLVNVALVFMVVXISYIYAD 22
                                                                                                                                                                                                                                                                                                                                                                        1 MKFLVNVALVFMVVYISYIYAD 22
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                                                                                                                                                                                                                                                                             5.6%; 8
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                        protein
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TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                         Conservative
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Best Local Similarity
Matches 60; Conserva
                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 22; Conservē
                        MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 30543
LENGTH: 286
                                            FEATURE
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                                                                                             0;
                                                                                                  Gaps
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0
                                              5.6%; Score 108; DB 5; Length 1189;
100.0%; Pred. No. 2.2;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IMP PC compatible
COMPUTER: IMP PC compatible
COMPUTER: IMP PC compatible
COMPUTER: Datentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/721,477
FILING DATE: 22-Nov-2000
CLASSIFICATION CURROWN>
PRIOR APPLICATION NUMBER: 08/974,549
FILING DATE: CONKNOWN>
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/851,843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 727
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
FILING DATE: 10-CT-1997
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-CCT-1997
APPLICATION NUMBER: WO PCT/US97/17885
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILLING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/911,312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 613:
                                                                                                                                                                                                                                                                                    Sequence 613, Application US/09721477; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Greeg B.
Harley, Calvin B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 01-OCT-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                1 MKFLVNVALVFMVVYISYIYAD 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS
                                                                                                  Conservative
                                                        Query Match
Best Local Similarity
Matches 22; Conserv
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13;

Gaps

91;

7

Search completed: January 29, 2002, 10:58:07 Job time: 2503 sec

us-09-763-397a-2.rapn

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

January 29, 2002, 10:15:49; Search time 144.96 Seconds (without alignments) 183.920 Million cell updates/sec Run on:

US-09-763-397A-2 Title: Perfect score:

1923 1 MKFLVNVALVFMVVXISYIY......DFFGISYYEKVLAKYKDDLE 350 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

219241 seqs, 76174552 residues Searched:

219241 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR\_68:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	circumsporozoite p	circumsporozoite p	circumsporozoite p		ozoite	merozoite surface	major merozoite su	probable major sur	apical membrane an	circumsporozoite p																			
SUMMARIES	ID	45	OZZQAF	A54529	A39756	S05428	S47282	SAZOGM	A45948	A45545	805603	SAZQK1	A54498	A26868	A24594	A32499	B44986	A44986	D44986	C44986	OZZQAB	OZZÓAL	OZZOAS	OZZOAC	OZZQAM	A60610	A44969	A29319	A32068	OZZQAV
	DB	~	Н	~	~	~	7	Н	~	7	7	-	~	~	~	~	7	7	~	~	-	Н	-	-	<del>, -</del>	~	7	~	~	-
	Length	424	412	442	388	405	651	1726	1726	400	1639	1631	1701	1701	1640	622	622	622	622	622	378	378	398	401	419	485	264	343	367	378
ď	Ouery Match	11.3	11.2	11.1	10.8	10.8	10.4	10.4	10.4	10.2	10.2	10.2	9.6	9.6		9.3		9.0		•	•	•				•	•		•	•
	Score	216.5	215.5	213.5	208.5	207.5	200.5	200.5	200.5	196.5	196.5	196	187.5	187.5	186	179	174	172.5	171.5	171	135	135	135	135	133	129	126	125	125	125
	Result No.	-	7	m	4	Ŋ	ø	7	∞	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	

circumsporozoite p	crecomsborozore b	circumsporozoite p	circumsporozoite p	thrombospondin-rel	circumsporozoite p	erythrocyte-bindin	circumsporozoite p	circumsporozoite p	66K merozoite surf	hypothetical prote	protein-tyrosine k	circumsporozoite p	rhoptry-associated	serine/threonine-s	. apical membrane an
A48571	D41130	C41156	A41156	S04531	OZZOMY	A37793	OZZÓMB	OZZOBK	A39238	E71616	T18287	A54504	S27833	H71621	A44944
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386	38/	387	395	559	367	1435	332	348	563	1247	1338	429	782	2485	295
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6.5	0.0	6.5	6.5	6.5	6.5	6.4	6.4	6.4	6.4	6.4	6.4	6.3	6.3	6.3	9
125 6.5	125 6.5	125 6.5	125 6.5	_	_	_	_	_	_	123 6.4	_	_	_	_	119.5 6.3

## ALIGNMENTS

RESULT

	A54533
	circumsporozoite protein - malaria parasite (Plasmodium falciparum) (strain T4, Thail
	C;Species: Plasmodium falciparum
-	C;Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 09-Jun-2000
	C; Accession: A54533
	R;del Portillo, H.A.; Nussenzweig, R.S.; Enea, V.
_	Mol. Biochem. Parasitol. 24, 289-294, 1987
	A; Title: Circumsporozoite gene of a Plasmodium falciparum strain from Thailand.
_	A; Reference number: A54533; MUID:87315205
_	A; Accession: A54533
	A;Status: preliminary
_	A; Molecule type: DNA
_	A; Residues: 1-424 <del></del>
	A; Cross-references: GB:M19752; NID:q160216; PIDN:AAA29555.1; PID:q160217
	C; Superfamily: circumsporozoite protein; thrombospondin type 1 repeat homology
	F;348-402/Domain: thrombospondin type 1 repeat homology <thr1></thr1>

## Length 424; DB 2; Score 216.5; 11.3%; Query Match

	Gaps	KC 72
	13; Gaps	KICKME
	Indels	DYENDIEK
:80-	12;	KPKDEL
red. No. 3.3e	3; Mismatches 12; Indels	
Ξ.	er G	SVTCG
Best Local Similarity 61.1%; Pred. No. 3.3e-U8;	Matches 44; Conservative 3	26 HHHKHKKLKQPGDGNPWSPCSVTCGKPKDELDYENDIEKKICKMEKC 72
al Sin	44;	HHHKH
Rest Poc	Matches	26 1
-	_	οy

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84 73 SSVFNVVNSNSG ò

QQ

RESULT 2
OracoAF
circumsporozoite protein - malaria parasite (Plasmodium falciparum) (isolate IMTM22)
C;Species: Plasmodium falciparum
C;Species: Plasmodium falciparum
C;Date: 15-Nov-1984 #sequence\_revision 15-Nov-1984 #text\_change 09-Jun-2000
C;Accession: A03388
R;Dame, J.B.; Williams; J.L.; McCutchan, T.F.; Weber, J.L.; Wirtz, R.A.; Hochmayer, W. Science 225, 593-599, 1984
A;Title: Structure of the gene encoding the immunodominant surface antigen on the spony; Aritle: Structure of the gene encoding the immunodominant surface antigen on the spony; Accession: A03388; MUID:84250215
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-412 < CDAM>A;Residues: 1-412 < CDAM>A;Cross-references: GB:K02194; NID:9160160; PIDN:AAA29524.1; PID:9160161
A;Experimental source: clone 768
C;Comment: Residues 1-16 are the probable signal sequence.
C;Comment: Residues 1-16 are the probable signal sequence.
C;Comment: There are 41 copies of a 4-residue repeating unit in the middle domain of C;Superfamily: circumsporozoite protein; thrombospondin type 1 repeat homology
F;336-390/Domain: thrombospondin type 1 repeat homology

```
A;Status: translation not shown
A;Status: translation not shown
A;Necule type: DNA
A;Nesidues: 1-405 <CAM>
A;Nesidues: 1-405 <CAM>
A;Coss-references: EMBL:X15363
A;Cross-references: EMBL:X15363
B;Caspers, P.; Gentz, R.; Mathle, H.; Pink, J.R.; Sinigaglia, F.
R;Caspers, P.; Gentz, R.; Mathle, H.; Pink, J.R.; Sinigaglia, F.
A;Caspers, P.; Gentz, R.; Muthle, H.; Pink, J.R.; Sinigaglia, F.
A;Title: The circumsporozoite protein gene from NF54, a Plasmodium falciparum isolate
A;Reference number: A45527; MUID:89364998
A;Reference preliminary
A;Relecule type: DNA
A;Residues: 1-405 <CAS>
A;Residues: 1-405 <C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Cross-references: GB:M22982; GB:J04650; NID:9160168; PIDN:AAA29527.1; PID:9160169
A; Cross-references: GB:M22982; GB:J04650; NID:9160168; PIDN:AAA29527.1; PID:9160169
B; Cockyer, M.J.; Marsh, K.; Newbold, C.I.
Mol. Biochem: Parasitol. 37, 275-280, 1989
A; Title: Wild isolates of Plasmodium falciparum show extensive polymorphism in T cell
A; Reference number: A60657; MUID:90114334
A; Accession: I60657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RO-71)
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merozoite surface antigen 1 - malaria parasite (Plasmodium falciparum) (strain RO-71

G:Species: Plasmodium falciparum

A;Variety: strain RO-71

C:Date: 06-Jan-1995 #sequence_revision 26-Jul-1996 #text_change 09-Jun-2000

C;Accession: S47282

Submitted to the EMBL Data Library, July 1994

A;Pescription: Plasmodium falciparum: recombination within the C-terminal region of a A;Reference number: S47282

A;Reference number: S47282

A;Rocession: S47282

A;Rocession: S47282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Title: DNA sequence of the gene encoding a Plasmodium falciparum malaria candidate A;Reference number: S05428; M0ID:89345189
A;Accession: S05428
                                                                                                                                                                                                                                                         - malaria parasite (Plasmodium falciparum) (isolate NF54)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5
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A;Residues: 319-336, 334-373 <LOC>
C;Superfamily: circumsporozoite protein; thrombospondin type 1 repeat homology
F;329-383/Pomain: thrombospondin type 1 repeat homology <THR1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: EMBL:235329; NID:9535257; PIDN:CAA84558.1; PID:9535258
A;Experimental source: strain RO-71
C;Superfamily: major merozoite surface antigen
C;Keywords: glycoprotein; merozoite; surface antigen
                                                                                                                                                                                                                                                                          circumsporozoite protein - malaria parasite (Plasmodium falciparum) (isolate C;Species: Plasmodium falciparum C;Species: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 09-Jun-2000 C;Accession: S05428; A45527; I60657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Status: preliminary; not compared with conceptual translation
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Pred. No. 1.4e-07;
4; Mismatches 9;
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1 Similarity 51.8%;
43; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic Acids Res. 17, 5854, 1989
                                              SSVFNVVNSSIG 377
84
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Best Local Similarity
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    SSVFNVVNSNSG
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        73
                                                                                366
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Cispeciaes: Plasmodium reichenowi
Cispeciaes: 14-Feb-1992 #sequence_revision 14-Feb-1992 #text_change 20-Aug-1999
Cispeciaes: 14-Feb-1992 #sequence_revision 14-Feb-1992 #text_change 20-Aug-1999
Cispeciaes: 18-Fig. 1992 Cispecial Astral, Astral,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Lockyer, M.J.; Schwarz, R.T.
R;Lockyer, M.J.; Schwarz, R.T.
Mol. Biochem. Parasitol. 22, 101-108, 1987
A;Title: Strain variation in the circumsporozoite protein gene of Plasmodium falciparum.
A;Reference number: A54529; MUID:87115616
A;Accession: A54529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           circumsporozoite protein - malaria parasite (Plasmodium falciparum) (strain Wellcome) (Species: Plasmodium falciparum C;Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 09-Jun-2000 C;Accession: A54529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ä
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A;Residues: 1-388 <LALD
A;Cross-references: GB:M60972; NID:g160228; PIDN:AAA29561.1; PID:g160229
A;Cross-references: GB:M60972; NID:g160228; PIDN:AAA29561.1; PID:g160229
C;Superfamily: circumsporozoite protein; thrombospondin type 1 repeat homology
F;312-366/Domain: thrombospondin type 1 repeat homology <THR1>
                                                                                        3;
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                                                                                                 Gaps
                                                                                                                                                                         --KPKDELDYENDIEKKICKME 70
                                                                                                 19;
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            Length 412;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: preliminary; not compared with conceptual translation A;Molecule type: DNA A;Residues: 1-442 <LOC>
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                DB 1;
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Pred. No. 5.8e-08;
1; Mismatches 12
            Score 215.5; DB 1
Pred. No. 3.8e-08;
2; Mismatches 7.
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                                                                                                                                                                                          KH----KKLKQPGDGNPWSPCSVTCG---
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Best Local Similarity 59.7%;
Matches 43; Conservative
                         11.2%;
62.2%;
                             Query Match
Best Local Similarity 62.23
Matches 46; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                 84
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                                                                                                                                                                                                                                                                                                                                                      71 KCSSVFNVVNSNSG
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Best Local S:
Matches 42
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Gispecies: Plasmodium falciparum (fragments c) Species: Plasmodium falciparum) (fragments c) Species: Plasmodium falciparum (c) Species: Plasmodium falciparum (c) Species: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 09-Jun-2000 (c) Accession: A45545 (c) Accession: A4545 (c) Accession: A4545 (c) Accession: A4546 (c) Accession: A4546 (c) Accession: A4546 (c) Accession: A4546 (c) Accession: A4545 (c) Accession: A4546 (c) Accession: A4546
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             - malaria parasite (Plasmodium falciparum)
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C;Species: Plasmodium falciparum
C;Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 09-Jun-2000
C;Accession: S05603; S04850
R;Myler, P.J.
submitted to the EMBL Data Library, April 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1606 GKFQDML----NISQHQCVKKQCP------ENSGCFRHLDEREECKCLLNYKQEGDKCV 1654
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287 NISQHQCVKKQCP-----QNSGCFRHLDEREECKCLLNYKQEGDKCVENPNPTCNENN 339
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A;Accession: $05603
A;Molecule type: mRnA
A;Residues: 1-1639 <MYL>
A;Cross-references: EMBL:X15063; NID:q9896; PIDN:CAA33163.1; PID:q9897
R;Myler, P.J.
                                                                                                                                                                                                                                                                                                                                                       43;
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                                                                                                                                                                                                                                                                             Score 200.5; DB 2;
Pred. No. 2.7e-06;
6; Mismatches 10;
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Pred. No. 8.5e-07;
5; Mismatches 8;
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                         A;Molecule type: DNA
A;Residues: 1-1726 <CHA>
A;Cross-references: GB:M37213
C;Superfamily: major merozoite surface antigen
C;Reywords: surface antigen
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10.2%;
Best Local Similarity 44.1%;
Matches 41; Conservative
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Best Local Similarity 43.3%;
Matches 45; Conservative
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A; Molecule type: mRNA
preliminary
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C;Species: Plasmodium falciparum
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jun-2000
C;Accession: A45948
R;Chang, S.P.; Kramer, K.J.; Yamaga, K.M.; Kato, A.; Case, S.E.; Siddiqui, W.A.
A;Title: Plasmodium falciparum: gene structure and hydropathy profile of the major meroz
A;Reference number: A45948; MUID:89005525
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Nucleic Acids Res. 14, 3311-3323, 1986
A;Title: Variation in the gene encoding a major merozoite surface antigen of the human A;Reference number: A23386; WUID:86205236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Accession: A23386
A; Molecule type: DNA
A; Residues: 1-1104 (AVBB1>
A; Cross-references: EMBL: X03831
A; Cross-references: EMBL: Lyon, J.A.; Wolff, R.
Nucleic Acids Res. 16, 1206, 1988
A; Title: Merozoite surface protein sequence from the Camp strain of the human malaria A; Accession: S06361: MUID: 88143999
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A.Residues: 1104-1726 <WEB2>
A.Crosszereferences: EMBL:X03831
C.Comment: The merozoite stages of different strains have strain-specific surface c.C.Comment: The merozoite stages of different strains have strain-specific surface c.C.Comment: P. falciparum has three stages: sporozoite, merozoite, and gametocyte. J.C.Superfamily: major merozoite surface antigen
C.Keywords: glycoprotein: merozoite; surface antigen; tandem repeat
F.1-19/Domain: signal sequence #status predicted <SIG>F.20-1736/Froduct: major merozoite surface antigen #status predicted <MAT>F.57-765/Region: 3-residue repeats (S-G-T)
F.77-765/Region: 3-residue repeats (T-E-E)
F.133,272,501,567,638,827,839,924,944,990,1016,1114,1221,1613,1658/Binding site: CR
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M
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C;Date: 30-Sep-1987 #sequence_revision 31-Mar-1991 #text_change 09-Jun-2000
C;Accession: A23386; S06361
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                                                                                                                                    43;
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Best Local Similarity 43.3%; Pred. No. 2.7e-06;
Matches 45; Conservative 6; Mismatches 10; Indels 43;
                                                                      651;
                                                                      Length
                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    50 GKPKDELDYENDIEKKICKMEKCSSVFNVVNSNSGCFRHLDEREECKCLL-
                                                                                                                                                                                                       50 GKPKDELDYENDIEKKICKMEKCSSVFNVVNSNSGCFRHLDEREECKCLL
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                                                                                                                                                                                                                                                                                                                                                                                        580 ENPNPTCNENNGGCDADAKCTEEDSGSNGKKITCECTKPDSYPL 623
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                                                                                                                                                                                                                                                                                                                                                   ------EDSGSNGKKITCECTKPDSKPI 121
                                        Score 200.5; DB 2;
Pred. No. 8e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   major merozoite surface antigen precursor N:Alternate names: 195K glycoprotein
                                                                                                                                    ;
9
                                                           10.4%;
illarity 43.3%;
Conservative
                                                       Query Match
Best Local Similarity
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probable major surface antigen (83K, 19K, 42K) precursor - malaria parasite (Plasmodi probable major surface antigen (83K, 19K, 42K) precursor - malaria parasite (Plasmodi C; Date: 29-Aug-1987 #sequence_revision 29-Aug-1987 #text_change 09-Jun-2000 C; Accession: A24594 M.J.; Odink, K.G.; Sandhu, J.S.; Riveros-Moreno, V.; Nicholl Nature 317, 270-273, 1985 A; Place of the precursor to the three major surface antigens of Pl A; Reference number: A24594 MID:86014355 A; Accession: A24594 A; Molecule type: DNA A; Redidues: 11640 A; Molecule type: C; Superfamily: major merozoite surface antigen C; Reywords: surface antigen C; Keywords: surface antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R:Tanabe, K:; Mackay, M.; Goman, M.; Scaife, J.G.
J. Mol. Biol. 195, 273-287, 1987
J. Mol. Biol. 195, 273-287, 1987
A;Title: Allellic dimorphism in a surface antigen gene of the malaria parasite Plasmod A;Reference number: A26868; MuID:88011243
A;Recession: A26868
A;Residues: 1-1701 <a href="https://dx.naper.nap-receives-receives-receives-receives-receives-receives-receives-receives-receives-receives-receives-receives-receives-receives-receives-receives-receives-receives-receives-receives-receives-receives-receives-receives-receives-receives-receives-receives-receives-receives-receives-receives-receives-receives-receives-receives-receives-receives-receives-receives-receives-receives-receives-receives-receives-receives-receives-receives-receives-receives-receives-receives-receives-receives-receives-receives-receives-receives-receives-receives-receives-receives-receives-receives-receives-receives-receives-receives-receives-receives-receives-receives-receives-receives-receives-receives-receives-receives-receives-receives-receives-receives-receives-receives-receives-receives-receives-receives-receives-receives-receives-receives-receives-receives-receives-receives-receives-receives-receives-receives-receives-receives-receives-receives-receives-receives-receives-receives-receives-receives-receives-receives-receives-receives-receives-receives-receives-receives-receives-receives-receives-receives-receives-receives-receives-receives-receives-receives-receives-receives-receives-receives-receives-receives-receives-receives-receives-receives-receives-receives-receives-receives-receives-receives-receives-receives-receives-receives-receives-receives-receives-receives-receives-receives-receives-receives-receives-receives-receives-receives-receives-receives-receives-receives-receives-receives-receives-receives-receives-receives-receives-receives-receives-receives-receives-receives-receives-receives-receives-receives-receives-receives-receives-receives-receives-receives-receives-receives-receives-receives-receives-receives-rece
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     major merozoite surface antigen precursor - malaria parasite (Plasmodium falciparum)
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C,Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 09-Jun-2000
C,Accession: A26868
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                                                                                                                                                                                                                                                                                                                                                                                     1581 GKFQDML----NISQHQCVKKQCP------ENSGCFRHLDEREECKCLLNYKQEGDKCV 1629
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F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-1701/Product: major merozoite surface antigen #status predicted
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                                                                                                                                                           Length 1701;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100 -----EDSGSNGKKITCECTKPDSKPI 121
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9.8%; Score 187.5; DB 2;
Best Local Similarity 41.3%; Pred. No. 2.3e-05;
Matches 43; Conservative 7; Mismatches 11;
                                                                                                                                                               DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 186; DB 2;
Pred. No. 2.8e-05;
4; Mismatches 4;
                                                                                                                                                       Score 187.5; DB 2
Pred. No. 2.3e-05;
7; Mismatches 11
C;Superfamily: major merozoite surface antigen C;Keywords: surface antigen
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Best Local Similarity
Matches 36; Conserva
                                                                                                                                                                                                                 Best Local Similarity
                                                                                                                                                                       Query Match
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C; Species: Plasmodium falciparum
C; Species: Plasmodium falciparum
C; Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 09-Jun-2000
C; Accession: A54498
M. G; Coppel, R. L.; McIntyre, P.; Langford, C.J.; Woodrow, G.; Brown, G.V.;
Mol. Biochem. Parasitol. 27, 291-302, 1988
A; Title: Variation in the precursor to the major merozoite surface antigens of Plasmodiu
A; Accession: A54498
A; MulD: 88142999
A; Accession: A54498
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A;Title: Polymorphism of the precursor for the major surface antigens of Plasmodium falc A;Reference number: A91030; WUID:86136024
A;Reference number: A25120
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F:1614-1631/Domain: membrane anchor #status predicted <MBN>
F:97,259,755,759,835,911,955,1049,1156,1165,1436,1563/Binding site: carbohydrate (Asn)
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C;Species: Plasmodium falciparum
C;Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 09-Jun-2000
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                                                                                            C.Superfamily: major merozoite surface antigen
C.Keywords: glycoprotein; merozoite; surface antigen
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-1639/Product: major merozoite surface antigen #status predicted <MAT>
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                                                                                                                                                                                                                                                                                                                                       Length 1639;
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Pred. No. 5.2e-06;
3; Mismatches 3; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                      Score 196.5; DB 2;
Pred. No. 4.9e-06;
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                                                                                                                                                                                                                                                                                                                                           10.2%;
ilarity 44.1%;
Conservative
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                                                                   Cross-references: EMBL:X15063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 10.2
Best Local Similarity 50.0
Matches 38; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                106 GKKITCECTKPDSKPI 121
                                 A; Residues: 1504-1639 <MYL2>
                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 41; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Date: 30-Sep-1987
C; Accession: A25120
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43;

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32;

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apical membrane antigen 1 - malaria parasite (Plasmodium falciparum)
C;Species: Plasmodium falciparum
C;Species: Plasmodium falciparum
C;Date: 12-Oct-1989 #sequence_revision 12-Oct-1989 #text_change 09-Jun-2000
C;Accession: A3249
E;Peterson, M.G.; Marshall, V.M.; Smythe, J.A.; Crewther, P.E.; Lew, A.; Silva, A.; Andé
Mol. Cell. Biol. 9, 3151-3154, 1989
A;Title: Integral membrane protein located in the apical complex of Plasmodium falciparu
A;Reference number: A32499; MUID:89384584
A;Accession: A32499
A;Residues: Dreliminary
A;Molecule type: DNA; mRNA
A;Residues: 1-622 cPET>
A;Residues: 1-622 cPET>
A;Residues: 1-622 cPET>
A;Cross-references: GB:M27133; NID:9160072; PID:9160073
C;Keywords: membrane protein; surface antigen
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9.3%; Score 179; DB 2;
Best Local Similarity 25.0%; Pred. No. 2.7e-05;
Matches 82; Conservative 22; Mismatches 86,
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106 GKKITCECTKPDSKPI 121
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P22622 P06719 P05691 P04922 P02894 O14628 P01501 Q14839 P03817 P09346

plasmodium

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KNOB\_PLAFA KNOB\_PLAFG RBP2\_PLAVB Y044\_UREPA

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(without alignments)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VERTEBRATE HOST).
-1- MISCELLANBOUS: THE C-TERMINAL REGION IS PROBABLY USED FOR ANCHORING THE PROTEIN TO THE CELL MEMBRANE. THE REPEAT SEQUENCES WOULD BE THE SURFACE ANTIGEN OF THE ORGANISM.
-1- SIMILARITY: CONTAINS 1 TSP TYPE-1 DOMAIN.
                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE-87115616; Pubmed-3543671;
LOCKYER M.J., Schwarz R.T.;
"Strain variation in the circumsporozoite protein gene of Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                     MOI. Biochem. Parasitol. 22:101-108(1987).
-!- FUNCTION: THE CIRCUMSPOROZOITE PROTEIN IS THE IMMUNODOMINANT SURFACE ANTIGEN ON THE SPOROZOITE (THE INFECTIVE STAGE OF THE MALARIA PARASITE THAT IS TRANSMITTED FROM THE MOSQUITO TO THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CIRCUMSPOROZOITE PROTEIN.
47 X 4 AA TANDEM REPEATS OF N-A-N-P.
BD57A9A152B85E03 CRC64;
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NCBL_TaxID=5854;
                                                                                                                            Plasmodium falciparum (isolate Wellcome).
Eukaryota, Alveolata, Apicomplexa, Haemosporida, Plasmodium.
NCBI_TaxID=5848;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11.1%; Score 213.5; DB 1; Length 59.7%; Pred. No. 8.8e-08; Live 4; Mismatches 12; Indels
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01-AUG-1992 (Rel. 23, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
CIRCUMSPOROZOITE PROTEIN PRECURSOR (CS).
                                                 01-AUG-1988 (Rel. 08, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
CIRCUMSPOROZOITE PROTEIN PRECURSOR (CS).
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PRINTS, PROJOS CRCMSPRZOITE.
SMART; SMO0209; TSP1; 1.
Malaria; Sporozoite; Repeat; Signal.
STGNAL 1
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InterPro; IPR000884; TSP1.
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MEDLINE-91201303; PubMed-2016283;
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Matches 43; Conserv
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                     01-AUG-1988 (Rel.
01-AUG-1988 (Rel.
20-AUG-2001 (Rel.
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Mol. Bioche
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -i- MISCELLANEOUS: THE C-TERMINAL REGION IS PROBABLY USED FOR ANCHORING THE PROTEIN TO THE CELL MEMBRANE. THE REPEAT SEQUENCES WOULD BE THE SURPACE ANTIGEN OF THE ORGANISM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDITRE-84250215; PubMed=6204383;
Dame J.B., Williams J.L., McCutchan T.F., Weber J.L., Wirtz R.A.,
Hochmeyer W.T., Maloy W.L., Haynes J.D., Schneider I., Roberts D.,
Sanders G.S., Reddy E.P., Diggs C.L., Miller L.H.;
"Structure of the gene encoding the immunodominant surface antigen of the sporozoite of the human malaria parasite Plasmodium falciparum."
Science 225:593-599(1984).
-!- FONCTION THE CIRCUMSPORZOITE PROTEIN IS THE IMMUNDOMINANT
SURPACE ANTIGEN ON THE SPOROZOITE (THE INFECTIVE STAGE OF THE
MALARIA PARASITE THAT IS TRANSMITTED FROM THE MOSQUITO TO THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CIRCUMSPOROZOITE PROTEIN.
41 x 4 AA TANDEM REPEATS OF P-N-A-N.
1EEEED3DE90965F8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19;
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Pred. No. 5.9e-08; 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                              Plasmodium falciparum.
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
                                                                                                                                                                                                                                                                                                                                    21-JUL-1986 (Rel. 01, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
CIRCUMSPOROZOITE PROTEIN PRECURSOR (CS).
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InterPro; IPR003067; Crcmsprzoite.
InterPro; IPR000884; TSP1.
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PRINTS; PR01303; CRCMSPRZOITE.
SMART; SM00209; TSP1; 1.
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62.2%;
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                                                                                                                                                                                                                                               STANDARD;
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                                                                       402 SSVFNVVNSSIG 413
                                        73 SSVFNVVNSNSG 84
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=5833;
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SEQUENCE
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P02893;
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CSP_PLAFW
IP CSP_PI
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Gaps

13;

DB 1; Length 442;

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Davis J.R., Cortese J.F., Herrington D.A., Murphy J.R., Clyde D.F., Thomas A.W., Baqar S., Cochran M.A., Thanassi J., Levine M.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Plasmodium falciparum (isolate ro-33 / Ghana)
      MEDLINE-92155298; PubMed-1346766;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        272
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194
197 AA;
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                                             Hackett C.S.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1;
                                                                                                                                                                                                                                                                                   VERTEBRATE HOST).
-!- MISCELLANEOUS: THE C-TERMINAL REGION IS PROBABLY USED FOR ANCHORING THE PROTEIN TO THE CELL MEMBRANE. THE REPEAT SEQUENCES WOULD BE THE SURFACE ANTIGEN OF THE ORGANISM.
-!- SIMILARITY: CONTAINS 1 TSP TYPE-1 DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26 HHHKHKKLKQPGDGNPWSPCSVTC------GKPKDELDYENDIEKKICKMEKC 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "DNA sequence of the gene encoding a Plasmodium falciparum malaria candidate vaccine autigen.";
Lal A.A., Goldman I.F.;
"Circumsporozoite protein gene from Plasmodium reichenowi, a
"Circumsporozoite protein gene from Plasmodium reichenowi, a
Cimipanzee malaria parasite evolutionarily related to the human
malaria parasite Plasmodium falciparum.";
J. Biol. Chem. 266:6686-6689(1991).
-: FUNCTION: THE CIRCUMSPOROZOITE PROPEIN IS THE IMMUNODOMINANT
SURPACE ANTIGEN ON THE SPOROZOITE (THE INFECTIVE STAGE OF THE
MALARIA PARASITE THAT IS TRANSMITTED FROM THE MOSQUITO TO THE
                                                                                                                                                                                                                                                                                                                                                                                                  PROBABLE.
CIRCUMSPOROZOITE PROTEIN.
62 X 4 AA TANDEM REPEATS OF N-A-N-P.
CO31EEFBEZE35604 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ch 10.8%; Score 208.5; DB 1; Length 388; I Similarity 58.3%; Pred. No. 1.7e-07; 42; Conservative 4; Mismatches 13; Indels 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Plasmodium falciparum (isolate NF54).
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Campbell J.R.;
Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CSP_PLAFO STANDARD; PRT; 397 AA. P19597; Q25798; 01-FEB-1991 (Rel. 17, Created) MAY-2000 (Rel. 39, Last sequence update) 20-AUG-2001 (Rel. 40, Last annotation update) CIRCUMSPOROZOITE PROTEIN PRECURSOR (CS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic Acids Res. 17:5854-5854(1989).
                                                                                                                                                                                                                                                                                                                                                                                       Malaria; Sporozoite; Repeat; Signal
                                                                                                                                                                                                                                                                                                          PIR; A39756, A39756.
InterPro; IPR003067; Crcmsprzoite.
InterPro; IPR000884; TSP1.
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MEDLINE-89345189; Pubmed-2668895;
Campbell J.R.;
                                                                                                                                                                                                                                                                                                                                              Pfam; PF00090; tsp_1; 1.
PRINTS; PR01303; CRCMSPRZOITE.
SMART; SM00209; TSP1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                           42245 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        73 SSVFNVVNSNSG 84
                                                                                                                                                                                                                                                                                                                                                                                                                                           388 AA;
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Best Local Similarity
Matches 42; Conserv
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SEQUENCE
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                                                                                                                                  SEQUENCE FROM N.A.

MEDLINE=89564998; PubMed=2671723;
Caspers P., Gentz R., Matile H., Pink J.R., Sinigaglia F.;
Caspers P., Gentz R., Matile H., Pink J.R., Sinigaglia F.;
The circumsporozoite protein gene from NF54, a Plasmodium falciparum isolate used in malaria vaccine trials."
Mol. Biochem. Parasitol. 35:185-190(1998).

-!- FUNCTION: THE CIRCUMSPOROZOITE PROTEIN IS THE IMMUNODOMINANT SURFACE ANTIGEN ON THE SPOROZOITE (THE INPECTIVE STAGE OF THE MALARIA PARASITE THAT IS TRANSMITTED FROM THE MOSQUITO TO THE VERTEBRATE HOST).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27; Gaps
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ID MSPI_PLAF3
STANDARD; PRT; 1682 AA.
AC P19588; 025921;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DF MEROZOITE SURFACE PROTEIN 1 PRECURSOR (MEROZOITE SURFACE ANTIGENS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CIRCUMSPOROZOITE PROTEIN.
43 X AA TANDEM REPEATS OF N-A-N-P.
A -> ANDHARDHA (IN REF. 4).
9E81146F59EBCEA3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 397;
"Plasmodium falciparum: in vitro characterization and human infectivity of a cloned line."; Exp. Parasitol. 74:159-168(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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Pred. No. 2e-07;
4; Mismatches 9;
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SIGNAL 1 16 PROBABLE.
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EMBL; W8386; AAA2921.1; -.
EMBL; M22982; AAA29527.1; -.
PIR; S05428; S05428;
PIR; A45527; A45527.
InterPro; IPR003067; Crcmsprzoite.
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PRINTS; PR01303; CRCMSPRZOITE.
SMART; SM00209; TSP1; 1.
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Best Local Similarity 51.8%;
Matches 43; Conservative 4
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(POTENTIAL)
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CARBOHYD
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CARBOHYD
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                                                                                                                                                                                                                      (POTENTIAL).

PTM: WEROZOTTE SURFACE ANTIGEN CONTAIN THE SEQUENCE OF 83 KDA, 4
KDA AND 19 KDA ANTIGENS WHICH ARE THE MAJOR SUBEACE ANTIGENS OF
MEROZOTTES. THE MATURATION TAKE PLACE DURING SCHIZONT.
                                        SEQUENCE OF 1-1061 FROM N.A.
MEDLINE-88166657; PubMed-3327688;
Certa U., Rotmann D., Matile H., Reber-Liske R.;
An aturally occurring gene encoding the major surface antigen
precursor p190 of Plasmodium falciparum lacks tripeptide repeats.";
EMBO J. 6:4137-4142(1987).
                                                                                                                               SEQUENCE OF 1032-1682 FROM N.A. MEDILNE-933547031, PubMed-762856; Tolle R., Bujard H., Cooper J.A.; "Plasmodium falciparum: variations within the C-terminal region of
                                                                                                                                                                                merozoite surface antigen-1.";
Exp. Parasitol. 81:47-54(1995).
-!- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
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(POTENTIAL)
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InterPro; IPR000561; EGF-like.
Pfam: PF00008; EGF; I.
Malaria; Mecozoite; Polyprotein; Repeat; Signal; Glycoprotein;
Transmembrane; GPI-anchor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10.4%; Score 200.5; DB 1; Length 1682; 43.3%; Pred. No. 3.4e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL.

MEMBRANE ANCHOR (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).
    Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           50 GKPKDELDYENDIEKKICKMEKCSSVFNVVNSNSGCFRHLDEREECKCLL-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      192462 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
                    NCBI_TaxID=5834;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100 -----
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TRANSMEM
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ID MSP1_P
AC P04934
Dr 13-AUG
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its mose by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                              SURFACE ANTIGENS)
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Interpro; IPR000561; EGF-like.
Pfam; PF00008; EGF; 1.
Malaria; Merozoite; Polyprotein; Repeat; Signal; Glycoprotein;
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                                                                                                           Plasmodium falciparum (isolate Camp / Malaysia).
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium
NCBL_TaxID-5835;
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                                                                                                                                                                                                                                                                 Weber J.L., Leininger W.M., Lyon J.A.; "Variation in the gene encoding a major merozoite s the human malaria parasite Plasmodium falciparum."; Nucleic Acids Res. 14:3311-3323(1986).
olocylly (Rel. 10, Last sequence update) 01-0CT-1996 (Rel. 34, Last annotation update) MEROZOITE SURFACE PROTEIN 1 PRECURSOR (MEROZOITE NOTE).
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MEDLINE=86205236; Pubmed=3517809;
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SEQUENCE OF 1104-1726 FROM N.A.
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|larity 43.3%;
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13-Aug-1987 (Rel. 05, Created)

STANDARD;

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                                                                                                                                                                                                                                                                                                                          "Plasmodium falciparum: gene structure and hydropathy profile of the major merozoite surface antigen (gpl95) of the Uganda-Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GKPKDELDYENDIEKKICKMEKCSSVFNVVNSNSGCFRHLDEREECKCLL----- 99
                                                                                                                                                                                                                                                                                                                                                                                                              (POTENTIAL).
PTM: MEROZOITE SURFACE ANTIGEN CONTAIN THE SEQUENCE OF 83 KDA, 4
KDA AND 19 KDA ANTIGENS WHICH ARE THE MAJOR SURFACE ANTIGENS OF
MEROZOITES. THE MATURATION TAKE PLACE DURING SCHIZONT.
                                                                                                                                                                                                                                                                                                                                                                              Exp. Parasitol. 67:1-11(1988).
-!- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR
                                                                                    01-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
MEROZOITE SURFACE PROTEIN 1 PRECURSOR (MEROZOITE SURFACE ANTIGENS)
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Pfam, PP00008; EGF: 1.
Malaria; Merzoite; Polyprotein; Repeat; Signal; Glycoprotein;
Transmembrane; GP-anchor.
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                                                                                                                                                                               Plasmodium falciparum (isolate Palo Alto / Uganda).
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium
                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE-89005525; PubMed-3049134;
Chang S.P., Kramer K.J., Yamaga K.M., Kato A., Case S.E.,
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Pred. No. 3.5e-06;
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P50495;
01-0CT-1996 (Rel. 34, Created)
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AA; 196174
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RESULT 8
MSP1_PLAFP
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-!- PTH: MEROZOITE SURFACE ANTIGEN CONTAIN THE SEQUENCE OF 83 KDA, 4 KDA AND 19 KDA ANTIGENS WHICH ARE THE MAJOR SURFACE ANTIGENS OF MEROZOITES. THE MATURATION TAKE PLACE DURING SCHIZONT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REVISIONS, SEQUENCE FROM N.A.
Pan W., Tolle R., Bujard H.;
Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR
                            13-AUG-1987 (Rel. 05, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
01-CCT-1996 (Rel. 34, Last annotation update)
MEROZOITE SURFACE PROTEIN 1 PRECURSOR (MEROZOITE SURFACE ANTIGENS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Polymorphism of the precursor for the major surface antigens of Plasmodium falciparum merozoites: studies at the genetic level."; EMBO J. 4:3823-3829(1985).
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Pfam; PF00008; EGF; 1.
Malaria; Merozoite; Polyprotein; Repeat; Signal; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 1630;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mackay M., Goman M., Bone N., Hyde J.E., Scaife J., Certa U., Stunnenberg H., Bujard H.;
                                                                                                                                                                                                                                                                        Plasmodium falciparum (isolate Kl / Thailand).
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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REPEAT.
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3.1e-06;
8;
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Pred. No. 6.1e-06;
5; Mismatches 8;
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TRIPEPTIDE SG(TP)
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N-L
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MEDLINE-86136024; Pubmed-3004972;
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Best Local Similarity 44.1'
Matches 41; Conservative
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STANDARD;
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MSP1\_PLAFW P04933;

RESULT 10 MSP1\_PLAFW

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1526 NISQHQCVKKQCP-----QNSGCFRHLDEREECKCLLNYKQEGDKCVENPNPTCNENN 1578
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SEQUENCE FROM N.A.
MEDLINE-88142999; PubMed-2449612;
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                                                                                                                                             STANDARD;
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1196
1588
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P13819;
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                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE-66014355; PubMed=2995820;
MHOLDER A.A., LOCKYER M.J., Odink K.G., Sandhu J.S., Riveros-Moreno V., Nicholls S.C., Hillman Y., Davey L.S., Tizard M.L.V., Schwarz R.T.,
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                                                                                                                                                                                                                                                                                                                                                                                                                           Holder A.A.;
Submitted (MAR-1991) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR
                                                                                                                      13-AUG-1987 (Rel. 05, Created)
17-AUG-1987 (Rel. 33, Last sequence update)
18-EBB-1996 (Rel. 33, Last annotation update)
MEROZOLITE SURFACE PROTEIN 1 PRECURSOR (MEROZOLITE SURFACE ANTIGENS)
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Pfam; PF00008; EGF; 1.
Malaria; Mcrozoite; POlyrotein; Repeat; Signal; Glycoprotein;
Transmembrane; GPT-anchor.
                                                                                                                                                                                                                                                                                                                                   Freeman R.R.; maintained the precursor to the three major surface antigens of Plasmodium falciparum merozoites."; Nature 317:270-273(1985).
                                                                                                                                                                                             Plasmodium falciparum (isolate Wellcome).
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium
NCBI_TaxID=5848;
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MEROZOITE SURFACE PROTEIN 1.
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ilarity 44.1%; Pred. No. 6.1e-06;
Conservative 5; Mismatches 8;
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                                                                                          STANDARD;
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Matches 41; Conserv
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REVISIONS

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"Variation in the precursor to the major merozoite surface antigens of Plasmodium falciparum.":
Mol. Biochem. Parasitol. 27:291-302(1988).
-:- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR
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                                                                                                                                                                                                                                         01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
01-OCT-1996 (Rel. 14, Last annotation update)
MEROZOTIE SURFACE PROTEIN 1 PRECURSOR (MEROZOTIE SURFACE ANTIGENS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (POTENTIAL).
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(POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Interproj IPR000561; EGF-like.
Pfam: PF00008; EGF: 1.
Malaria; Merozoite; Polyprotein; Repeat; Signal; Glycoprotein; Transmembrane; GF1-anchor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1701;
                                                                                                                                                                                                                                                                                                                                                                                Plasmodium falciparum (isolate FC27 / Papua New Guinea).
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBL_TaxID=5837;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 50 GKPKDELDYENDIEKKICKMEKCSSVFNVVNSNSGCFRHLDEREECKCLL
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Pred. No. 2.7e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-LINKED (GLCNAC.
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N-LINKED (GLCNAC
N-LINKED (GLCNAC
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                                                                                                                                                                                         PRT; 1701 AA
                            1579 GGCDADAKCTEEDSGSNGKKITCECTKPDSYPL 1611
------EDSGSNGKKITCECTKPDSKPI 121
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CARBOHYD
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1581 GKFQDML----NISQHQCVKKQCP-----ENSGCFRHLDEREECKCLLNYKQEGDKCV 1629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      42
                                                                                                                                                                                                                                                                                     parasite
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -1- PTM: MEROZÓITE SURFACE ANTIGEN CONTAIN THE SEQUENCE OF 83 KDA, 4 KDA AND 19 KDA ANTIGENS WHICH ARE THE MAJOR SURFACE ANTIGENS OF MEROZOITES. THE MATURATION TAKE PLACE DURING SCHIZONT.
                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-86136024; PubMed-3004972; MEDLINE-86136024; PubMed-3004972; MEDLINE-86136024 M., Bone N., Hyde J.E., Scaife J., Certa U., Stunnenberg H., Bujard H.; Pulymorphism of the precursor for the major surface antigens of Jasamodium falciparum merczoltes: studies at the genetic level."; EMBO J. 4:3823-3829(1985).
                                                                                                                            01-AUG-1988 (Rel. 08, Created)
90-AMY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last anoncation update)
MEROZOITE SURFACE PROTEIN 1 PRECURSOR (MEROZOITE SURFACE ANTIGENS)
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(POTENTIAL)
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InterPro; IPR000561; BGF-11ke.
Pfam; PF00008; BGF; 1.
Malaria; Merozoite; Polyprotein; Repeat; Signal; Glycoprotein;
Transmembrane; GPI-anchor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (POTENTIAL)
                                                                                                                                                                                                                                                         MEDLINE-88011243; PubMed-3079521;
Tanabe K., Mackay M., Goman M., Scaife J.G.;
"Allelic dimorphism in a surface antigen gene of the malaria
                                                                                                                                                                                                   Guinea).
Plasmodium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEROZOITE SURFACE PROTEIN 1
                                                                                                                                                                                                                                                                                                                                                       Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases
                                  1630 ENPNPTCNENNGGCDADATCTEEDSGSSRKKITCECTKPDSYPL 1673
                       ------EDSGSNGKKITCECTKPDSKPI 121
                                                                                                                                                                                             Plasmodium falciparum (isolate mad20 / Papua New
Eukaryota, Alveolata, Apicomplexa, Haemosporida,
NCBI_TaxID=70153;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-LINKED (GLCNAC...
                                                                                                      PRT; 1701 AA
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REVISIONS TO 1403; 1569 AND 1629.
                                                                                                                                                                                                                                                                                            Plasmodium falciparum.";
J. Mol. Biol. 195:273-287(1987).
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PIR; A26868; A26868.
PIR; B25120; B25120.
                                                                                                       STANDARD;
                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (POTENTIAL).
                                                                                                                                                                           (PMMSA) (P190).
                    100 -----
                                                                                                                           01-AUG-1988
30-MAY-2000
30-MAY-2000
                                                                                                      MSP1_PLAFM
P08569;
                                                                                                                                                                                                                                                                                                                                             Tanabe K.;
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                                                                                                                                                                                                                                                                                1581 GKFQDML----NISQHQCVKKQCP-----ENSGCFRHLDEREECKCLLNYKQEGDKCV 1629
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APTCAL MEMBRANE ANTIGEN 1.
EXTRCELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-N (IN REF. 1; AAA29476).
H -> N (IN REF. 1; AAA29476).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Peterson M.G., Marshall V.M., Smythe J.A., Crewther P.E., Lew A., Silva A., Anders R.F., Kemp D.J.;
"Integral membrane protein located in the apical complex of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-AUG-1991 (Rel. 19, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
APICAL MEMBRANE ANTIGEN 1 PRECURSOR (MEROZOITE SURFACE ANTIGEN).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
My 3FC2EC59AF96EA98 CRC64;
                                                                                                                                                                                43;
                                                                                                                                Length 1701;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Plasmodium falciparum (isolate FC27 / Papua New Guinea).
Eukaryota, Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5837;
                                                                                                                                                                                Indels
                                                                                                                                                                                                                                50 GKPKDELDYENDIEKKICKMEKCSSVFNVVNSNSGCFRHLDEREECKCLL-
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InterPro; IPR003298; Apmem_Ag1.
Pfam; PF00430; AMA-1; 1.
Malaria; Signal; Transmembrane; Antigen; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                1630 ENPNPTCNENNGGCDADATCTEEDSGSSRKKITCECTKPDSYPL 1673
                                                                                                                                                                                                                                                                                                                                        ------EDSGSNGKKITCECTKPDSKPI 121
                                                                                                                             Score 187.5; DB 1;
Pred. No. 2.7e-05;
                                                                                                                                                                                11;
                                                                                                                                                                             7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        622 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE=89384584; Pubmed=2701947;
  1196 1196 N-LJ
1588 1588 N-LJ
1701 AA; 193768 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-AUG-1991 (Rel. 19, Created)
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                                                                                                                             Query Match 9.8%;
Best Local Similarity 41.3%;
Matches 43; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PK66 FROM P.KNOWLESI.
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P22621;
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EMBL; M58545; AAA29718.1; +.
547
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162
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371
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P50489;
            DOMAIN
CARBOHYD
                                                            CARBOHYD
CARBOHYD
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  TRANSMEM
                                   CARBOHYD
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                                                                                     12;
                                                                                                                                                                                                                                  340
                                                                                                                                                                                                                                                         249
                                                                                                                                                                         - PNAN----PDGNCEDIPHYNEFSAIDLGNAEKYDKMDEPQHYGKSLTPLEELYKPNDKS 189
                                                                                                                                                                                                                                                                                                      250 GRGONYWEHPYOKSDOPKOYEQHLTDYEKİKEGKPLDKFGNIYDYHYEHSSPSSTKSSSP 309
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                                                                                                                               DEMRHFYKDNKYVKNLD--ELTLCSRHAGNMIPDNDKNSNYKYPAVYDDKDKKKCHILYIA 253
                                                                                                                                                             79 VNSNSG----CFRHLDEREECKCLLEDSGSNGKKITCECTKPDSKPIVQYDNF-NANPNAN 134
                                                                                      Gaps
                                                                                                             DHHHHHHHHKKLKQPGDGNPWSPCSVTCGKPKDELDYENDIEKKIC---KMEKCSSVFNV 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOI. Blochem. Parasitol. 42:285-287(1990).
-!- FUNCTION: INVOLVED IN PARASITE INVASION OF ERYTHROCYTES.
-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-!- SIMILARITY: STRONG TO AMA-1 FROM P.CHABAUDI AND P.FRAGILE, AND PK66 FROM P.KNOWLESI.
                                                                                                                                                                                                                                                     190 LYQYIKANSKFIGITELSNTFINNAGOHGHMHGNEREDERTLTKEYEDIVLKEFTYMINF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
APICAL MEMBRANE ANTIGEN 1 PRECURSOR (MEROZOITE SURFACE ANTIGEN).
                                                                                     Indels 138;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Plasmodium falciparum (isolate 7G8).
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium
                                                               Length 622;
 -> M (IN REF. 1; AAA29476).
-> R (IN REF. 1; AAA29476).
7D41335E249FA18F CRC64;
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                                                              9.3%; Score 179; DB 1; L
25.0%; Pred. No. 3.1e-05;
tive 22; Mismatches 86;
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InterPro; IPR003298; Apmem_Agl.
Pfam; PF02430; AMA_1; 1.
Malaria; Signal; Transmembrane;
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72009 MW;
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   496
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622 AA;
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SEQUENCE FROM N.A.
                                                                            Similarity
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P50492;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                      14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       236 EDIVLKEFTYMINFGRGQNYWEHPYQKSDQPKQYEQHLTDYEKIKEGKPLDKFGNIYDYH 295
                                                                                                                                                                                                                                                                                                                                                                                                                                   KICKMEKCSSVFNVVNSNSG----CFRHLDEREECKCLLEDSGSNGKKITCECTKPDSKPI 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               122 VQYDNF-NANPNAN-PNAN----PDGNCEDIPHVNEFSAIDLGNAEKYDKMDEPQHYGKS 175
                                                                                                                                                                                                                                                                                                                                                                                          190 ISPMTLDHMRDFYKNNEYVKNLDELTLCSRHAGNMNPDNDKNSNYKYPA-VYDY-ND--- 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----KKCHILYIAAQENNGPRYCNKDESKRNSMFCFRPAKDKSFQNYTYL-----SKNV 294
                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                            16 ISYIYADHHHHHHKHKKL------KQPGDGNPWSPCSVTCGKPKDELDYENDIEK 64
POTENTIAL.

(YTOPLASMIC (POTENTIAL).

N-LINKED (GLCNAC...) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        176. LTPLEELYKPNDKSLYQYIKANSKFIGITELSNTFINNAGQHGHMHGNEREDERTLTKEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SURFACE ANTIGEN)
                                                                                                                                                                                                                                                                                                      Indels 153;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 171.5; DB 1; Length 622;
Pred. No. 0.0001;
3; Mismatches 84; Indels 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Plasmodium falciparum (isolate Camp / Malaysia).
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       295 V--DNWEKVCPRKNLENAKFGLWVDGNCEDIPHVNEFSANDLFECNKL----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             296 YEHSSPSSTKSSSPSNVKSASLATRLMK--KFKAEIRDFFGISYYEK 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1C9C8715D8E2915F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-02001 (Rel. 40, Last annotation update)
APICAL MEMBRANE ANTIGEN 1 PRECURSOR (MEROZOITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          622 AA
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                                                                                                                                                                                         622 AA;
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Matches 82; Conserv
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11;
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                                                                                                                                                                                                                                        277 RPAKDKSFQNYTYL----SKNVV--DNWEKYCPRKNLENAKFGLAVDGNCEDIPHVNEF 329
                                                                                                                                                                                                                                                                                                   213 NAGQHGHMHGNEREDERTLTKEYEDIVLKEFTYMINFGRGQNYWEHPYQKSDQPKQYEQH 272
                                                                                                                                                                                                                                                                                                              153 SAIDLGNAEKYDKMDEPQHYGKSLTPLEELYKPNDKSLYQYIKANSKFIGITELSNTFIN 212
                                                                                                                                                      Query Match 8.9%; Score 171.5; DB 1; Length 622;
Best Local Similarity 23.9%; Pred. No. 0.0001;
Matches 74; Conservative 24; Mismatches 77; Indels 135; Gaps
                                                                                                                                                                                          45 CSVTCGKPKDELDYENDIEKKIC---KMEKCSSVFNVVNSNSG---CFRHLDEREECKCL 98
                                                                                  (POTENTIAL)
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Search completed: January 29, 2002, 11:13:36 Job time: 812 sec

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Sequence

Sequence

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Sequence Sequence

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KH----KKLKQPGDGNPWSPCSVTCG------KPKDELDYENDIEKKICKME 70
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US-08-113-288B-18
Sequence 18, Application US/08313288B
Sequence 18, Application US/08313288B
Sequence 18, Application US/08313288B
SEQUENCE 18, Application US/08313288B
SEQUENCE 18, Application US/0831328B
STITLE OF INVENTION: CLONING, EXPRESSION AND USES OF A TITLE OF INVENTION: CLONING, EXPRESSION AND USES OF A TITLE OF INVENTION: CLONING, EXPRESSION AND USES OF A MUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: ADDRESSE:
STREET: 1185 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/313,288B
FILING DATE: January 5, 1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REGISTRATION NUMBER: 40028-A-PCT-US
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRAX: (212) 278-0400
TELEFRAX: (212) 391-0526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 215.5; DB 1;
Pred. No. 3.2e-12;
----hes 7;
                  US-08-929-329-5
US-08-755-587-16
US-08-639-501-2
US-09-044-948-2
US-09-164-908-2
US-09-150-741-2
US-08-189-469-2
US-08-189-462-4
US-08-189-462-4
US-08-515-251A-2
US-09-347-402-47
US-08-974-186-47
US-08-974-186-47
US-08-974-186-47
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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Best Local Similarity 62.2
Matches 46; Conservative
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STATE: New York
COUNTRY: USA
  LENGTH:
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Sequence 3, Appli
Sequence 3, Appli
Sequence 9, Appli
Sequence 35, Appli
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59.139 Million cell updates/sec
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                                                                                                                                   Search time 133.18 Seconds
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Sequence 4
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/cgn2_6/ptodata/2/laa/5B_COMB.pep:*
/cgn2_6/ptodata/2/laa/6A_COMB.pep:*
/cgn2_6/ptodata/2/laa/6B_COMB.pep:*
/cgn2_6/ptodata/2/laa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/laa/PCTUS_COMB.pep:*
                  GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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US-08-760-797A-1

US-08-760-797A-3

US-08-932-929B-1

US-08-932-929B-3

US-08-932-929B-3

US-08-926-703-9

US-08-455-625-35

US-08-455-625-35

US-08-455-625-35

US-08-455-685-35

US-08-455-685-35

US-08-455-685-35

US-08-456-424

US-08-133-288B-14

US-08-133-288B-14

US-08-139-13

US-08-139-13

US-08-290-919-12

US-08-290-919-12

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US-08-290-919-17

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Maximum Match 100%
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Maximum DB :
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                                                                                                                                   Run on:
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Gaps

19;

Indels

Length 412;

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29 KH-----KKLKQPGDGNPWSPCSVTCG------KPKDELDYENDIEKKICKME 70
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10.9%; Score 210.5; DB 4;
63.4%; Pred. No. 9.9e-12;
tive. 1; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 3, Application US/08760797A
Patent No. 5928902
GENERAL INFORMATION:
APPLICANT: De Wilde, Michel
APPLICANT: Cohen, Joseph
TITLE OF INVENTION: Hybrid Protein Between CS
TITLE OF INVENTION: from Plasmodium and HBSAG
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
TITLE OF INVENTION: from Plasmodium and HBSAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
                                                                                                                                                                                                                                       OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                         ADDRESSEE: SmithKline Beecham Corporation STREET: 709 Swedeland Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  B45015-1FWC2
                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/932,929B FILING DATE:
                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/760,797
FILING DATE: 04-DEC-1996
APPLICATION NUMBER: 08/442,612
FILING DATE: 17-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: BAUMMELS: 33,833
REGISTRATION NUMBER: 33,833
RECISTRATION NUMBER: B45015-1
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                      MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 424 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 63.4<sup>§</sup>
Matches 45; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 610-270-5090
                                                                                STREET: 709 Sweueraus
CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   single
                        NUMBER OF SEQUENCES: 4
                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              71 KCSSVFNVVNS 81
                                                                                                                                            USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS:
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US-08-760-797A-3
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                                                                                                                                            COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 210.5; DB 2; Length 423;
Pred. No. 9.9e-12;
1; Mismatches 6; Indels 19; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29 KH-----KKLKQPGDGNPWSPCSVTCG------KPKDELDYENDIEKKICKME 70
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APPLICANT: Cohen, Joseph
TITLE OF INVENTION: Hybrid Protein Between CS
                                                                                                                                                                     Sequence 1, Application US/08760797A
Patent No. 5928022
GENERAL INFORMATION:
APPLICANT: De Wilde, Michel
APPLICANT: Cohen, Joseph
TITLE OF INVENTION: Hybrid Protein Between CS
TITLE OF INVENTION: Hrom Plasmodium and HBsAG
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER FRADABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
COMPUTER: IBM COMPATIBLE
COMPATION SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
FILING DATE: 04-DEC-1996
                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: SmithKline Beecham Corporation STREET: 709 Swedeland Road CITY: King of Prussia STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   B45015-1C2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 435
PRIOR APPLICATION DARP:
FILING DATE: 17-MAY-1995
ATTORNEY/AGRUT INFORMATION:
NAME: Baumelster, Kirk
REGISTRATION NUMBER: 33,833
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/08932929B Patent No. 6169171 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: B4.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 10.9%;
Best Local Similarity 63.4%;
Matches 45; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : 423 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 423 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 610-270-5090
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                                                         388 KCSSVFNVVNSSIG 401
                                     71 KCSSVFNVVNSNSG 84
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         71 KCSSVFNVVNS 81
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                                                                                                                                                                                                                                                                                                                                                                                                                                     USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                        19406
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US-08-760-797A-1
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                                                                                                                                                        US-08-760-797A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
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29 KHKKLKQPGD-----KPKDELDYEND 61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Pacleti, Enzo
APPLICANT: de Taisne, Charles
APPLICANT: de Taisne, Charles
APPLICANT: de Taisne, John A.
TITLE OF INVENTION: MALARIA RECOMBINANT POXVIRUS VACCINE
NUMBER OF SEQUENCES: 143
ADDRESSEE: CURTIS, Morris & Safford, P.C.
STREET: 530 Fifth Avenue, 25th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/257,073
FILING DATE: 09-JUN-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/075,783
FILING DATE: 11-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/852,305
FILING DATE: 18-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/672,183
FILING DATE: 20-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Frommer, William S.
REGISTRATION NUMBER: 25.506
REFERENCE/DOCKET NUMBER: 25.506
REFERENCE/DOCKET NUMBER: 45.310-2570
  B45015-1FWC2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: New York COUNTRY: NUITED STATES OF AMERICA ZIP: 10036 COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           170 IEKKICKMEKCSSVFNVVNSSIG 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 9, Application US/08257073 Patent No. 5766597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62 IEKKICKMEKCSSVFNVVNSNSG 84
                   TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5096
TELEFAX: 610-270-5090
                                                                                                                                                                                                                                                                                                                          10.8%;
51.8%;
                                                                                                            INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 424 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-932-9298-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (212) 840-3333
TELEFAX: (212) 840-0712
TELEEX: 425066 CURTMS
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
  REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 51.8
Matches 43; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-257-073-9
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Pred. No. 1.9e-11;
4; Mismatches 9; Indels 27
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Patent No. 6169171
GENERAL INFORMATION
GENERAL INFORMATION: De Wilde, Michel
APPLICANT: Cohen, Joseph
TITLE OF INVENTION: Hybrid Protein Between CS
TITLE OF INVENTION: from Plasmodium and HBsAG
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                   SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/760,797A FILING DATE: 04-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 709 Swedeland Road CITY: King of Prussia STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: DOS
SOFTWARE: FASLSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/932,929B
                                                                                  FILING DATE: 04-DEC-1996
CLASSIECTATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/442,612
FILING DATE: 17-RAY-1995
ATTONNEY, AGGENT INFORMATION:
NAME: BAUMELSEEV, Kirk
REGISTRATION NUMBER: 33,833
REFERENCE/DOCKET NUMBER: 33,833
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
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APPLICATION NUMBER: 08/760,797
FLING DATE: 04-DEC-1996
APPLICATION NUMBER: 08/442,612
FILING DATE: 17-MAY-1995
ATTORNEY/ARGNY INFORMATION:
NAME: Baumelster, Kirk
REGISTRATION NUMBER: 33,833
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       170 IEKKICKMEKCSSVFNVVNSSIG 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62 IEKKICKMEKCSSVFNVVNSNSG 84
                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 424 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-760-797A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
10.8%;
Best Local Similarity 51.8%;
Matches 43; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE
COMPUTER: IBM COMPATIBLE
                                                                                                                                                                                                                                                                                                                                           TELEFAX: 610-270-5090
OPERATING SYSTEM: DOS
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CLASSIFICATION:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/060,988
FILING DATE: 14-MAY-1993
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 35, Application US/08455625
; Patent No. 5932218
                                                                                                                                                                                                                                                                    /label= X
/note= "X =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Svenson, Leonard R. REGISTRATION NUMBER: 30330 REFERENCE/DOCKET NUMBER: 11 TELECOMMUNICATION INFORMATION: 703-205-8000
                                                                                                                                                                                                                                NAME/KEY: Modified-site LOCATION: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 66 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: 703-205-8050
                                                                                                                                                                                                                                                                                                                                                                                                         25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 22040-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                              TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                            single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
CLASSIFICATION: 435
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COTHER INFORMATION:
US-08-290-919-3
                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                        TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                        LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 8
US-08-455-625-35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           250 GRGQNYWEHPYQKSDQPKQYEQHLTDYEKIKEGKPLDKFGNIYDYHYEHSSPSSTKSSSP 309
                                                                                                                                                                                                                                                  79 VNSNSG----CFRHLDEREECKCLLEDSGSNGKKÍTCECTKPDSKPIVQYDNF-NANPNAN 134
                                                                                                                                                                                                                                                                                                                 254 AQENNGPRYCNKDESKRNSMECKS- A FRPAKDISFONYTYLSKNVV--DNWEKVCPRKN 306
                                                                                                                                                                                                                                                                                                                                                                         135 -PNAN----PDGNCEDIPHVNEFSAIDLGNAEKYDKMDEPQHYGKSLTPLEELYKPNDKS 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels 133; Caps
                                                                                                                                                                                                                      22 DHHHHHHKHKKLKQPGDGNPWSPCSVTCGKPKDELDYENDIEKKIC---KMEKCSSVFNV 78
                                                                                                                                                                                                                                                                                                                                                                                                 Length 628;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: HOLDER, ANTHONY A.
APPLICANT: GLACKMAN, MICHAEL J.
APPLICANT: CHAPPEL, JONATHAN A.
APPLICANT: CHAPPEL, JONATHAN A.
TITLE OF INVENTION: VACCINE
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN DARBY & CUSHMAN, L.L.P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/290,919
FILING DATE: 04-OCT-1994
CLASSIFICATION 1435
PRIOR APPLICATION NUMBER: GB 9203821.5
FILING DATE: 22-FEB-1992
PRIOR APPLICATION NUMBER: POT/GB93/00367
FILING DATE: 22-FEB-1993
ATTORNEY/AGENT INFORMATION:
NAME: RCHULLS, PAUL N.
REGISTRATION NUMBER: 16,773
                                                                                                                                              Query Match
9.1%; Score 175.5; DB 1;
Best Local Similarity 25.0%; Pred. No. 3.5e-08;
Matches 82; Conservative 24; Mismatches 89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 1100 NEW YORK AVENUE, N.W. CITY: WASHINGTON STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       310 SNVKSASLATRLMKKFKAEIRDFFGISY 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        378 RRIKSAFLPT---GAFKADRYKSHGKGY 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: U.S.A.
ZIP: 20005-3918
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 3, Application US/08290919 Patent No. 5720959
                                                        peptide
internal
                      single
; TYPE: amino acid
; STRANDEDNESS: singl;
; TOPOLGX: linear
; MOLECULE TYPE: peptid
; FRAGMENT TYPE: intern
US-08-257-073-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-290-919-3
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GENERAL INFORMATION:

APPLICANT: Berzofsky, Jay A.

APPLICANT: Berzofsky, Jay A.

APPLICANT: Abless, Jeffrey D.

APPLICANT: Pendleton, C. D.

APPLICANT: Nara, Peter

APPLICANT: Nara, Peter

APPLICANT: OF INVENTION: COMPOSITE SYNTHETIC PEPTIDE CONSTRUCT

TITLE OF INVENTION: ELICITING NEUTRALIZING ANTIBODIES AND CYTOTOXIC T

TITLE OF INVENTION: LYMPHOCYTES AGAINST HIV

NUMBER OF SEQUENCES: 36

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC COMPALIDLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     81 SNSGCFRHLDEREECKCLLEDSGSNGKKITCECTKPDSKPI 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 212242/HCM/MJL/6BC8/
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 61-3000
TELERAX: 6714627 CUSH
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 53 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6.8%; Score 131; DB 1;
61.0%; Pred. No. 1.5e-05;
tive 3; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Birch, Stewart, Kolasch & Birch STREET: P.O. Box 747 CITY: Falls Church STATE: Virginia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Berzofsky, Jay A.
APPLICANT: Ahlers, Jeffrey D.
APPLICANT: Pendleton, C. David
APPLICANT: Bendleton, C. David
APPLICANT: Shirai, Mutsunori
TITLE OF INVENTION: MULTIDETERMINANT PEPTIDES THAT ELLCIT
TITLE OF INVENTION: HELPER T-LYMPHOCYTE, CYTOTOXIC T LYMPHOCYTE AND
TITLE OF INVENTION: NEUTRALIZING ANTIBODY RESPONSES AGAINST HIV-1
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                        Gaps
                                                                                                              /label- peptide
/note- "peptide from P. falciparum CS antigen"
                                                                                                                                                                                                                                                                                                                 31 KKLKQPGDGNP------WSPCSVTCGKPKDELDYENDIEKKICKMEKCS 73
                                                                                                                                                                                                               Score 128.5; DB 2; Length 66;
Pred. No. 3.4e-05;
3; Mismatches 11; Indels 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OCHEVILES, 10% COMPACTANCE
OPERATING SYSTEM: Windows95
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/455,685
FILING DATE: 31-MAY-1995
PROR APPLICATION DATA:
APPLICATION NUMBER: 08/60,988
FILING DATE: 14-MAY-1993
APPLICATION NUMBER: 07/847,311
FILING DATE: 29-MG-1991
FILING DATE: 29-MG-1991
APPLICATION NUMBER: 07/751,998
FILING DATE: 29-MG-1991
APPLICATION NUMBER: 07/18,692
FILING DATE: 26-JAN-1988
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 08830/022003 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E: Fish & Richardson P.C. 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 35, Application US/08455685 Patent No. 6214347 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Beattle, Ingrid A. REGISTRATION NUMBER: P-42,306
                                                                                                                                                                                                               6.7%;
51.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPALIALE
                                                                                                                                                                                        Query Match
Best Local Similarity 51.00,
-hog 29, Conservative
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617/542-8906
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 66 amino acids
                MOLECULE TYPE: peptide FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; MOLECULE TYPE: peptide US-08-455-685-35
                                                                     NAME/KEY: Peptide
COCATION: 1.66
OTHER INFORMATION: OTHER INFORMATION: US-08-455-625-35
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          amino acid
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STREET: 225
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                                                       FEATURE:
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                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: MULTIDETERMINANT PEPTIDES
TITLE OF INVENTION: THAT ELICIT
TITLE OF INVENTION: HELPER T-LYMPHOCYTE, CYTOTOXIC T LYMPHOCYTE AND
TITLE OF INVENTION: HELPER T-LYMPHOCYTE, CYTOTOXIC T LYMPHOCYTE AND
NUMBER OF INVENTION: NEUTRALIZING ANTIBODY RESPONSES AGAINST HIV-1
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                             -----WSPCSVTCGKPKDELDYENDIEKKICKMEKCS 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31 KKLKQPGDGNP------WSPCSVTCGKPKDELDYENDIEKKICKMEKCS 73
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    Length 66;
                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: US
ZIP: 02110-2804
COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/060,988A
6.7%; Score 128.5; DB 4
51.8%; Pred. No. 3.4e-05;
tive 3; Mismatches 11
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APPLICATION DATA:
APPLICATION NUMBER: 07/447,311
FILING DATE: 06-MAR-1992
APPLICATION NUMBER: 07/751,998
FILING DATE: 29-MG-1991
APPLICATION NUMBER: 07/748,692
FILING DATE: 26-JAN-1988
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                     US-08-060-988A-35; Sequence 35, Application US/08060988A; Patent No. 6294322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER: P-42,306
                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Berzofsky, Jay A.
APPLICANT: Ahlers, Jeffrey D.
APPLICANT: Pendleton, C. David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 08
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Nara, Peter
APPLICANT: Shirai, Mutsunori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Beattie, Ingrid A.
Query Match 6.7%
Best Local Similarity 51.8%
Matches 29; Conservative
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Best Local Similarity 51.8
Matches 29; Conservative
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 66 amino acids
                                                                                     31 KKLKQPGDGNP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY:
STATE:
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60 -NDIEKKICKMEKCSSVFNVVNSNSGCFRHLDEREECKCLLEDSGSNGKKITCECTKPDS 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                --KKLKQPGDGNPWSPCSVTCGK----PKDELDYE--
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21.0%; Pred. No. 0.0017;
ive 46; Mismatches 104; Indels 128;
                                                                                                                                                                                           16;
                                                                                                                                                                                           10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Jessell, Thomas M. and Avihu Klar TITLE OF INVENTION: CLONING, EXPRESSION AND USES OF A TITLE OF INVENTION: NOVEL SECRETED PROTEIN, F-SPONDIN NUMBER OF SEQUENCES: 20 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6.5%; Score 125; DB 6; 40.0%; Pred. No. 0.00093;
                                                                                                                                                                                           10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SSEE: Cooper & Dunham LLP
F: 1185 Avenue of the Americas
New York
New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                       US-08-313-288B-14; Sequence 14, Application US/08313288B Sequence 14, Application US/08313288B Patent No. 5750502; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 14: SEQUENCE CHARACTERISTICS:
       FILING DATE: 26-OCT-1987
APPLICATION NUMBER: 649,903
FILING DATE: 12-SEP-1984
APPLICATION NUMBER: 115,634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 6.5%;
Best Local Similarity 21.0%;
Matches 74; Conservative 4
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amino acid
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                                                                                                                                                           Query Match
Best Local Similarity
Matches 24; Conserv
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                                                                     SEQ ID NO:9:
LENGTH: 378
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                                                                                                                                                                                                                                                                                                                          RESULT 13
                                                                                                        5171843-9
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                                                                                                 COMPOSITE SYNTHETIC PEPTIDE CONSTRUCT
ELICITING NEUTRALIZING ANTIBODIES AND CYTOTOXIC T
LYMPHOCYTES AGAINST HIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels 13; Gaps
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/note= "peptide from P. falciparum CS antigen"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31 KKLKQPGDGNP------WSPCSVTCGKPKDELDYENDIEKKICKMEKCS 73
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Pred. No. 3.4e-05;
3; Mismatches 11; Indels 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; PATENT NO. 5171843
APPLICANT: NUSSENZWEIG, VICTOR
TITLE OF INVENTION: IMMUNOGENIC POLYPEPTIDE AND METHOD FOR
; PURIFYING IT
                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/05142
                                                                            APPLICANT:
TITLE OF INVENTION: COMPOSITE SYNTHETIC PEPTIDE
TITLE OF INVENTION: ELICITING NEUTRALIZING ANTI
TITLE OF INVENTION: LYMPHOCYTES AGAINST HIV
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Birch, Stewart, Kolasch & Birch
STREET: P.O. BOX 747
CITY: Falls Church
STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRICR APPLICATION DATA:
APPLICATION NUMBER: US 08/060,988
FILING DATE: 14-MAY-1993
ATORNEY/AGENT INFORMATION:
NAME: Svensson, Leonard R.
REGISTRATION NUMBER: 30330
RECISTRATION NUMBER: 1173-434P
TELECHORE: 703-205-8050
TELECHORE: 703-205-8050
                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 13-MAY-1994
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/175,112
FILING DATE: 30-MAR-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 754,645
FILING DATE: 9-JUL-1985
                                                        Sequence 35, Application PC/TUS9405142 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 703-205-8050
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
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ilarity 51.8%;
Conservative
                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 66 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
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CTHER INFORMATION: /;
PCT-US94-05142-35
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Matches 29; Conserv
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ZIP: 22040-0747
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                                              PCT-US94-05142-35
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5171843-9
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MOLECULE TYPE: protein HYPOTHETICAL: NO
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MEDIUM TYPE: Floppy
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Matches 61; Conserva
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                                                                                                                                                                                                                                                                                                                                             COUNTRY: US
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APPLICANT: Hoffman, Stephen L.
APPLICANT: Hedstrom, Richard C.
APPLICANT: Sedegah, Martha
TITLE OF INVENTION: POLYNUCLEOTIDE VACCINE PROTECTIVE
TITLE OF INVENTION: DELIVERING POLYNUCLEOTIDE PROTECTION AND VECTOR FOR TITLE OF INVENTION: DELIVERING POLYNUCLEOTIDE VACCINES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;;
                                                        319 NII---DNNPQEPSPNPEGKDENPNGFDLDENPENPPNPDIPEQKPNIPEDSEKEVPSD 375
 -----WEPLDVPDE----PEDDQPRPRGDNSSVQKPEE 318
                                   119 KPIVQYDNFNANPNANP----NANPDG-----NCE-----PHVNEFSAIDL--- 157
                                                                                                                                                 376 VPKNPEDDREENFDIPKKPENKHDNONNL-----PNDKS------DRNIPYSPLPPKV 422
                                                                                                                                                                                      211 INN-----AGGHGHMHGNEREDERTLTKEYEDIVLKEFTYMINFGRGQNYWEHPYQ 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                              158 -----GNAEKYDKMDEPQHYGKSLTPLEELYKPNDKSLYQYIKANSKFIGITELSNTF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   42 WSPCSVTCG-----KPKDELDYENDIEKKICKMEKCSSVFNVVNSNSG 84
                                                                                                                                                                                                                                                                 262 KSDQPKQYEQHLTDYEKIKEGKPLDKFGNIYDYHYEHSSPSSTKSSSPSNVK 313
                                                                                                                                                                                                                                                                                                        -----EHEKPDNNKKKGESDNK 494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 3; Length 478;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER REDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/155,888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 124.5; DB 3;
Pred. No. 0.0015;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Naval Medical Res. & Dev. Cmd
STREET: Bldg. 1, T-12 8901 Wisconsin Ave
CITY: Bethesda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9; Mismatches
                                                                                                                                                                                                                            423 LDNERKQSDPQSQDNNGNRHVPNSEDRET ---
                                                                                                                                                                                                                                                                                        Sequence 2, Application US/08155888 Patent No. 6066623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Spewack, A. David
REGISTRATION NUMBER: 24,743
REFERENCE/DOCKET NUMBER: N.C.
TELECOMMUNICATION INFORMATION:
TELEFAX: (202) 295-6759
TELEFAX: (202) 295-1022
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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274 TSEIQEQ-CEEERCPPK-
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CORRESPONDENCE ADDRESS
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COUNTRY: USA
ZIP: 20889-5606
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Best Local Similarity
Matches 25; Conserv
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RESULT

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APPLICANT: Chitais, Chetan
APPLICANT: Miler, Louis H.
APPLICANT: Miler, Louis H.
APPLICANT: Peterson, David S.
APPLICANT: Wellems, Thomas E.
TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
TORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            979 GNSLNHEEVKEHTSNSDNVQQSGGIVNMNVEKELKDTLENPSSSLDEGKAHEELSEPNLS 1038
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6.4%; Score 124; DB 2; L
illarity 23.1%; Pred. No. 0.0081;
Conservative 36; Mismatches 113;
                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Knobbe Martens Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: NIH121.001CP1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 235-850
TELEFAX: (619) 235-0176
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
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FILING DATE: 07-DEC-1995
CLASSIFICATION: 435
ATTORNEY/AGBNT INFORMATION:
NAME: Israelsen, Ned
REGISTRATION NUMBER: 29,655
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Sequence 4, Application US/08568459A Patent No. 5849306
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                                                   GENERAL INFORMATION:
APPLICANT: Sim, Kim L.
APPLICANT: Chitnis, Chetan
APPLICANT: Miller, Louis H.
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Search completed: January 29, 2002, 10:24:00 Job time: 506 sec ,

us-09-763-397a-2.rai

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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5833;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
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1 MKFLVNVALVFMVVYISYIY......DFFGISYYEKVLAKYKDDLE
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                 GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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Maximum Match 100%
Listing first 45 summaries
                                                                                  OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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NON_TER
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26 HHHKHKKLKQPGDGNPWSPCSVTCG------KPKDELDYENDIEKKICKMEKC 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01.NOV-1996 (TrEMBLrel. 01, Created)
01.NOV-1996 (TrEMBLrel. 01, Last sequence update)
01.NOV-1996 (TrEMBLrel. 1), Last sequence update)
01.JUN -2001 (TrEMBLrel. 1), Last annotation update)
01.JUN -2001 (TrEMBLRel. 1), Last annotation update)
01.JUN -2001 (TrEMBLREL) (CS) PRECURSOR, VARIANT 2 (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 424;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Plasmodium falciparum.
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5833;
                                                                                                                                    Alveolata; Apicomplexa; Haemosporida; Plasmodium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12; Indels
                                                                                                                                                                                                                                                                                                                                                 Jongwutiwes S., Tanabe K., Kanbara H.;
Submitted (MAR-1992) to the EMBL/GenBank/DDBJ databases.
EMBL; M83169; AAA29547.1;
EMBL; M83149; AAA29562.1;
                                                                                                                                                                                                                                                                                                       Submitted (MAR-1992) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                    SMART; SM00209; TSP1; 1.
SEQUENCE 424 AA; 45592 MW; F20CEB60636DB98E CRC64;
                                                                        01.NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
CIRCUMSDROZOITE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 216.5; DB 5;
Pred. No. 7.5e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3; Mismatches
                                                    424 AA.
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                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                          Interpro; IPR000884; TSP1.
Interpro; IPR003067; Crcmsprzoite.
Pfam: PF00090; tsp_1: 1.
PRINTS; PR01303; CRCMSPRZOITE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLIND=91270295; PubMed=2052038;
Lockyer M.J.;
                                                                                                                                                                                          MEDLINE=84250215; PubMed=6204383;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
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1 Similarity 61.1%;
44; Conservative 3
                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         402 SSVFNVVNSSIG 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q99256 PRELIMINARY;
Q99256;
                                                                                                                              Plasmodium falciparum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             73 SSVFNVVNSNSG 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                              [1]
SEQUENCE FROM N.A.
    93 SSVFNVVNSSIG
                                                                                                                                               NCBI_faxID=5833;
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                                                                                                                                         Eukaryota;
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                                                                027425
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Q99256
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Q27425
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Dame J.B., Williams J.L., McOutchan T.F., Weber J.L., Wirtz R.A., Dame J.B., Williams J.L., Haynes J.D., Schneider I., Roberts D., Sanders G.S., Reddy P.E., Diggs C.L., Miller L.H.;
"Structure of the gene encoding the immunodominant surface antigen on the sporozoite of the human malaria parasite Plasmodium falciparum."; Science 225:593-599(1984).
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-1- MISCELLANEOUS: THE C-TERMINAL REGION IS PROBABLY USED FOR ANCHORING THE PROTEIN TO THE CELL MEMBRANE. THE REPEAT SEQUENCES WOULD BE THE SURFACE ANTIGEN OF THE ORGANISM.

EMBL, MS7489, AAA63422.1;

InterPro; IPR000884; TSP1.

InterPro; IPR000884; TSP1.

PRINTS; PR01303; CRCMSPEZOITE.

PRINTS; PR01303; CRCMSPEZOITE.

SMART; SM00209; TSP1.
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                                                                                                  MOI. Biochem. Parasitol. 45:179-182(1991).

-i- FUNCTION: THE CIRCUMSPOROZOITE PROTEIN IS THE IMMUNODOMINANT
SURFACE ANTIGEN ON THE SPOROZOITE (THE INFECTIVE STAGE OF THE
MALARIA PARASITE THAT IS TRANSMITTED FROM THE MOSQUITO TO THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels 13;
"Clonal variation in the Plasmodium falciparum circumsporozoite
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5833;
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Submitted (MAR-1992) to the EMBL/GenBank/DDBJ databases.
EMBL; M83155; AAA29568.1; --
EMBL; M83155; AAA29565.1; --
EMBL; M83158; AAA29565.1; --
EMBL; M83158; AAA29571.1; --
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q27246 PRELIMINARY; PRT; 432 AA. Q27246; 01-NOY-1996 (TrEMBLrel. 01, Created) 01-NOY-1996 (TrEMBLrel. 01, Last sequence update) 01-JUN-2001 (TrEMBLrel. 17, Last annotation update) CIRCUMSPOROZOITE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=84250215; PubMed=6204383;
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61.1%;
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Best Local Similarity
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la Cruz V.F.;
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STRAIN-BI.
STRAIN-BI.
Ge Stricker K., Vuust J., Jepsen S., Oeuvray C., Theisen M.;
de Stricker K., Vuust J., Jepsen S., Oeuvray C., Theisen M.;
"Sequence variation in the non-repeat region of the Plasmodium
falciparum glutamate rich protein (GLURP) from Brazil, Senegalese, and
Burmese field isolates and from laboratory strains.";
Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AJZ69941; CAB64167.1;
Interpro; IPR000884; TSP1.
Interpro; IPR0008067; Cromsprzoite.
Pfam: PP00090; tsp.1:
PRINTS; PR01303; CRCMSPRZOITE.
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"Sequence variation in the non-repeat region of the Plasmodium
falciparum glutamate rich protein (GLORP) from Brazil, Senegalese, and
Burmese fleld isolates and from laboratory strains.";
Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AJ269978; CAB64197.1;
InterPro; IPR000884; TSP1.
InterPro; IPR000808, Cromsprzoite.
Pfam; PF00090; LSP_1: 1.
PRINTS; PR01303; CRCMSPRZOITE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26 HHHKHKKLKQPGDGNPWSPCSVTCG------KPKDELDYENDIEKKICKMEKC 72
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                                                                                                                                                                                                                                          Plasmodium falciparum.
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5833;
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                                                                                                                                                                   (TrEMBLrel. 13, Last sequence update)
(TrEMBLrel. 17, Last annotation update)
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 5;
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63.8%; Pred. No. 1.3e-09;
tive 1; Mismatches 11
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                                                                                                                                                 01-MAY-2000 (TrEMBLrel. 13,
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Best Local Similarity 63.8
Matches 44; Conservative
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                                                                                                              PRELIMINARY;
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410 SSVFNVVNSSIG 421
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01-JUN-2001
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26 HHHKHKKLKQPGDGNPWSPCSVTCG------KPKDELDYENDIEKKICKMEKC 72
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                                                                                                                                                                                      Length 432;
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NCBL_TaxID=5833;
                                                                                                                                                                                                                           12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         la Cruz V.F.; Submitted (MAR-1992) to the EMBL/GenBank/DDBJ databases
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                                                                                                                              432 AA; 46414 MW; 8787E6005578873A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
CIRCUMSPOROZOITE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ch 11.3%; Score 216.5; DB 5; 11 Similarity 61.1%; Pred. No. 7.7e-09; 44; Conservative 3; Mismatches 12;
                                                                                                                                                                                    Score 216.5; DB 5;
Pred. No. 7.7e-09;
3; Mismatches 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        432 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mol. Biochem. Parasitol. 0:0-0(0).
EMBL; M83165; AAA2543.1; -.
Interpro: IPR000884; TSP1.
Interpro: IPR003067; Crmsprzoite.
Pfam; PF00090; tsp_1; 1.
                                 InterPro; IPR000884; TSP1.
InterPro; IPR003067; Crcmsprzoite.
PRAM; PF00090; tsp_1; 1.
PRINTS; PR01303; CRCMSPRZOITE.
SMART; SM00209; TSP1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-838;
MEDLINE-84250215; PubMed-6204383;
                                                                                                                                                                                                                         3;
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EMBL; M83166; AAA29544.1; -.
EMBL; M83168; AAA29546.1; -.
                                                                                                                                                                                    ch
11.3%;
1 Similarity 61.1%;
44; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                           SSVFNVVNSSIG 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PR01303; CRCM;
SMART; SM00209; TSP1;
                                                                                                                                                                                                                                                                                                                                      73 SSVFNVVNSNSG 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              73 SSVFNVVNSNSG 84
                                                                                                                                                                                      Query Match
Best Local Similarity
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Gaps

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InterPro; IPR000884; TSP1.
InterPro; IPR003067; Crcmsprzoite.
Pfam; PF00090; tsp_1; 1.
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MEDLINE-84250215; PubMed=6204383;
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SMART; SM00209; TSP1; 1.
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59.7%;
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                                                                                                                                                                                                               Query Match 11.1:
Best Local Similarity 59.7;
Matches 43; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Plasmodium falciparum
                                                                                                                                                                                                                                                                                                                           73 SSVFNVVNSNSG 84
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Best Local Similarity
                                                                                                                                                            117 1
117 AA;
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[1]
SEQUENCE FROM N.A.
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                                                                                                                                                            NON_TER
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13; Gaps
                                                                                                      Gaps
                                                                                                                          26 HHHKHKKLKQPGDGNPWSPCSVTCG------KPKDELDYENDIEKKICKMEKC 72
                                                                                                                                           Jongwutiwes S., Tanabe K., Hughes M.K., Kanbara H., Hughes A.L.;
"Allelic variation in the circumsporozoite protein of Plasmodium facilitation final disclates.";
Am. J. Trop. Med. Hyg. 51:659-668(1994).
EMBL: M83154; AAA29567.1; -.
ENBL: M83154; AAA29567.1; -.
Enterpro: IPR003067; Crcmsprzoite.
Ffam; PF00090; tsp_l: STP1:
Ffam; PR00309; TSP1: 1.
SWART; SW0209; TSP1: 1.
                                                                                                      13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 213.5; DB 5; Length 115;
Pred. No. 2.9e-09;
4; Mismatches 12; Indels 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Plasmodium falciparum.
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5833;
                                                                                                                                                                                                                                                                                                                                      Plasmodium falciparum.
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5833;
                                                                            Length 80;
                                                                                                      Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         025795;
01-NOV-1996 (TrEMBLrel. 01, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
CIRCUMSPOROZOITE PROTEIN (FRAGMENT).
                                       BFC6C970CEF0FA3E CRC64;
                                                                                                                                                                                                                                                                                            01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UNA-2001 (TrEMBLrel. 17, Last annotation update)
CIRCUMSPOROZOITE PROTEIN (FRAGMENT).
                                                                                                      11;
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                                                                          Score 215.5; DB 5
Pred. No. 1.3e-09;
1; Mismatches 11
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MEDLINE=95077069; PubMed=7985759;
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illarity 59.7%;
Conservative 4
                             80
9102 MW;
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Best Local Similarity 63.8%;
Matches 44; Conservative
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   SM00209; TSP1; 1.
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Matches 43; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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80
80 AA;
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72 SSVFNVVNS 80
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                              NON_TER
SEQUENCE
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                  NON_TER
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      SMART;
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Q25795
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Dame J.B., Williams J.L., McCutchan T.F., Weber J.L., Wirtz R.A., Hockmeyer W.T., Maloy W.L., Haynes J.D., Schneider I., Roberts D., Sanders G.S., Reddy P.E., Diggs C.L., Miller L.H.:
"Structure of the gene encoding the immunodominant surface antigen on the sporozoite of the human malaria parasite Plasmodium falciparum."; Science 225:593-599(1984).
Doolan D.L., Saul A., Good M.F.; "Geographically restricted heterogeneity of the Plasmodium falciparum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26 HHHKHKKLKQPGDGNPWSPCSVTCG------KPKDELDYENDIEKKICKMEKC 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 135 HIBOYLKKIONSLSTEWSPCSVTCGNGIOVRIKPGSANKPKDQLDYENDIEKKICKMEKC 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 213.5; DB 5; Length 416; Pred. No. 1.3e-08;
                                                       circumsporozoite protein: relevance for vaccine development. Submitted (FEB-1992) to the EMBL/GenBank/DDBJ databases.
EMBL; M7723; AAA29517.2; ...
InterPro; IPR003067; Crcmsprzoite.
InterPro; IPR003067; Crcmsprzoite.
Prin; PF001909; LSP_1. 1.
PRINTS: PR01303; CROMSPRZOITE.
SMART; SM00209; TSP1: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 117;
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                                                                                                                                                                                                                                                                                                                                                                                                  13110 MW; D96BE20944A7C726 CRC64;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11.1%; Score 213.5; DB 5;
59.7%; Pred. No. 2.9e-09;
tive 4; Mismatches 12;
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Jongwithwes S., Tanabe K., Kanbara H.;
Jongwithwes S., Tanabe K., Ranbara H.;
Mall Biochem. Parasitol. 0:0-0(0).
EMBL; M83172; AAA29550.1;
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de Stricker K., Vuust J., Jepsen S., Oeuvray C., Theisen M.;
"Sequence variation in the non-repeat region of the Plasmodium
falchparum glutamate rich protein (GLURP) from Brazil, Senegalese, and
Burmese field isolates and from laboratory strains.";
Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ269961; CAB64180.1;
InterPro: IPR000884; TSP1.
InterPro: IPR003067; Cromsprzoite.
Pfam: PF00090; tsp_l: 1.
PRINTS; PR01303; CRCMSPRZOITE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-835A;
MEDLINE-84250215; PubMed-6204383;
Dame J.B., Williams J.L., McCutchan T.F., Weber J.L., Wirtz R.A.,
Dame J.B., Williams J.L., Haynes J.D., Schneider I., Roberts D.,
Sanders G.S., Reddy P.E., Diggs C.L., Miller L.H.;
Structure of the gene encoding the immunodominant surface antigen on
the sporozoite of the human malaria parasite Plasmodium falciparum.";
Science 225:593-599(1984).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12 HIEQYLKTIQNSLSTEWSPCSVTCGNGIQVRIKPGSANKPKDELDYENDIEKKICKMEKC 71
Plasmodium falciparum.
Eukaryota: Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBL_TaxID=5833;
                                                                                                                                                                                                                                                                                                                                                                                                                         Length 80;
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
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                                                                                                                                                                                                                                                                                                                                                               9047 MW; BA769C90DB031C3E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
CIRCUMSPOROZOITE PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                      11.1%; Score 212.5; DB 5;
11arity 62.3%; Pred. No. 2.2e-09;
Conservative 2; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Jongwutiwes S., Tanabe K., Kanbara
Mol. Biochem. Parasitol. 0:0-0(0).
EMBL; M83160; AAA29573.1; -.
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InterPro; IPR003067; Crcmsprzoite.
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PRINTS; PR01303; CRCMSPRZOITE.
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Best Local Similarity
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Q25837
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                                     HHHKHKKLKQPGDGNPWSPCSVTCG------KPKDELDYENDIEKKICKMEKC 72
     13;
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Pred. No. 1.3e-08;
4; Mismatches 12; Indels 13
                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBL_TaxID=5833;
   12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (MAR-1992) to the EMBL/GenBank/DDBJ databases
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Mol. Blochem. Parasitol. 0:0-0(0).
EMBL. M83173; AAA29551.;
InterPro. IPR000884; TSP1.
InterPro: IPR000884; TSP1.
InterPro: IPR000807; Cromsprzoite.
Pfam; PF00090; tsp.1; 1.
PRINTS; PR01303; CRCAMSPRZOITE.
SEQUENCE 442 AA; 47414 MW; BFAF9D939D7862FF CRC64;
                                                                                                                                                                                                                                                                      01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
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1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
CIRCUMSPOROZOITE PROTEIN (FRAGMENT).
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     Mismatches
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1 Similarity 59.7%;
43; Conservative
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MEDLINE-84250215; PubMed-6204383;
Dame J.B., Williams J.L., McCutchan T.F., Weber J.L., Wirtz R.A.,
Hockmeyer W.T., Maloy W.L., Haynes J.D., Schneider I., Roberts D.,
Sanders G.S., Reddy P.E., Diggs C.L., Miller L.H.;
"Structure of the gene encoding the immunodominant surface antigen on
the sporozoite of the human malaria parasite Plasmodium falciparum.";
Science 225:593-599(1984).
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NCBI_TaxID=5833;
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SEQUENCE 115 AA; 12974 MW; 6BB538287260DA90 CRC64;
                           SEQUENCE 115 AA; 13018 MW; C0A23F5805688237 CRC64;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
CIRCUMSPOROZOITE PROTEIN (FRAGMENT).
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                                                           Score 212.5; DB 5
Pred. No. 3.4e-09;
4; Mismatches 12
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Mol. Biochem. Parasitol. 0:0-0(0).
EMBL; M83162; AAA29575.1;
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Interpro; IPR003067; Crcmsprzoite.
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PROSITE; PS50092; TSP1; 1
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Best Local Similarity 59.7%;
Matches 43; Conservative
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PS50092; TSP1; 1.
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          SM00209; TSP1;
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Dame J.B., Williams J.L., McCutchan T.F., Weber J.L., Wirtz R.A., Hockmeyer W.T., Maloy W.L., Haynes J.D., Schneider I., Roberts D., Sanders G.S., Reddy P.E., Diggs C.L., Miller L.H., "Structure of the gene encoding the immunodominant surface antigen on the sporozoite of the human malaria parasite Plasmodium falciparum."; Science 225:593-599(1984).
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Pred. No. 1.5e-08;
                                                                                                                                                       plasmodium falciparum (isolate K1 / Thailand).
Eukaryota, Alveolata, Apicomplexa, Haemosporida, Plasmodium.
NCBI_TaxID=5839;
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                                     01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
420 AA.
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Mol. Biochem. Parasitol. 0:0-0(0).
EMBL; M83174; AAA29552.1;
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InterPro; IPR003067; Crcmsprzoite.
Pfam; FR00090; tsp_1; 1.
PRINTS; PR01303; CROMSPRZOITE.
PROSITE; PS50092; TSP1; 1.
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59.78;
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Best Local Similarity 59.77
Matches 43; Conservative
                                                                                                                      CIRCUMSPOROZOITE PROTEIN.
  PRELIMINARY;
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SEQUENCE 420 AA; 45
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SEQUENCE FROM N.A.
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Compugen Ltd
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027336 plasmodium P90588 plasmodium Q927u8 chlamydia p 09m0s8 arabidopsis 097909 tragelaphus 007099 caenorhabdi Q966w4 arabidopsis Q9655 butyrivibri Q98556 butyrivibri Q97kk gadus morhu Q94kv7 hordeum vul Q94kv7 hordeum vul Q9601 arabidopsis Q95eg3 arabidopsis Q91m6 orobanche c Q94kf7 vibrio chol G32608 edwardsiell Description 027336 090288 090708 090708 0020045 020045 0908535 098535 097177 0946E0 095535 095537 095537 095537 095537 095537 095537 095537 095537 5 2 8 10 10 DB Query Match Length Score 44.5

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MEDLINE-9329437; PubMed-8515780;
MEDLINE-9329437; PubMed-8515780;
Lal A.A. Goldman I.F., Collins W.E., Kumar N.;
"Sequence of a 27-kilodalton gamete antigen of Plasmodium reichenowi and comparison with Ffg27 of Plasmodium falciparum.";
MMOI. Biochem. Parasitol. 59:175-176(1993).
EMBL: L08799; AAB42050.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Shirai M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi K., Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa T.; Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa T.; Comparison of Whole genome sequences of Chlamydia pneumoniae J138 from Japan and CWL029 from USA."; Nucleic Acids Res. 28:2311-2314(2000).
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MEDLINE=20150255; PubMed=10684935;
Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
White O., Hickey E.K., Peterson J., Umayam L.A., Utterback T.,
Berry K., Bass S., Linher K., Weidman J., Khouri H., Craven B.,
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NCBL_TaxID=5854;
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Pred. No. 1.8e-07;
1; Mismatches 0; Indels
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Bacteria; Chlamydiales; Chlamydiaceae; Chlamydophila.
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
CT488 HYPOTHETICAL PROTEIN.
CPN0600 OR CPJ0606 OR CP0141.
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MEDLINE=99206606; PubMed=10192388;
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Best Local Similarity 93.8
Matches 15; Conservative
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SECURINCE FROM N.A. Spiegel L.A., Huang E.N., Nascimento L.U., de la Bastide M., Vil D.M., Spiegel L.A., Huang E.N., Shah R., O'Shaughnessy A., Rodriguez M., Preston R.R., Matero A., Shah R., O'Shaughnessy A., Rodriguez M., Shekher M., Schutz K., See L.H., Swaby I., Habermann K., Dedhia N.N., Mewes H.W., Lemcke K., Mayer K.F.X., Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                            Gaps
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Bowman C., Dodson R., Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L., Eisen J., Fraser C.M.; "Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.";
Nucleic Acids Res. 28:1397-1406(2000).
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                                                                                                                                                                                                                                                                                                                Length 246;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      D6D9BCC70DFACOAE CRC64;
                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
MODIFICATION METHYLASE (EC 2.1.1.73) (CYTOSINE-SPECIFIC
                                                                                                                                                                                                                               Complete proteome.
Sentence 246 AA; 27619 MW; F3990B645AA0083B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    49.5%; Score 48; DB 10;
53.3%; Pred. No. 56;
                                                                                                                                                                                                                                                                                                                   Score 48; DB 2;
Pred. No. 7.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT; 1512 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                        InterPro; IPR000934; Ser_thr_phosphtse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00145; DNA methylase; 3. PRINTS; PR00105; C5METTRFRASE. SMART; SM00439; BAH; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Methyltransferase; Transferase.
SEQUENCE 1512 AA; 171154 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00094; C5_MTASE_1; 1. PROSITE; PS00095; C5_MTASE_2; 1.
                                                                                                                 49.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
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217 RPIDGFGNIRGIHY 230
                                                                                                                                                                                                                                                                                                                                                                                                          1 KPLDKFGNIYDYHY 14
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Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               METHYLTRANSFERASE).
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Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
Gardner A., Green P., Hawkins T., Hiller L., Jier M., Johnston L.,
Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
Lightning J., Lloyd C., Mcmurray A., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen R.,
Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J.,
Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
Watson A., Weinstock L., Willkinson-Sproat J., Wohldman P.;
"2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoldea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 46; DB 5; Length 207;
Pred. No. 13;
3; Mismatches 5; Indels
                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
Waterston R.;
Submitted (APR-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AF000264; AAC71122.1;
HSSP; P54149; IFVG.
InterPro; IPR02569; PMSR.
Pfam; PF01055; PMSR; 1.
ProDom; PD003489; PMSR; 1.
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Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases.
EMBL: U20741; AAA68327.1; -
SEQUENCE 339 AA; 38264 MW; DAE289FF34B70503 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                       Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24151 MW; 1CD4968C847A1013 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                339 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
MEDLINE-94150718; Pubmed-7906398;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       47.48;
50.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1998 (TrEMBLrel. 08,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                :|||||| | | ::
119 EPLDKFYQAEDYHQKY 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 47.4
Best Local Similarity 50.0
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 KPLDKFGNIYDYHYEH 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nature 368:32-38(1994).
                                                                            Nature 368:32-38(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       207 AA;
                                                                                                                                 SEQUENCE FROM N.A. STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COSMID F35D2.
                                                                                                                                                                                            Latreille P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Connell M.;
                                                     elegans."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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Q20045
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WEDLINE-94150718; PubMed-7906398;

WEDLINE-94150718; PubMed-7906398;

WILSON R., Ainscough R., Anderson K., Baynes C., Berks M.,

Bonfleld J., Button J., Connell M., Copsey T., Cooper J., Coulson A.,

Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,

Jones M., Kershaw J., Kirsten J., Hillier L., Jier M., Johnston L.,

Lightning J., Lloyd C., Mcmurray A., Mortimore B., O'Callaghan M.,

Parsons J., Percy C., Rifken L., Roopera A., Saunders D., Shownkeen R.,

Smaldon N., Smith A., Sonnhammer E., Staden R., Valston J.,

Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Schatzl H.M., Wopfner F., Weidenhofer G., Gilch S.;
"Analysis of 27 mammalian and 9 avian PrPs reveals high conservation of non-structural regions of the prion protein.";
Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
HSSP; p04165, IEIG.
HIGHPRO: IPR002935; Kininogen.
InterPro: IPR000817; Prion.
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Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
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01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
SIMILAR TO DROSOPHILIA ECDYSONE-INDUCED PROTEIN 28/29 KDA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24651 MW; 99FD0BAF0B6A0077 CRC64;
                                                                                                                                                               Last sequence update)
Last annotation update)
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                                                                            227 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 47; DB
Pred. No. 10;
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                                                                                                                                    Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PFam; PF00377; prion; 1.
PRINTS; PR00334; KININGGEN.
PRINTS; PR00341; PRION.
SMART; SM00157; PRP; 1.
PROSITE; PS00291; PRION.1; 1.
PROSITE; PS00706; PRION.2; 1.
                                                                                                                                                                                                                                                                                                                                                               Bovidae; Bovinae; Tragelaphus
                                                                                                                                                                                                                                                                         Tragelaphus angasii (nyala).
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57.18;
                                                                                                                           01-MAY-1999 (TrEMBLrel. 10, 01-MAY-1999 (TrEMBLrel. 10, 01-JUN-2001 (TrEMBLrel. 17,
                                                                                                                                                                                                                    PRION PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 48.5
Best Local Similarity 57.1
Matches 8; Conservative
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                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  :|| ||| |: ||
123 RPLTHFGNDYEDHY 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          F43E2.5.
Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 KPLDKFGNIYDYHY 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       227 2
227 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=66437;
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NON_TER
SEQUENCE
                                                                      097909
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                    RESULT
                                            906160
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ပ Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.; "2.2 Mb of contiguous nucleotide sequence from chromosome III of

Gaps ;

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Last sequence update)
Last annotation update)

Created) PRT;

08, 08, 08,

793 AA.

PRELIMINARY;

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SEQUENCE FROM N.A.

Kalmokoff M.L., Lu D., Whitford M.F., Teather R.M.;

"Evidence for two new lantibiotics (butyrivibriocin OR79A and OR79B),

"Evidence for two new annearobe Butyrivibrio fibrisolvens.
Isolated from the rumen annearobe Butyrivibrio fibrisolvens.
Identification of the structural gene encoding butyrivibriocin
                                                                                                                                            Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae;
Butyrivibrio.
                                                                                01-NOV-1998 (TERBELFEL. 08, Last sequence ol-NOV-1998 (TERBELFEL. 08, Last annotat. HYPOTHETICAL 92.6 KDA PROTEIN (FRAGMENT) Butyrivibrio fibrisolvens.
                                                                      01-NOV-1998 (TrEMBLrel.
                                                                                                                                                                                                   NCBI_TaxID=831;
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RESULT
085356
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RA Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,
RA White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,
RA White O., Alonso J., Chao H., Chen H., Cheuk R.F., Chin C.W..
RA Chung M.K., Conn L., Conway A.R., Creasy T.H., Dewar K.,
RA Chung M.K., Conn L., Conway A.R., Creasy T.H., Dewar K.,
RA Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,
RA Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,
RA Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,
RA Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,
RA Lin X., Liu S.X., Luros J.S., Maitl R., Marialall A.,
RA Milltscher J., Miranda M., Nayven M., Nierman W.C., Osborne B.I.,
RA Sana H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,
RA Utterback T., Van Aken S., Vaysberg M., Vysotskaia V.S., Walker M.,
RA WH. Salzer C.M., Venter J.C., Davis R.W.;
RA W.D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;
RT "Sequence and analysis of chromosome I of the plant Arabidopsis
                                                                          ö
                                                                                                                                                                                                                                                                                                                                                             Arabidopsis thaliana (Mouse-ear cress).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nature 408 (816-820(2000).

**Interpose RESIDUES IN BETA-D-GALACTOSIDES.

GALACTOSE RESIDUES IN BETA-D-GALACTOSIDES.

GALACTOSE RESIDUES IN BETA-D-GALACTOSIDES.

EMBL; AC074360; AAG60136.1; -.

Interpro; IPR001944; Glyco_hydro_35.

Pfam; PF02140; Gal_Lectin; 1.

Pfam; PF01301; Glyco_hydro_35; 1.

PR01304; Glyco_hydro_35; 1.
                                                                              Gaps
                                                                            ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 779;
                                     Score 45; DB 5; Length 339;
Pred. No. 32;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Glycosidase; Hydrolase; Hypothetical protein.
SEQUENCE 779 AA; 86342 MW; 888813DF318890B0 CRC64;
                                                                                                                                                                                                                                                                                                01-JUN-2001 (TrEMBLrel. 17, Last sequence update) 01-JUN-2001 (TrEMBLrel. 17, Last annotation update) BETA-GALACTOSIDASE (EC 3.2.1.23) (LACTASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 10;
80;
                                                                                                                                                                                                                                              779 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ProDom; PD005612; Gal_lectin; 1.
PROSITE; PS01182; GLYCOSYL_HYDROL_F35; 1.
PROSITE; PS50228; SUEL_LECTIN; 1.
                                                                                                                                                                                                                                                                                     Created)
                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN-CV. COLUMBIA;
MEDLINE-21016719; PubMed-11130712;
                                            46.48;
                                                                                                                                                                                                                                                                                   01-JUN-2001 (TrEMBLrel. 17, 01-JUN-2001 (TrEMBLrel. 17, 01-JUN-2001 (TrEMBLrel. 17, 01-JUN-2001 (TrEMBLrel. 17,
                                                                                 Conservative
                                                                                                                                                                                                                                                PRELIMINARY;
                                              Query Match
Best Local Similarity
                                                                                                                                          |:| ||:::||
188 PIDPFGSLFDY 198
                                                                                                                   2 PLDKFGNIYDY 12
                                                                                 9
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SEQUENCE
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                                                                                 Matches
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MEDLINE-94150718: pubMed-7906398;
Milson R., Ainscough R., Anderson K., Baynes C., Berks M.,
Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
Jones M., Kershaw J., Kirsten J., Laister N., Latrelle P.,
Lightning J., Lloyd C., Nemurray A., Mortimore B., O'Callaghan M.,
Lightning J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen R.
Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J.,
Thierry Mieg J., Thomas K., Yaudin M., Vaughan K., Watston P.,
Matson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.;
2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                              ;;
                                                                                                                                                                                                                                                          DB 2; Length 793;
                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nature 368:32-38(1994).

EMBL; Z68493; CAA97795.1; -.

InterPro; IPR003839; DUF215.

PROUGNGE 336 AA; 38680 MW; 4F8AAADE8FD43D90 CRC64;
Submitted (MAX-1998) to the EMBL/GenBank/DDBJ databases EMBL; AF065647; AAC19356.1; -. Hypothetical protein. NON_TER 793 793
                                                                                                                                                8EE72F58A098D997 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01, Created)
05, Last sequence update)
17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                              Score 44.5;
Pred. No. 98;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                       793 AA; 92557 MW;
                                                                                                                                                                                                                                                              45.9%;
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                                                                                                                                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1996 (TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16
                                                                                                                                                                                                                                                                                                                                                                                                              5 KFGNIY-DYHYEH 16
                                                                                                                                                                                                                                   Query Match
Best Local Similarity
9; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 KFGKIYIDYLYDH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         elegans."
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                                                                                                                                                               SEQUENCE
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Gaps

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Indels

5;

Mismatches

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Conservative

Query Match Best Local Similarity Matches 8; Conserv

|||:|||: |PLDEFGNLNQPKYGH 326 PLDKFGNIYDYHYEH 16

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Score 45; Pred. No. 8

46.4%;

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Proctor R.H., Seo J.-A., Plattner R.D.;

"Characterization of four clustered and coregulated genes associated
"Characterization of four clustered and coregulated genes associated
"The fumonish biosynthesis in Fusarium verticillioides.";

"Labmitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.";

"SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.

EMBL, AFI55773, AAG27132.1;

"R InterPro; IPR001128; CYL_2450.

"R InterPro; IPR001109; FlavAyin'ike.

"R InterPro; IPR001094; FlavAyin'icyt_redctse.

"R InterPro; IPR001133; Oxidored_FAD.

"R Pfam; PF00667; FAD_binding; 1.

"R Pfam; PF00175; oxidored_FAD.
"R Pfam; PF00175; oxidored_FAD.
"R Pfam; PF00175; oxidored_FAD."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreales; Nectriaceae; Gibberella.
NCBI_TaxID=117187;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1115;
Length 656;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5C6D2B947AE86C25 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAY 2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
MODIFICATION METHYLASE (EC 2.1.1.73) (CYTOSINE-SPECIFIC
                                                                                                                                                                                                                       01-WAR-2001 (TrEMBLrel. 16, Created)
01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                   3;
DB 10;
96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 44; DB 3; 1
Pred. No. 1.7e+02;
6; Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PR00385; P450.
PROSITE; PS00086; CYTOCHROME_P450; UNKNOWN_1.
                                                                                                                                                                                         PRT; 1115 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1404 AA
                                 3; Mismatches
   Score 44;
                   Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Heme; Monooxygenase; Oxidoreductase.
SEQUENCE 1115 AA; 123276 MW; 5C6
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45.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 37.5%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRINTS; PR00369; FLAVODOXIN.
PRINTS; PR00371; FPNCR.
                 Best_Local Similarity 53.8
Matches 7; Conservative
                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 KPLDKFGNIYDYHYEH 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                              Gibberella moniliformis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         T6G15.160 OR AT4G13610.
                                                                                        ||||| ::||:|
414 KPLDHPADLYDFH 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 KPLDKFGNIYDYH 13
                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. STRAIN=M-3125;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=3702;
 Query Match
                                                                                                                                                                                                          Q9HGEO;
                                                                                                                                                     RESULT 13
Q9HGE0
                                                                                                                                                                                         Q9HGE0
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                                                   Gaps
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Eukaryota: Viridiplantae: Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta: Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldeae;
NCBI_TaxID=4513;
                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.

Arvidsson A.-K., Wraith A., Jonsson-Rylander A.-C., Larhammar D.;

Arvidsson A.-K., Wraith A., Jonsson-Rylander A.-C., Larhammar D.;

Cloning of a neuropeptide Y/Peptide YY receptor from the Atlantic

cod: the Yb receptor.

Regul. Pept. 0:0-0(1998).

EMBL: AF073925; AAD02833.1;

InterPro: IPR000276; GPCR_Rhodpsn.
                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Paracanthopterygii; Gadiformes; Gadoidei; Gadidae;
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                 Length 336;
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                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 7), Last sequence update)
01-JUN-2001 (TrEMBLrel. 7), Last annotation update)
ARABINOXYLAN ARABINOFURANOHYDROLASE ISOEKXYME AXAH-II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       42260 MW; D2A9C9516C4998E2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           656 AA; 71999 MW; 4D04531E6948415A CRC64;
                                                                                                                                                                                                                                       01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
NEUROPEPTIDE Y/PEPTIDE YY RECEPTOR YB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lee R.C., Burton R.A., Hrmova M., Fincher G.B.; "Barley arabinoxylan arabinofuranohydrolases."; Blochem. J. 0:0-0(2001).
EMBL; AF320325; AAK21880.1; -. Hydrolase.
SEQUENCE 656 AA; 71999 MW; 4D04531E6948415A
                Score 44; DB 5;
Pred. No. 46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                656 AA.
                                                                                                                                                                                                         374 AA
                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                         PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00001; 7tm_1; 1.
PRINTS; PR00237; GPCRRHODOPSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         45.4%;
                45.4%;
                                                                                                                                                                                                                                                                                                                          Gadus morhua (Atlantic cod).
                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 45.4
Best Local Similarity 42.9
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Receptor; Neuropeptide
SEQUENCE 374 AA; 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 PLDKFGNIYDYHYE 15
                                                                                                     ||::| |||:
189 FGSVYIYHYQ 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    374 AA;
              Query Match
Best Local Similarity
Matches 6; Conserv
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SEQUENCE FROM N.A.
                                                                                 6 FGNIYDYHYE 15
                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=8049;
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                                                                                                                                                                                                                         Q9YHX1
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                                                                                                                                                                                                       Q9YHX1
                                                                                                                                                                     RESULT 11
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SEQUENCE FROM N.A.

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Arabidopsis thaliana (Mouse-ear cress).
Arabidopsis thaliantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.

STRAIN-CV. COLUMBIA;

BIDLINE-20044094;

GENGER R.K., ROVAC K.A., Dennis E.S., Peacock W.J., Finnegan E.J.;

GENGER R.K., ROVAC K.A., Dennis E.S., Peacock W.J., Finnegan E.J.;

"Multiple DNA methyltransferase genes in Arabidopsis thaliana.";

"Multiple DNA methyltransferase genes in Arabidopsis thaliana.";

"In the Mol. Biol. 41:269-278(1999)

-1 - CATALYTIC ACTIVITY: S-ADENOSYL-L-METHIONINE + DNA CYTOSINE = S-ADENOSYL-L-HOMOCYSTEINE + DNA 5-METHYLCYTOSINE.

-1 - SIMLARITY: TO C-5 CYTOSINE-SPECIFIC DNA METHYLASE FAMILY.

BNBL; AF138283; AAF1482.1; -..

HISSP: P20589; IOCT.
Bevan M., Murphy G., Ridley P., Hudson S., Bancroft I., Mewes H.W., Mayer K.F.X., Schueller C.;
Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                   Score 44; DB 10; Length 1404;
Pred. No. 2.2e+02;
3; Mismatches 5; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 17, Last annotation update)
MODIFICATION METHYLASE (EC 2.1.1.73) (CYTOSINE-SPECIFIC
                                                                       EU Arabidopsis sequencing project;
Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT; 1517 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HSPF; ELOSSY; LOLD.
InterPro: IPR001025; BAH.
InterPro: IPR001025; C5_DNA_meth.
InterPro: IPR001048; EF hand.
InterPro: IPR001048; EF hand.
Pfam: PF00145; DNA_methylase; 3.
PRINTS; PR00105; C5METTRFRASE.
SWART; SW00109; C5METTRFRASE.
PROSITE; PS000994; C5_MTASE_1: 1.
PROSITE; PS00095; C5_MTASE_2: 1.
                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 46.7%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 || |: :||| :|
102 KPSKKYKKLYDYFFE 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 KPLDKFGNIYDYHYE 15
                                                                 SEQUENCE FROM N.A.
                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  09SEG3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 15
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DR PROSITE; PS00018; EF_HAND; UNKNOWN_1.

KW Methyltransferase. Transferase.

SQ SEQUENCE 1517 AA; 171324 MW; AF0B810C3AFDB54A CRC64;

Query Match

Best Local Similarity 45.4%; Score 44; DB 10; Length 1517;

Best Local Similarity 46.7%; Pred. No. 2.4e+02;

Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps

Qy 1 KPLDKFGNIYDYHYE 15
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Db 159 KPSKKYKKLYDYFFE 173

Search completed: January 29, 2002, 11:12:09 Job time: 765 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

January 29, 2002, 10:26:33; Search time 144.96 Seconds (without alignments) 8.408 Million cell updates/sec

US-09-763-397A-3 97 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 1 KPLDKFGNIYDYHYEH 16 Scoring table:

219241 seqs, 76174552 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

pir1:\* pir2:\* pir3:\* pir4:\* PIR\_68:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		dР			SUMMARIES	
Result No.	Score	Query Match	Length	DB	ID	Description
П	97	100.0	217	~	S27829	qametocytoqenesis
7	48	49.5	246	~	H72057	conserved hypothet
Э	48	49.5	246	~	C86566	CT488 hypothetical
4	48	49.5	1512	ď	G85090	hypothefical prote
2	46	47.4	207	7	T34041	
φ	45	46.4	339	~	T16273	
7	45	46.4	392	7	C72427	pyruvate synthase
89	44.5	45.9	316	7	G65021	transaldolase (EC
σ	44.5	45.9	316	~	A85889	transaldolase A [1
10	44.5	45.9	507	7	S23422	catalase (EC 1.11.
11	44	45.4	336	7	T19665	hypothetical prote
12	44	45.4	591		CBBY2	L-lactate dehydrog
13	44	45.4	867		JH0225	L96 protein - Tipu
14	44	45.4	1072	7	A38457	占
15	44	45.4	1404		T06663	DNA (cytosine-5-)-
16	44	45.4	1519	7	G71402	DNA (cytosine-5-)-
17	44	45.4	1534	7	S59604	DNA (cytosine-5-)-
18	43	44.3	358	-	A48952	triacylglycerol li
19	43	44.3	540	~	A70358	topoisomerase I -
20	43	44.3	009	~	C82126	conserved hypothet
21	43	44.3	1594	~	T43072	
22	42	43.3	169	~	G84155	hypothetical prote
23	42	43.3	273	~	G81778	Q)
24	42	43.3	395	~	T15302	hypothetical prote
25	42	43.3	490	7	T49616	hypothetical prote
56	42	43.3	1182	~	G71607	probable integral
27	42	43.3	1683	~	S56811	probable membrane
28	41.5	42.8	385	7	T11848	gibberellin 20-oxi
58	41.5	42.8	687	~	JQ1044	arylphorin precurs

replication factor	hypothetical prote	lysine-rich surfac	cytochrome P450 3	DNA-binding protei	probable GT-11ke t	probable 3-hydroxy	dynein heavy chain	hypothetical prote	hypothetical prote	deoxynucleotide mo	bioC protein homol	probable trascript	site-specific DNA-	3-isopropylmalate	hypothetical prote
B37281	D96840	S58472	A40843	S39484	F96797	F71660	T30299	T38490	T07456	KIBPD4	B64456	T41149	S15908	C70322	T27670
~	~	-	~	~	7	~	~	~	~	7	٦	7	~	7	7
273	274	294	503	575	603	720	1114	798	87	241	251	332	358	364	398
42.3	42.3	42.3	42.3	42.3	42.3	42.3	42.3	41.8	41.2	41.2	41.2	41.2	41.2	41.2	41.2
			_	_	_	4	-	2.	0	40	0	0	0	0	0
41	41	41	4	4	4	4	4	40.5	•	•	`	4	4	4	4

## ALIGNMENTS

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gametocytogenesis onset-specific protein - malaria parasite (Plasmodium falciparum)

C;Species: Plasmodium falciparum C;Date: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 09-Jun-2000

C; Accession: \$27829
R; Alano, P.; Premawansa, S.; Bruce, M.; Carter, R.
submitted to the EMBL Data Library, April 1991
A; Reference number: \$27829
A; Reference number: \$27829
A; Accession: \$27829
A; Molecule type: mRNA
A; Residues: -1-217 ALA>
A; Residues: -1-217 ALA>
A; Cross-references: GB:X84904; EMBL:M38286; NID:q1340125; PID:e139902; PID:g1340126

ö Gaps . 0 Length 217; Indels 100.0%; Score 97; DB 2; L ilarity 100.0%; Pred. No. 4.6e-08; Conservative 0; Mismatches 0; Query Match Best Local Similarity Matches 16; Conserv

1 KPLDKFGNIYDYHYEH 16 QQ δ

10 KPLDKFGNIYDYHYEH 25

## ~ RESULT

Cispecies: Chlamydophila pneumoniae (strains Nilternate names: ct488 hypothetical protein (Species: Chlamydophila pneumoniae, Chlamydia pneumoniae (Species: Charcession: H72057; C81609 #sequence\_revision 23-Apr-1999 #text\_change 11-May-2000 Rikalman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood, Nature Genet. 21, 385-389, 1999 A; Title: Comparative genomes of Clamydia pneumoniae and C. trachomatis. A; Reference number: A72000; MUID:99206606 A; Reference number: A72000; MUID:99206606 A; Molecule type: DNA A; Residues: 1-246 cARN> A; Molecule type: DNA A; Residues: 1-246 cARN> A; Cross-references: GB:AE001645; GB:AE001363; NID:94376896; PIDN:AAD18745.1; PID:9437 A; Experimental source: strain CWL029 R; Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hicke, C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBOy, R.; Kolonay, J.; McClarty, G.; Salzbe, Nucleic Acids Res: 28, 1397-1406, 2000

A;Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39 A;Reference number: A81500; MUID:20150255 A;Accession: C81609

A;Status: preliminary A;Molecule type: DNA A;Residues: 1-246 <REA> A;Cross-references: GB:AE002175; GB:AE002161; NID:g7189069; PIDN:AAF38023.1; PID:g718

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A;Cross-references: EMBL:U28741; NID:9861290; PID:9861293; PIDN:AAA68327.1; CESP:F35D
A;Experimental source: strain Bristol N2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C72427
pyruvate synthase (EC 1.2.7.1) alpha chain - Thermotoga maritima (strain MSB8)
pyruvate pames: pyruvate--ferredoxin 2-oxidoreductase alpha subunit
C;Species: Thermotoga maritima
C;Species: Thermotoga maritima
C;Date: 11-Jun-1999 #sequence_revision 18-Jun-1999 #text_change 21-Jul-2000
C;Accession: C72427; A54346
E;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hic Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A, Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ó
                                                                                                                                                                                                                                                                                            A;Cross-references: EMBL:AF000264; PIDN:AAC71122.1; GSPDB:GN00020; CESP:F43E2.5
A;Experimental source: strain Bristol N2; clone F43E2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
0
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C;Species: Caenorhabditis elegans
C;Date: 20-Sep_1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
                     hypothetical protein F43E2.5 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 29-0ct-1999 #sequence_revision 29-0ct-1999 #text_change 29-0ct-1999
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A;Gene: CESP:F35D2.1
A;Introns: 76/1; 102/1; 136/3; 174/1; 240/2; 268/1; 298/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Accession: T16273
R;Connell, M.
Submitted to the EMBL Data Library, June 1995
A;Description: The sequence of C. elegans cosmid F35D2.
A;Reference number: Z18488
A;Accession: T16273
A;Accession: T16273
A;Atcus: preliminary; translated from GB/EMBL/DDBJ
                                                                          C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #tex
C;Accession: T34041
R:Latreille, P. Submitted to the EMBL Data Library, April 1997
A;Description: The sequence of C. elegans cosmid F43E2.
A;Reference number: Z21467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 45; DB 2;
Pred. No. 13;
4; Mismatches
                                                                                                                                                                                                                             A;Status: prelimināry; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-207 <LAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 46; DB 2,
Pred. No. 5.3;
3; Mismatches
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Best Local Similarity 54.5
Matches 6; Conservative
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119 EPLDKFYQAEDYHQKY 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 50.0
Matches 8; Conservative
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188 PIDPEGSLEDY 198
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A; Residues: 1-339 <CON>
                                                                                                                                                                                                                                                                                                                                                                           A; Gene: CESP:F43E2.5
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A; Introns: 83/3
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                                                                                                                                                                                                                                                                                                                                                 C; Species: Chlamydophila pneumoniae, Chlamydophila pneumoniae (strain J138)
C; Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C; Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 02-Mar-2001
C; Accession: C86566
C; Accession: C86566
A; Title: Comparison of Whole genome sequences of chlamydia pneumoniae J138.
A; Reference number: A86491; MUID: 20330349
A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein A74908990 [imported] - Arabidopsis thaliana C. Species: Arabidopsis thaliana (mouse-ear cress) C. Species: Arabidopsis thaliana (mouse-ear cress) C. Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 16-Feb-2001 C. Accession: G85090 R. Arabidopsis Genome Sequencing Consortium, The Cold Sprin Nature 402, 769-777, 1999 Arabidopsis Genome Sequencing Consortium, The Cold Sprin Nature 402, 769-777, 1999 Arabidopsis of Chromosome 4 of the plant Arabidopsis thaliana. A Hecession: G85090 A85001; MUID:20083488
                          C;Genetics:
A;Gene: CPN0606; CP0141
C;Superfamily: unassigned probable phosphoesterases; phosphoesterase core homology
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                                                                                                                                                                             ;
0
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Pred. No. 25;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 2;
                                                                                                                                  DB 2;
                                                                                                                                  Score 48; DB 2;
Pred. No. 3.1;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 48; DB 2
Pred. No. 3.1;
2; Mismatches
A; Experimental source: strain AR39, HL cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     57.18;
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53.3%;
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KPASKYKKIYDYFFE 173
                                                                                                                   Query Match
Best Local Similarity 57.1*
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 KPLDKFGNIYDYHYE 15
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217 RPIDGFGNIRGIHY 230
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Best Local Similarity 5
".....ag 8; Conservat
                                                                                                                                                                                                                                1 KPLDKFGNIYDYHY 14
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Best Local Similarity
Matches 8; Conserva'
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A; Molecule type: DNA
A; Residues: 1-1512 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-246 <STO>
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A; Map position: 4
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G85090
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Hic

4 15:23:47 2002

Mon Keb

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A.Title: Genome sequence of enterohemorrhagic Escherichia coli 0157:H7.

A.Reference number: A85480; MUD:21074935; PMID:11206551

A.Accession: A85889
A.Status: preliminary
A.Molecule type: DNA
A.Rolscule type: DNA
A.Kross references: GB:AE005174; NID:q12516839; PIDN:AAG57573.1; GSPDB:GN00145; UWGP:
A.Experimental source: strain 0157:H7, substrain EDL933
C.Genetics:
A.Gene: tala
C.Superfamily: human transaldolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       methylotrophic yeast Han
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C; Species: Pichla angusta
C; Species: Pichla angusta
C; Date: 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change 20-Apr-2000
C; Date: 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change 20-Apr-2000
C; Date: 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change 20-Apr-2000
R; Diddion, T.; Roggenkamp, R.
FEBS Lett. 303, 113-116, 1992
A; Title: Targething signal of the peroxisomal catalase in the methylotrophic yeas
A; Reference number: $23422; MUID:92299073
A; Recession: $23422
A; Molecule type: DNA
A; Residues: 1-507 < DID>A; Residues: 1-507 < DID>A; Cross-references: EMBL:X56501; NID:92775; PIDN:CAA39856.1; PID:92776
C; Superfamily: catalase
C; Superfamily: catalase
C; Keywords: chromoprotein; heme: iron; metalloprotein; oxidoreductase
F; 55, 104, 138/Active site: His, Ser, Asn #status predicted
F; 348/Binding site: heme iron (Tyr) (axial ligand) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein C33A12.11 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jul-2000
C;Accession: T19665
R;Wilkinson, J.
Submitted to the EMBL Data Library, January 1996
A;Reference number: Z19159
A;Accession: T19665
A;Accession: T
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A;Introns: 149/3; 202/3; 270/3
C;Superfamily: Caenorhabditis elegans hypothetical protein C33A12.9b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11;
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Pred. No. 26;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  catalase (EC 1.11.1.6) - yeast (Pichia angusta)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               45.9%; Score 44.5; 33.3%; Pred. No. 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | | | : | : | | 189 KPMDPYVVEEDPGVKSVRNIYDYYKQH 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 KPLDKF------GNIYDYHYEH 16
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    Nature 409, 529-533, 2001
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Matches 8; Conserv
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Matches 9; Conserv
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                                                                                       A; Molecule type: DNA
A; Residues: 'MR',1-392 <NEL>
A; Cross-references: GB:AE001690; GB:AE000512; NID:g4980496; PIDN:AAD35111.1; PID:g49805G
A; Experimental source: strain MSB
A; Note: an incorrect initiation codon was used
A; Note: an incorrect initiation codon was used
Biochemistry 3.M.; Adams, M.W.
Biochemistry 33, 1000-1007, 1994
A; Title: Characterization of an ancestral type of pyruvate ferredoxin oxidoreductase fro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Gene: TM0017
C;Superfamily: pyruvate synthase alpha chain; 2-oxoacid ferredoxin oxidoreductase homolc
C;Keywords: coenzyme A; oxidoreductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C; Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 31-Mar-2001
C;Accession: A65889
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
Iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ပိ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Species: Escherichia coll
C;Species: Escherichia coll
C;Species: Escherichia coll
C;Species: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 12-Nov-1999
C;Accession: G55021
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.;
A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coll K-12.
A;Reference number: A64720; MUID:97426617
A;Status: nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                   A; Reference number: A54346; MUID:94137707
A; Accession: A54346; MUID:94137707
A; Accession: A54346
A; Status: preliminary
A; Mcedule type: protein
A; Residues: 1-43 < BLA>
A; Experimental source: etrain not at a contract of a
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Note: sequence extracted from NCBI backbone (NCBIP:143495)
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Pred. No. 15;
4; Mismatches
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Pred. No. 16;
3; Mismatches
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16;
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A; Reference number: A72200; MUID:99287316
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Best Local Similarity 33.3%;
Matches 9; Conservative .4
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53.3%;
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Best Local Similarity
Matches 8; Conserv
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A; Reference number: JH0225; MUID:91078646
A; Accession: JH0225; MUID:91078646
A; Accession: JH0225
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-867 < HOM>
A; Cross - reference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Gallus gallus (Chicken)
C;Date: 20-Mar-1992 #sequence_revision 20-Mar-1992 #text_change 29-Sep-1999
C;Date: 20-Mar-1992 #sequence_revision 20-Mar-1992 #text_change 29-Sep-1999
C;Accession: A38457; S16429
J. Cell Biol. 113, 405-416, 1991
A;Title: Laminin receptors in the retina: sequence analysis of the chick integrin alp A;Reference number: A38457; MUID:91185416
A;Accession: A38457
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C:Keywords: cell adhesion; cytoskeleton; phosphoprotein; transmembrane protein
F;81-591/Product: L-lactate dehydrogenase (cytochrome) #status predicted <MAT>F;88-159/Domain: cytochrome b5 core homology <CB5>F;200-504/Domain: (S)-2-hydroxy-acid oxidase homology <2HY>F;213,146/Binding site: heme iron (His) (axial ligands) #status experimental F;429,459,493,513/Bunding site: FMN (Lys, Asp, Arg, Arg) #status experimental F;453/Active site: His #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JH0225

196 protein - Tipula iridescent virus

196 protein - Tipula iridescent virus

C; Species: Tipula iridescent virus

C; Date: 16-Jul-1999 #Sequence_revision 16-Jul-1999 #text_change 21-Jul-2000

C; Accession: JH0225

R;Home, W.A.: Tajbakhsh, S.; Seligy, V.L.

R;Home, W.A.: Tajbakhsh, S.; Seligy, V.L.

R;Home, W.A.: 1990

A;Title: Molecular cloning and characterization of a late Tipula iridescent
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A;Molecule type: mRNA
A;Residues: 1-1072 <DEC>
A;Cross-references: GB:X56559; NID:g63541; PIDN:CAA39909.1; PID:g63542
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Pred. No. 72;
1; Mismatches
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Pred. No. 56;
0; Mismatches
                                                                                                                                                                                                                                                                                                            ore 44; DB 1
red. No. 36;
Mismatches
                                                                                                                                                                                                                                                                                                                   Score 44;
Pred. No.
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Best Local Similarity 58.3.
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198 PLDNIINLYDFEY 210
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A; Molecule type: protein
A; Molecule type: protein
B; Molecule type: 197-465, 0', 467-513, 'E', 515-591 < LED>
B; Mochimic SB, 305-316, 1976
Biochimic SB, 305-316, 1976
Bi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: protein
A; Residues: 80,82-164,'E',166-394 <GHR>
R; Guiard, B.; Lederer, F.; Jacq, C.
Rature 255, 422-423, 1975
A; Title: More similarity between bakers' yeast L-(+)-lactate dehydrogenase and liver mid
A; Reference number: A93173; MUID:75156546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    L-lactate dehydrogenase (cytochrome) (EC 1.1.2.3) precursor - yeast (Saccharomyces cerev N;Alternate names: cytochrome b2; flavocytochrome B2; protein YM958.08c; protein YML054 C;Species: Saccharomyces cerevisiae
C;Species: 24-Apr-1984 #sequence_revision 31-Mar-1993 #text_change 21-Jul-2000 C;Accession: A24583; S49806; A91136; A93173; A23095; A90671; A00175
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBO J. 4, 3265-3272, 1985
A;Title: Structure, expression and regulation of a nuclear gene encoding a mitochondrial
A;Reference number: A24583; MUID:86135959
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A;Residues: 'N',82-94 <GUI2>
R;Lederer, F.; Cortial, S.; Becam, A.M.; Haumont, P.Y.; Perez, L.
Bur. J. Blochem. 152, 419-428, 1985
A;Title: Complete amino acid sequence of flavocytochrome b2 from baker's yeast.
A;Reference number: A91154; MUID:86030284
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A;Reference number: A44532; MUID:90230315
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A;Residues: 1-591 <GUI1>
A;Cross-references: EMBL:X03215; NID:93632; PIDN:CAA26959.1; PID:93633
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Eur. J. Biochem. 139, 59-74, 1984
A;Title: Primary structure of flavocytochrome b2 from baker's yeast.
A;Reference number: A91136; MUID:84132029
A;Accession: A91136
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                                                              Length 336;
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A;Residues: 88-121, fo',123-164,'E',166-183 <GUI3>
R;Xia, Z.; Mathews, F.S.
J. Mol. Biol. 212, 837-863, 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R; Devlin, K.; Churcher, C. submitted to the EMBL Data Library, November 1994 A; Reference number: $49800 A; Accession: $49806
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A;Gene.SGD:CYB2; MIPS:YML054c
A;Cross-references: SGD:S0004518; MIPS:YML054c
A;Map position: 13L
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                                                              Score 44;
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A; Residues: 1-591 <DEV>
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Gaps

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DNA (cytosine-5-)-methyltransferase (EC 2.1.1.37) T6G15.160 - Arabidopsis thaliana N.Alternate names: protein T6G15.160
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 05-May-2000
C:Accession: T06663
R:Bevan, M.: Murphy, G.; Ridley, P.: Hudson, S.; Bancroft, I.; Mewes, H.W.; Mayer, K.F.X submitted to the Protein Sequence Database, April 1999
A:Reference number: 215791
A:Residues: 1-1404 <BEV>
A:Residues: 1-1404 <BEV>
A:Residues: 1-1404 <BEV>
A:Cossion: T06663
A:Molecule type: DNA
A:Residues: 1-1404 <BEV>
A:Cossion: T0665
A:Experimental source: cultivar Columbia; BAC clone T6G15
C:Genetics: A:Genetics: A:G
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Pred. No. 98;
3; Mismatches 5; Indels
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Best Local Similarity 46.7%;
Matches 7; Conservative
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Search completed: January 29, 2002, 10:26:34 Job time: 645 sec THIS PAGE BLANK (USPTO)

Mature Pseudomonas
Ford OmpA signal

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Recombinant protein; CDC/NIIMALVAC-1; multivalent; malaria; vaccine; T-cell epitope; tetanus toxoid; antigenic epitope; treatment; circumsporozoite protein; CSP; sporozoite surface protein-2; SSP-2; liver stage antigen-1; LSA-1; merozoite surface protein-1; MSP-1; apical membrane antigen-1; AMA-1; erythrocyte binding antigen-175; EBA-175; rhoptry associated protein-1; RAP-1; gamete specific antigen; Pfg27; antiparasitic; prevention; anti-CDC/NIIMALVAC-1 antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Plasmodium falciparum Pfg27 antigenic epitope, P591.
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AAR10437
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AAB32984
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AAG07900
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WO200011179-A1.
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RESULT
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S. epidermidis ope
S. epidermidis ope
Amino acid sequenc
Soybean POP2/CAF1
Soybean POP2/CAF1
Pollyeptide with 1
Pseudomonas glumae
Pseudomonas glumae
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3.813 Million cell updates/sec
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| SIDS8/gcgdata/geneseq/geneseqp/AA1980.DAT:*
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| SIDS8/gcgdata/geneseq/geneseqg/geneseqg/AB19999.DAT:*
| SIDS8/gcgdata/geneseq/geneseqg/aB18/AB2000.DAT:*
| SIDS8/gcgdata/geneseq/geneseqg/aB18/BA2001.DAT:*
           GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                         hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
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AAY35228
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AAY71534
AAP91951
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Sequence:

Scoring table:

Pseudomonas glumae

Human protein sequ Human polypeptide C glutamicum prote Human polypeptide

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Human polypeptide Human polypeptide Bacteriophage 192

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06-JUN-2000 (first entry)
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WO200011179-A1

19-AUG-1999; 21-AUG-1998;

02-MAR-2000

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The present sequence is that of recombinant protein CDC/NIIMALVAC-1, which is a multivalent, multistage malarial vaccine. The recombinant protein comprises, melitin signal peptide, (His)6 tag. T-cell epitope from tetanus toxoid and 21 antigenic epitopes from circumsporozoite protein (CBP), sporozoite surface protein-2 (SSP-2), liver stage antigen-1 (LSA-1), merozoite surface protein-1 (MSP-1), MSP-2, apical membrane antigen-1 (AMA-1), erythrocyte binding antigen-175 (EBA-175), rhoptry associated protein-1 (AMP-1) and gamete specific antigen, Pfg27. These epitopes were obtained at different stages of the life cycle of plasmodium faltiparum. CDC/NIIMALVAC-1 vaccine has antiparasitic activity and can used for treatment and prevention of malarial infections. Anti-CDC/NIIMALVAC-1 antibodies can be used for detecting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Monoclonal antibodies useful in vaccines against malaria transmission - recognise continuous epitope in the sexual stages of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Continuous epitope of Plasmodium falciparum in the gametocyte stage.
                                                                                                                                                                                    Novel recombinant protein as vaccine for treating malarial infection comprises antigenic peptides obtained from different stages of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Epitope; monoclonal antibody; malaria; vaccine; immunisation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 97; DB 21;
100.0%; Pred. No. 4.5e-08;
iive 0; Mismatches 0;
         (NAIM-) NAT INST IMMUNOLOGY.
(USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P. falciparum in biological samples
                                                                                                                                                                                                                                                                                     Claim 3; Page 43-44; 52pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AA.
                                                                                                                                                                                                                                           plasmodium falciparum life cycle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAR96217 standard; peptide; 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         91US-0779494; 93US-0120225.
                                                                              Lal AA, Shi YP, Hasnain SE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              91US-0779494
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 transmission; sexual stage.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 KPLDKFGNIYDYHYEH 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1996-179336/18.
                                                                                                                         WPI; 2000-237654/20.
N-PSDB; AAZ51336.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
Matches 16; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   350 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24-0CT-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24-OCT-1991;
14-SEP-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-AUG-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US5502168-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAR96217;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kumar N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAR96217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          δλ
                                                                                                                                                The present sequence is the antigenic epitope P591, derived from gamete specific antigen, Pfg27 of the sexual stage of Plasmodium falciparum. It is used in the construction of recombinant protein comprises, melitinis signal peptide, (His)6 tag. The recombinant protein comprises, melitini signal peptide, (His)6 tag. The recombinant protein comprises, melitini signal peptide, (His)6 tag. Treell epitope from tetanus toxoid and 21 antigenic epitopes from Treell epitope from tetanus toxoid and 21 antigenic epitopes from Treell epitope antigen-1 (LSA-1), merozoite surface protein-2 (SSP-2), SMSP-2, apical membrane antigen-1 (AMA-1), erythrocyte binding antigen-175 (EBA-175), rhoptry associated protein-1 (RAP-1) and gamete specific antigen, Pfg27. These epitopes were obtained at different stages of the life cycle of P. falciparum. CDC/NIIMALVAC-1 vaccine has antiparasitic activity and can used for treatment and prevention of malarial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Recombinant protein; CDC/NIIMALVAC-1; multivalent; malaria; vaccine; T-cell epitope; tetanus toxoid; antigenic epitope; treatment; SSP-2; circumsporozoite protein; CSP; sporozoite surface protein:2; SSP-2; apical membrane antigen:1; LSA-1; merozoite surface protein-1; MSP-1; MSP-2; BBA-175; rhoptry associated protein-1; RAP-1; gamete specific antigen; Pf927; antiparasitic; prevention; anti-CDC/NIIMALVAC-1 antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                Novel recombinant protein as vaccine for treating malarial infection comprises antigenic peptides obtained from different stages of plasmodium falciparum life cycle -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23..350
/label= Mature_CDC/NIIMALVAC-1
/note= "Recombinant multivalent malarial vaccine"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 97; DB 21;
100.0%; Pred. No. 1.5e-09;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "Derived from Honey bee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Recombinant vaccine CDC/NIIMALVAC-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY70278 standard; Protein; 350 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P. falciparum in biological samples
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            - Apis sp.
- Clostridium tetani.
- Plasmodium falciparum.
                                                                                                                    Claim 2; Page 17; 52pp; English
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Gaps

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Length 350; Indels

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                                                                                                                             AAR96217 is a continuous epitope derived from Plasmodium falciparum in the sexual stage of development. The epitope was identified using monoclonal antibodies (MADS) 686, 1662, 19F1 and 11612 (ATCC HBILIS5, HBILIS6, HBILIS7, HBILIS7, HBILIS7, HBILIS7, HBILIS7, HBILIS7, HBILIS7, HBILISS, HBI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             S. epidermidis open reading frame protein sequence SEQ ID NO:892.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Staphylococcus epidermidis SR1 strain; infection; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63.9%; Score 62; DB 17; Length 20; 100.0%; Pred. No. 0.0011; live 0; Mismatches 0; Indels
                                                                      Claim 1; Column 15-16; 17pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAG81899 standard; Protein; 202 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   03-SEP-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     vaccination; endocarditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 63.9
Best Local Similarity 100.
Matches 11; Conservative
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Plasmodium falciparum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-316495/33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 KPLDKFGNIYD 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200134809-A2
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AAG81899
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AAH52304 to AAH53970 represent nucleic acids (I) encoding polypeptides (II), given in AAG81454 to AAG83120, from Staphylococcus epidermidis. (I) and (II) can have antibacterial activity and therefore can be used in vaccination. The nucleic acids (I) may be used to produce the used in vaccination The nucleic acids (I) may be used to produce the used to produce hosts cells which express the polypeptides. (II) (and/or nucleic acids) may then be polypeptides. The polypeptides (II) (and/or nucleic acids) may then be used to vaccinate subjects and to raise antibodies against the bacteria. The polypeptides may also be used to assay for other Inhibitors of their activity and therefore identify compounds that may be used for the reatment of S. epidermidis infections, e.g. endocarditis. AAH53971 to AAH55090 represent specifically claimed S. epidermidis genomic DNA polynucleotide sequences from the present invention. AAH55091 to AAH55091 to the present invention of the present invention.

N. B. The present invention specifically claims all the polynucleotide sequence listing of the present specification,
                                                                                                                                                                                                                                                                            ö
                AAH55098 represent oligonucleotide sequences and primers which are used in the exemplification of the present invention.

N.B. The present invention specifically claims all the polynucleotide sequences given in the sequence listing of the present specification, however the sequence listing only goes up to SEQ ID NO:4454 so even though sequences are given in the disclosure for SEQ ID NO:4465 to 4472, no sequences are present for SEQ ID NO:4465 to 4464.
                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleic acids encoding polypeptides from Staphylococcus epidermidis, useful for vaccinating against infections, e.g. endocarditis -

    S. epidermidis open reading frame protein sequence SEQ ID NO:1110.

polynucleotide sequences from the present invention. AAH55091 to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Staphylococcus epidermidis SR1 strain; infection; diagnosis;
                                                                                                                                                                                                                                  Score 52; DB 22; Length 202;
Pred. No. 0.64;
3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 18; Page 322; 2188pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAG82008 standard; Protein; 312 AA.
                                                                                                                                                                                                                                     53.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      vaccination; endocarditis.
                                                                                                                                                                                                                                Query Match
Best Local Similarity 60.0
Matches 9; Conservative
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41 qpidkfgeiydlnpe 55
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                                                                                                                                                                             Sequence
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89 AA

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standard; Protein;
                                                                           (first entry)
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                                                                                                                                                                                                                    01-DEC-1999;
                                                                                                                                                                                                                                      02-DEC-1998;
                                                                            12-OCT-2000
                                                                                                                                                          Glycine max.
                                                                                                                                                                                                 08-JUN-2000
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                                     AAY71539
                                                         AAY71539
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                            AAY71539
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C. pneumoniae causes respiratory disease such as pneumonia and bronchitis and is thought to be a contributing factor in heart disease, sarcoidosis, sinusitis, purulent oitiis media, erythema nodosum or pharyngitis. The polypeptides encoded by the open reading frames of the C. pneumoniae genome (see AAY34584-Y35879) can be used in immunogenic compositions as vaccines. Vectors containing C. pneumoniae nucleotides sequences can also be used as immunogenic compositions, especially where the vector directs the expression of a neutralising epitope of C. pneumoniae.
however the sequence listing only goes up to SEQ ID NO:4454 so even though sequences are given in the disclosure for SEQ ID NO:4465 to 4472, no sequences are present for SEQ ID NO:4455 to 4464.
                                                                                                                                                                                                                                                            Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis; sinusitis; purulent otitis media; erythema nodosum; pharyngitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                         Gaps
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Pred. No. 3.9;
2; Mismatches 4; Indels
                                                                       Length 312;
                                                                                          Indels
                                                                                                                                                                                                                                            Amino acid sequence of a Chlamydia pneumoniae protein.
                                                                                          3;
                                                                       DB 22;
                                                                                          3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genome sequence of Chlamydia pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Page 1074; Disclosure; 1912pp; English.
                                                                       Score 52;
Pred. No.
                                                                                                                                                                                   AAY35228 standard; Protein; 262 AA.
                                                                                                                                                                                                                                                                                      vaccine; neutralising epitope.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       49.5%;
57.1%;
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                                                                                                                                                                                                                                                                                                                                                                                      98US-0107078
97FR-0014673
                                                                        53.6%;
60.0%;
                                                                                                                                                                                                                          13-SEP-1999 (first entry)
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8; Conservative
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233 rpidgfgnirgihy 246
                                                                                            Conservative
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                                                                                                                1 KPLDKFGNIYDYHYE 15
                                                                                                                                  55
                                                                                                                                                                                                                                                                                                         Chlamydia pneumoniae
                                                                                                                           :|:|||| ||| :|
41 qpidkfgeiydlnpe
                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1999-357842/30.
                                                                262 AA;
                                           312 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                    (GEST ) GENSET
                                                                                                                                                                                                                                                                                                                                                                                      04-NOV-1998;
21-NOV-1997;
                                                                                                                                                                                                                                                                                                                              W09927105-A2
                                                                                                                                                                                                                                                                                                                                                                    20-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                03-JUN-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Griffais R;
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Best Local S
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                                                                                                                                                                                                        AAY35228
                                             Sequence
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AAY35228
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                                                      Soybean; POP2 transcription factor; CAF1 transcription factor; ADH2 gene; glucose-repressible alcohol dehydrogenase gene; cell metabolism; transgenic plant; herbicide; expressed sequence tag; EST.
Soybean POP2/CAF1 transcription factor encoded by expressed sequence tag.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New nucleic acids encoding transcription factor in plants and seeds, useful for producing transgenic plants, antibodies and selecting a polynucleotide that affects transcription factor polypeptide expression
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 44;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Soybean POP2/CAF1 transcription factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (DUPO ) DU PONT DE NEMOURS & CO E I. (PION-) PIONEER HI-BRED INT INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Helentjaris TG;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            45.48;
46.78;
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Best Local Similarity 46.7
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 KPLDKFGNIYDYHYE 15
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rpvgnfknindynyg
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Mon Feb

Glycine max.

08-JUN-2000

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AAW09620-W09625 are modified lipase sequences derived from Pseudomonas
                                                                                                                                                     New polypeptide with lipase activity – used for prodn. of fatty acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 glumae lipase modified to have reverse stereoselectivity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pseudomonas; Chromobacterium; modification; variant; optical isomer; steroeselectivity; drug preparation; 1,4-dihydropyridine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lipase of modified stereo:selectivity - useful for prepn. of optically active isomer 1,4-di:hydro:pyridine cpd., as intermediate
                                                                                                                                                                                                                                  The polypeptide has good stability and high lipase activity. I for prodo. of fatty acids from triglycerides, as a reagent for quantitative analysis of troglycerides, and as a catalyst for transesterifying fats and oils.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "wild-type Phe replaced with Leu,
important substitution for producing
a lipase of reverse stereoselectivity"
                                                                                                                                                                                                                                                                                                                                                             DB 10; Length 319; 32;
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                                                                                                                                                                                                                                                                                                                                                                      Score 43; DB
Pred. No. 32;
1; Mismatches
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                                                                                                                                                                                                    Claim 1; page 12; 16pp; German
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88JP-0058376.
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                                                                                                                                                                   from triglyceride(s), etc.
                                                                                                                                                                                                                                                                                                                                                                        Query Match 44.3
Best Local Similarity 63.6
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note=
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                                 (TOXN ) TOYO JOZO CO.
                                                                                                WPI; 1989-293865/41.
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                                                                                                                                                                                                                                                                                                                                                                                                                                           4 DKFGNIYDYHY 14
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21 dkfanvodywy 31
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                                                                                                                                                                                                                                                                                                                        AA;
                                                                 Ohta H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Key
Misc-difference
                                                                                                                  N-PSDB; AAN9133]
                                                                                                                                                                                                                                                                                                                        319
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14-MAR-1988;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22-JAN-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pseudomonas
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                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW09624;
                                                                 Sagai H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10
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              Soybean; POP2 transcription factor; CAF1 transcription factor; ADH2 gene; glucose-repressible alcohol dehydrogenase gene; cell metabolism; transgenic plant; herbicide.
                                                                                                                                                                                                                                                                                                                                                                                    New nucleic acids encoding transcription factor in plants and seeds, useful for producing transgenic plants, antibodies and selecting a polynucleotide that affects transcription factor polypeptide expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence is a CAF1 (also known as POP2) transcription factor from srl.pk0126.b4 clone isolated from soybean root cDNA library srl. CAF1 protein has been shown to bind to another transcription factor CCR4 and regulate the expression of glucose-repressible alcohol dehydrogenase (ADH2) gene. The present sequence is useful for producing transgenic plants with altered levels of POP2/CAF1 transcription factor to control expression of various genes or transgenes. The CAF1 protein may also be used to design or identify inhibitors of cell metabolism that may be useful as herbicides.
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Pred. No. 21;
Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chromobacterium viscosum var paralipoliticum.
                                                                                                                                                                                                                                                      ΕΙ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 10; Page 38-39; 46pp; English.
                                                                                                                                                                                                                                                                                                     Allen SM, Weng Z, Helentjaris TG;
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                                                                                                                                                                                                                                                  (DUPO ) DU PONT DE NEMOURS & (PION-) PIONEER HI-BRED INT
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85 rpvgnfknindynyg 99
                                                                                                                                                                                                                                                                                                                                     WPI; 2000-412328/35
N-PSDB; AAD01326.
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Best Local Similarity
Matches 7; Conserv
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                                                                                                              WO200032782-A2
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                                                                                                                                                                                   01-DEC-1999;
                                                                                                                                                                                                                  02-DEC-1998;
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Sequence

DE3908131-A 05-0CT-1989

Lipase.

AAP91951;

AAP91951 RESULT

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Gaps

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species cepacia and glumae and from Chromobacterium viscosum (AAW09625 only). The lipase variants were created in an attempt to find important substitution sites that affect the stereoselectivity of the lipase enzyme. Important substitutions found for Pseudomonas species were Phe221Leu, Val266Leu and Leu2871le. Lipase variants of reverse stereoselectivity are used to produce optically active
                                                                                                                                                                                                                                                                                                                                                                                                                                Pseudomonas glumae lipase modified to have reverse stereoselectivity.
                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pseudomonas; Chromobacterium; modification; variant; optical isomer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lipase of modified stereo:selectivity - useful for prepn. of optically active isomer 1,4-di:hydro:pyridine cpd., as intermediate for prepn. of drugs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Jabel= substitution
/note= "wild-type Phe replaced with Leu,
important substitution for producing
a lipase of reverse stereoselectivity"
                                                                                                                                                                               DB 17; Length 319;
32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          steroeselectivity; drug preparation; 1,4-dihydropyridine;
                                                                                                                                                                                                              Indels
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                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                  Score 43;
                                                                                                                                                                                              Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 9-10; 10pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
221
                                                                                                                                                                                                                                                                                                                                             AAW09625 standard; Protein; 319 AA.
                                                                                                                                                                                44.3%;
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Best Local Similarity
'-has 7; Conserve
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dkfanvvdywy 31
                                                                                                                                                                                                                                         4 DKFGNIYDYHY 14
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                                                                                                                                       319 AA;
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                                                                                                           drug preparation.
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Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                          AAW09625
                                                                                                                                          Sequence
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319

Sequence

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                                                                                                                                                                                                                                                                             /label= substitution
/note= "Leu to Phe, in wild-type sequence a Leu residue
is present at position 292 of mature P. glumae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AARR88009-R88018 are protein variants of Pseudomonas glumae lipase. The
                                                                                                                                                                                                  Mutant; lipase; enzymatic detergent; substitution; variant; improved; hydrophobicity.
                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ased surface hydrophobicity - useful in enzymatic detergent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "possible site for His to Arg substitution"
                                                                                                                                                                                                                                                                                                                                                      for Thr to Tyr substitution"
                                                                                                                                                                                                                                                                                                                                                                          "possible site for Leu to Arg substitution"
                                                                                                                                                                                                                                                                                                                                                                                              "possible site for Thr to Val substitution"
                                                                                                                                                                                                                                                                                                                                                                                                                   to Arg substitution"
                                                                                                                                                                                                                                                                                                                                                                                                                                        for Leu to Arg substitution"
                                                                                                                                                                                                                                                                                                                                                                                                                                                           to Phe substitution"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  for Thr to Leu substitution"
                                                                                                                                                                                                                                                                                                                                "possible site for Phe to Arg substitution"
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0
DB 17; Length 319; 32;
                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Suerbaum HMU;
                      .;
3
                                                                                                                                                                                Mature Pseudomonas glumae lipase L292F variant.
                                                                                                                                                                                                                                                                                                                                                                                                                    for Thr
                                                                                                                                                                                                                                                                                                                                                                                                                                                              for Val
 Score 43; DB 1
Pred. No. 32;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pseudomonas lipase variant with increased
                                                                                                                                                                                                                                                                                                                                                                                                                                                            'note= "possible site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             has improved in-the-wash performance,
                                                                                                                                                                                                                                                                                                                                                       "possible site
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                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                     AAR88018 standard; protein; 319 AA
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                                                                                                                                                                                                                                                                                                                                                                                                            /note= "possible
234
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                                                                                                                                                                                                                                                                                                                lipase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           94EP-0201761.
 44.3%;
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                                                                                                                                                               (first entry)
                       Conservative
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                                                                                                                                                                                                                                                                                                                                             Misc-difference 129
                                                                                                                                                                                                                                                            Key
Misc-difference 292
                                           14
                                                                21 dkfanvvdywy 31
                                                                                                                                                                                                                                       Pseudomonas glumae.
                                                                                                                                                                                                                                                                                                                         23
   Query Match
Best Local Similarity
                                           4 DKFGNIYDYHY
                                                                                                                                                                                                                                                                                                                                                                 Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                       Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20-JUN-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO9535381-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             De Vlieg J,
Verrips CT;
                                                                                                                                                              02-AUG-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-DEC-1995
                                                                                                                                          AAR88018;
                                                                                                  12
                        Matches
                                                                                                            AAR88018
                                                                                                                       δ
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7

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δ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             /label= substitution
/note= "Thr to Tyr, in wild-type sequence a Thr residue
is present at position 129 of mature P. glumae
lipase"
                                                                                                                                                                                                                                                                                                                                                                                  Mutant; lipase; enzymatic detergent; substitution; variant; improved; hydrophobicity.
sequences are based upon the wild-type P. glumae sequence disclosed in EP407225-A (UNILEYER PLC). The lipase variants may contain one cor more of the amino acid substitutions indicated in the features table. Using these variants it was shown that lipases can be modified in a such a way that interaction with the substrate can be improved without forming large hydrophobic areas on the modified lipase surface which allow aggregation of lipase molecules; the lipase variants show improved in the-wash lipolytic activity and may
                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       to Arg substitution"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "possible site for Leu to Phe substitution"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'note= "possible site for Leu to Arg substitution"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "possible site for Thr to Val substitution"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'note= "possible site for Thr to Arg substitution"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'note= "possible site for Val to Phe substitution"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note- "possible site for Thr to Leu substitution"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'note= "possible site for His to Arg substitution"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "possible site for Phe to Arg substitution"
                                                                                                                                                                               ö
                                                                                                                                                        17; Length 319;
                                                                                                                                                                              3; Indels
                                                                                                                                                                                                                                                                                                                                                            Mature Pseudomonas glumae lipase T129Y variant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'note= "possible site for Leu
                                                                                                                                                     DB 32;
                                                                                                                                                       Score 43; DB ]
Pred. No. 32;
1; Mismatches
                                                                                              be used in enzymatic detergent compsns.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
129
                                                                                                                                                                                                                                                                                     AAR88010 standard; protein; 319 AA.
                                                                                                                                                       44.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               94EP-0201761
                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                  Best Local Similarity 63.6
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note-
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                                                                                                                                                                                                      4 DKFGNIYDYHY 14
                                                                                                                                                                                                                            21 dkfanvvdywy 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Misc-difference 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Misc-difference 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Misc-difference 134
                                                                                                                                                                                                                                                                                                                                                                                                                     Pseudomonas glumae
                                                                                                                    319 AA;
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                                                                                                                                                                                                                                                                                                              AAR88010;
                                                                                                                     Sequence
                                                                                                                                                        Query Match
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/note* "Leu to Arg, in wild-type sequence a Leu residue is present at position 134 of mature P. glumae
                                                                                                                                                                          AAR88009-R88018 are protein variants of Pseudomonas glumae lipase. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mutant; lipase; enzymatic detergent; substitution; variant; improved;
                                                                                                                                                                                     sequences are based upon the wild-type P. glumae sequence disclosed in EP40725-A (UNILEVER PLC). The lipase variants may contain one or more of the amino acid substitutions indicated in the features table. Using these variants it was shown that lipases can be modified in a such a way that interaction with the substrate can be improved without forming large hydrophobic areas on the modified lipase surface which allow aggregation of lipase molecules. the lipase variants show improved in the wash lipolytic activity and may be used in enzymatic detergent compsns.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                    Pseudomonas lipase variant with increased surface hydrophobicity has improved in-the-wash performance, useful in enzymatic detergent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "possible site for Thr to Leu substitution"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "possible site for Thr to Arg substitution"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "possible site for His to Arg substitution"
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                                                                                                                                                                                                                                                                                                                                                                                                                          Length 319;
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 Suerbaum HMU;
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т
                                                                                                                                                                                                                                                                                                                                                                                                                            DB 17;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  for Thr
                                                                                                                                                                                                                                                                                                                                                                                                                                          ed. No. 32;
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                            Score 43;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "possible site
 Frenken LGJ, Peters H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /label= substitution
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR88011 standard; protein; 319 AA.
                                                                                                                                       Claim 12; Page -; 33pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                            44.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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292
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282
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Misc-difference 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'note=
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Misc-difference 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'note-
                                                   WPI; 1996-058418/06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 DKFGNIYDYHY 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ||| |: || |
21 dkfanvvdywy 31
                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pseudomonas glumae.
                                                                                                                                                                                                                                                                                                                                                                        319 AA;
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Misc-difference
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De Vlieg J,
Verrips CT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            02-AUG-1996
                                                                                                                                                                                                                                                                                                                                                                        Sequence
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Search completed: January 29, 2002, 10:21:41 Job time: 417 sec
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Matches 7; Conservative
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Misc-difference 234
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21 dkfanvvdywy
                         Misc-difference
                                                 Misc-difference
                                                                        Misc-difference
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                                                                                                                                                                                        15-JUN-1995;
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                                                                                                                                        WO9535381-A1
                                                                                                                                                                28-DEC-1995
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                                                                                                                                                                                                                                                                 AAR88009-R88018 are protein variants of Pseudomonas glumae lipase. The sequences are based upon the wild-type P. glumae sequence disclosed in EP407255-A (UNILEYER PLC). The lipase variants may contain one or more of the amino acid substitutions indicated in the features table. Using these variants it was shown that lipases can be modified in a such a way that interaction with the substrate can be improved without forming large hydrophobic areas on the modified lipase surface which allow aggregation of lipase molecules. The lipase variants show improved in the wash lipolytic activity and may be used in enzymatic detergent compsns.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                       Pseudomonas lipase variant with increased surface hydrophobicity has improved in the wash performance, useful in enzymatic detergent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  to Arg substitution"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               233
/note= "possible site for Thr to Arg substitution"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "possible site for Phe to Arg substitution"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "possible site for Thr to Tyr substitution"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        148
/label= substitution
/note= "Thr to Val, in wild-type sequence a Thr is present at position 148 of mature P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 17; Length 319; 32;
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                                                                                                                                           Suerbaum HMU;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "possible site for Leu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 43;
Pred. No.
                                                                                                                                            Peters H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAR88012 standard; protein; 319 AA.
                                                                                                                                                                                                                                              Claim 12; Page -; 33pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    44.3%;
                                                      95WO-EP02349
                                                                               94EP-0201761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                            Frenken LGJ,
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                                                                                                       (UNIL ) UNILEVER NV. (UNIL ) UNILEVER PLC.
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dkfanvvdywy 31
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Best Local Similarity
Matches 7; Conserv
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Misc-difference
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    WO9535381-A1
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                                                      15-JUN-1995;
                                                                               20-JUN-1994;
                                                                                                                                            De Vlieg J,
Verrips CT;
                             28-DEC-1995
                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
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Gaps

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Indels

1; Mismatches

Score 43; DB 17; Length 319; Pred. No. 32;

44.3%;

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AAR88009-R88018 are protein variants of Pseudomonas glumae lipase. The sequences are based upon the wild-type P. glumae sequence disclosed in Ep407225-A (UNIEUREVER PLC). The lipses variants may contain one or more of the amino acid substitutions indicated in the features table. Using these variants it was shown that lipases can be modified in a such a way that interaction with the substrate can be improved without forming large hydrophobic areas on the modified lipase surface which allow aggregation of lipase molecules. the lipase variants show improved in the wash lipolytic activity and may
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pseudomonas lipase variant with increased surface hydrophobicity has improved in-the-wash performance, useful in enzymatic detergent
                                                                                                                                                                                                                                                        /note= "possible site for Leu to Phe substitution"
note= "possible site for Leu to Arg substitution"
                                                          Val to Phe substitution"
                                                                                                                            to Leu substitution"
                                                                                                                                                                                          /note= "possible site for His to Arg substitution"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Suerbaum HMU;
                                                                                                                               Thr
                                                              for
                                                                                                                               for
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                                                                 'note= "possible site
                                                                                                                               "possible site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 12; Page -; 33pp; English.
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Verrips CT;
                                                                                                                                   /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (UNIL ) UNILEVER NV. (UNIL ) UNILEVER PLC
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Sequence 4
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                                US-08-544-332-42

US-08-961-083-72

US-08-061-38E-8

US-08-026-138E-8

US-08-026-138E-8

US-08-21-193A-56

US-08-940-086A-56

US-08-940-086A-56

US-08-244-701B-12

US-08-244-701B-11

US-08-244-701B-8

US-08-244-701B-8

US-08-248-4

US-08-809-261A-4

US-08-809-261A-4

US-08-692-892-4

US-08-713-939A-4
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PRIOR APPLICATION DATA.
APPLICATION DATE: US 07/779,494
FILING DATE: 24-OCT-1991
TELEPHONE: (202) 861-3000
TELEPHONE: (202) 861-300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (202) 861-3000
TELEFAX: (202) 822-0944
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 63.5
Best Local Similarity 100.
Matches 11; Conservative
TOPOLOGY: linear
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RESULT 2
US-08-034-650-10
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                                                                                                                                   Search time 133.18 Seconds
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Sequence 3,
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/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/FCTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
                                      Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                  212252 segs, 22503292 residues
                                                                                                                                     ٠.
                  GenCore version
Copyright (c) 1993 - 2000
                                                                                                                                 January 29, 2002, 10:24:00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

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Gapop 10.0 , Gapext 0.5
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97
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seq length: 200000000
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Match I
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39.5
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Maximum DB s
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ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz 6 No. 5955652ris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
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Patent No. 595562
GENERAL INFORMATION:
APPLICANT: Ecker, Joseph
APPLICANT: Alonso, Jose
TITLE OF INVENTION: PLANT GENES FOR SENSITIVITY TO ETHYLENE
TITLE OF INVENTION: AND PATHOGENS
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 358;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3; Indels
                                        MEDIUM TYPE: FILIPOPY disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/449,015
FILING DATE: 24-MAY-1995
CLASSIFICATION NUMBER: US 07/727,235
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/727,235
FILING DATE: 03-JUL-1991
ATTORNEY/AGENT INFORMATION:
NAME: KOKULIS, PAUL N.
REGISTRATION NUMBER: 16,773
REFERENCE/POCKET NUMBER: PNK/5970/91731
TELECOMMUNICATION DATA
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/819,288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               core 43; DB 1;
red. No. 15;
Mismatches 3
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: UI
TELECOMMUNICATION INFORMATION
TELEPHONE: 215-568-3100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (202) 861-3000
TELEFAX: (202) 822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : 358 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 44.3
Best Local Similarity 63.6
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    , MOLECULE TYPE: protein US-08-449-015-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
CLASSIFICATION: 435
                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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COUNTRY: US
ZIP: 19103
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US-08-819-288-3
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Patent No. 5804409
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: FRENKEN, Leon G.
APPLICANT: VESRER, Christiaan
TITLE OF INVENTION: PRODUCTION OF ACTIVE PSEUDOMONAS GLUMAE
TITLE OF INVENTION: LPASE IN HOMOLOGOUS OR HETEROLOGOUS HOSTS
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
                                                                                         APPLICANT: BOS, Jannetje W.
APPLICANT: FERNERN, Leon G.
APPLICANT: VERRIES, Cornelis T.
APPLICANT: VISSER, Christiaan
TITLE OF INVENTION: PRODUCTION OF ACTIVE PSEUDOMONAS GLUMAE
TITLE OF INVENTION: LIPASE IN HOMOLOGOUS OR HETEROLOGOUS HOSTS
NUMBER OF SEQUENCES: 13
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APPLICATION NUMBER: US/08/034,650

FILING DATE:
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Pred. No. 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Kokulis, Paul N.
REGISTRATION NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 16,773
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 861-3000
TELEFAX: (202) 822-0944
TELEFAX: (714627 CUSH
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                       ADDRESSEE: CUSHMAN, DARBY & CUSHMAN STREET: 1615 L. Street, N.W. CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/727,235
FILING DATE: 03-UUL-1991
ATTORNEY/AGENT INFORMATION:
Sequence 10, Application US/08034650 patent No. 5641671 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                44.38;
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Best Local Similarity 63.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        , MOLECULE TYPE: protein US-08-034-650-10
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ZIP: 20036-5601
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US-08-449-015-10
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APPLICANT: KANANAKA, SHIGERU
APPLICANT: YAMANAKA, SHIGERU
APPLICANT: MANAKA, SHIGERU
APPLICANT: MINA, KIYOSHI
APPLICANT: MINA, KIYOSHI
APPLICANT: BTO, YUZURU
APPLICANT: TANITA, YUKO
APPLICANT: TANITA, YUKO
APPLICANT: TANITA, YUKO
APPLICANT: TANITA, YUKO
APPLICANT: MASHIGHUI, KENICHI
TILLE OF INVENTION: BACILLUS-DERIVED TRANSGLUTAMINASE
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLEAND, MAIER & NEUSTADT,
ADDRESSEE: OP.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22202
                      TITLE OF INVENTION: Plant Genes for Sensitivity to Ethylene TITLE OF INVENTION: and Pathogens NUMBER OF SEQUENCES: 82

RUBBER OF SEQUENCES: 82

ADDRESSE: Woodcock, Washburn, Kurtz, Mackiewicz & Norris STREET: One Liberty Place, 46th floor CITY: Philadelphia STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 1321;
      Trustees of The University of Pennsylvania
VENTION: Plant Genes for Sensitivity to Ethylene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IRAPPY disk
COMPUTER: IRAPPY disk
COMPUTER: IRAP
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/07744A
FILING DATE: 15-JUNE-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/261,822
FILING DATE: JUNE 17, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Beardell, Lori Y:
NAME: READALLOATION NUMBER: 34, 293
M. REGISTRATION NUMBER: 34, 293
M. REGISTRATION NUMBER: 34, 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 39.5; DB 5;
Pred. No. 2.4e+02;
4; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEPAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        40.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1321 amino acids
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Best Local Similarity 58.3
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
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PCT-US95-07744A-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz & No. 5650553ris
STREET: One Liberty Place, 46th floor
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                        1;
                                                                                                                                                                             Length 1294;
                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 3, Application US/08261822A
Patent No. 565053
GENERAL INFORMATION:
APPLICANT: EXAMPLE TITLE OF INVENTION: Plant Genes for Sensitivity to Ethylene TITLE OF INVENTION: and Pathogens
NUMBER OF SEQUENCES: 82
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz & No. 565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 1321;
                                                                                                                                                                                                                   0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTE: USAN
ZIP: 19103
COMPUTE: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/261,822A
FILING DATE: 17-JUN-1994
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Beardell, Lori Y.
REGISTRATION NUMBER: 34,293
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION SEQ ID NO: 3:
SEQUENCE (215) 568-3130
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHRRACTERISTICS:
                                                                                                                                                                             Score 39.5; DB 2;
Pred. No. 2.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 39.5; DB 1;
Pred. No. 2.4e+02;
4; Mismatches 0;
                                                                                                                                                                                                                      4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 3, Application PC/TUS9507744A GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     40.7%;
                                                                                                                                                                         Query Match
Best Local Similarity 58.3%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 1321 amino acids
TYPE: amino acid
STRANDEDNESS: single
SEQUENCE CHARACTERISTICS:
LENGTH: 1294 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; MOLECULE TYPE: protein US-08-819-288-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear MOLECULE TYPE: peptide
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678 LDEFWGHLYDFH 689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      678 LDEFWGHLYDFH 689
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                                                                                                                                                                                                                                                              3 LDKF-GNIYDYH 13
                                                                   linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      USA
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PCT-US95-07744A-3
                                                                 TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: F
STATE:
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APPLICANT: NAKAYAMA, NO. 5656471iyuki
APPLICANT: NAKAMOTO, Shinya
TITLE OF INVENTION: LACTATE OXIDASE WITH AN IMPROVED THERMAL
TITLE OF INVENTION: STABILITY AND GENE OF THE SAME
NUMBER OF SEQUENCE: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 2; Length 242;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 22202
COMPUTER READABLE FORM:
MEDTUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/625,876
FILING DATE: 01-APR-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 39; DB 2
Pred. No. 44;
2; Mismatches
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION
APPLICATION NUMBER: US 08/596,864
FILING DATE: 09-FEB-1996
APPLICATION NUMBER: UP 021963/1995
FILING DATE: 09-FEB-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: UP 226316/1995
FILING DATE: 04-SEP-1995
FILING DATE: 29-JAN-1996
ATPORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REGISTRATION NUMBER: 24,618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-95947
FILING DATE: 30-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-146186
FILING DATE: 13-JUN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 10-786-0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E: YOUNG & THOMPSON 745 South 23rd Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application US/08625876
Patent No. 5656471
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION TELEPHONE: 703-413-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISICS:
LENGTH: 242 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             44.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       135 DKFNASFDRIILYDWHYE 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 DKFGN-----IYDYHYE 15
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Best Local Similarity 44.4
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: 703-412
TELEPHONE: 703-413-2220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: PATCH, Andrew J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        , MOLECULE TYPE: protein US-08-989-667-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: YOUNG
STREET: 745 Sout
CITY: Arlington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: Virginia COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 9
US-08-625-876-2
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APPLICANT: YAMANAKA, SHIGERU
APPLICANT: YAMANAKA, SHIGERU
APPLICANT: MINA, KIYOSHI
APPLICANT: SUZUKI, SHUNICHI
APPLICANT: STAVITA, YUGURU
APPLICANT: FTAVITA, YUGURU
APPLICANT: YOKOZEKI, KENZO
APPLICANT: HASHIGUCHI, KENICHI
APPLICANT: PORCESS: 9
CORRESPONDENCE ADDRESS: 9
CORRESPONDENCE ADDRESS: 7
ADDRESSER: DELON, SPIVAK, MCCLELLEAND, MAIER & NEUSTADT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 242;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: P.C. STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400 CITY: ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/989,667
                                                                COMPUTER: L. L. COMPUTER: COMPUTER: COMPUTER: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/596,864
FILING DATE: 09-FEB-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           40.2%; Score 39; DB
44.4%; Pred. No. 44;
tive 2; Mismatches
                                                                                                                                                                                   CLASSIFICATION: 97 FEB-1290
CLASSIFICATION: 97 FEB-1290
CLASSIFICATION DATA: 97 FEB-1290
PRIOR APPLICATION DATA: 97 FEB-1295
FILING DATE: 09 FEB-1995
PRIOR APPLICATION DATA: 97 E26316/1995
FILING DATE: 04 SEB-1995
PRIOR APPLICATION DATA: 97 PRIOR APPLICATION DATA: 97 PRIOR APPLICATION NUMBER: 97 PRIOR APPLICATION NUMBER: 29 JAN 1996
ATTORNEY/AGENT INFORMATION: REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 10-786-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3200
                                   E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-989-667-3
; Sequence 3, Application US/08989667
; Patent No. 5948662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 242 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              135 DKFNASFDRIILYDWHYE 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 DKFGN-----IYDYHYE 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; MOLECULE TYPE: protein US-08-596-864-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
Matches 8; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: MINAGAWA, Hirotaka
APPLICANT: NAKAYAMA, NO. 56564711yuki
APPLICANT: NAKAYAMA, NO. 56564711yuki
APPLICANT: NAKAMOTO, Shinya
TITLE OF INVENTION: LACTATE OXIDASE WITH AN IMPROVED THERMAL
TITLE OF INVENTION: STABILITY AND GENE OF THE SAME
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                               Score 39; DB 1; Length 374;
Pred. No. 71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     40.2%; Score 39; DB 1; Length 374;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. 71;
0; Mismatches
                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRECT AFFLICATION NUMBER: USA/08/625,876
ELLING DATE: 01-APR-1996
CLASSIFICATION: 435
PRIOR APPLICATION ONTA:
APPLICATION NUMBER: JP 7-95947
FILING DATE: 30-MAR-1995
PRIOR APPLICATION NUMBER: JP 7-146186
FILING DATE: 13-UNH-1995
APPLICATION NUMBER: JP 7-146186
FILING DATE: 13-UNH-1995
APPLICATION NUMBER: JP 7-146186
FILING DATE: J3-UNH-1995
AFFORNEY/AGENT INFORMATION:
NAME: PATCH, Andrew J
REGISTRATION NUMBER: 32,925
RECISTRATION NUMBER: PF-1612
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 521-2297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMpatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 12
US-07-863-169A-5
; Sequence 5, Application US/07863169A
; Patent No. 5420245
                                                                                                                                                                                                                                                                                                                                                                    Sequence 6, Application US/08625876; Patent No. 5656471; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: YOUNG & THOMPSON
STREET: 745 South 23rd Street
                               40.2%;
57.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 374 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (703) 685-057
TELEX: 248425 EMBON
INFORMATION FOR SEQ ID NO:
                               Query Match 40.2
Best Local Similarity 57.1
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 57.1
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; MOLECULE TYPE: protein US-08-625-876-6
                                                                                                                                                                                           361 KGLDLFDNPYGYEY 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           361 KGLDLFDNPYGYEY 374
                                                                                                                                                        1 KPLDKFGNIYDYHY 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY:
                                                                                                                                                                                                                                                                                                           RESULT 11
US-08-625-876-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: MINAGAWA, HIROTAKA
APPLICANT: NAKAYAMA, NO. 56564711yuki
APPLICANT: NAKAYAMA, NO. 56564711yuki
APPLICANT: NAKAYANO, Shinya
TITLE OF INVENTION: LACTATE OXIDASE WITH AN IMPROVED THERMAL
TITLE OF INVENTION: STABILITY AND GENE OF THE SAME
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 39; DB 1; Length 374; Pred. No. 71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CALP: 22202

CAPPE: 22202

CAPPE: ELOPPY disk

COMPUTER: IBM PC COMPATIBLE

COMPUTER: IBM PC COMPATIBLE

COMPUTER: IBM PC COMPATIBLE

OURREATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/625,876

FILING DATE: 01-APR-1996

FILING DATE: 30-MAR-1995

PRIOR APPLICATION NUMBER: P7-146186

FILING DATE: 13-JUN-1995

ATPORNEY/AGENT INFORMATION:

REGISTRATION NUMBER: 32,925

ATPORNEY/AGENT INFORMATION:

TELEFRA: (703) 521-2297

TELEFRA: (703) 521-2297

TELEFRA: (703) 685-0573

TELER: 248425 EMBON

INFORMATION FOR SEQ ID NO: 15 FORWATION: 15 FORWATION FOR SEQ ID NO: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                      REFERENCE/DOCKET NUMBER: PF-1612
TELECOMUNICATION INFORMATION:
TELEPHONE: (703) 521-2297
TELEFAX: (703) 685-0573
TELEX: 248425 EMBON
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 374 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 4, Application US/08625876
Patent No. 5656471
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E: YOUNG & THOMPSON 745 South 23rd Street
REGISTRATION NUMBER: 32,925
                                                                                                                                                                                                                                                                                                                                                                                                                                                             40.28;
57.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 374 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 40.2
Best Local Similarity 57.1
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                       ; MOLECULE TYPE: protein US-08-625-876-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein US-08-625-876-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | || | | | | | | 361 KGLDLFDNPYGYEY 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 KPLDKFGNIYDYHY 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 745 South CITY: Arlington STATE: Virginia COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                 linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
                                                                                                                                                                                                                                                                              TYPE: ami
TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-625-876-4
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STATE: ILANDE STATES OF AMERICA
ZIP: 77210
COUNTRY: UNITED FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/429,964
FILING DATE: 27-APR-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 39; DB 2;
Pred. No. 72;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: ARNOLD, WHITE & DURKEE STREET: P.O. BOX 4433
                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/424,268
FILING DATE: 4/24/95
CLASSIFICATION: 435
                                                                                             STATE: New Jersey
COUNTRY: United States of America
ZIP: 07065-0907
                                                                                                                                                                                                                                                                                                                                                                                                 18858PC
                                                                                                                                                                                                              OPERATING SYSTEM: System 7.5.3 SOFTWARE: Microsoft Word 5.1 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                   ATTORNEY AGENT INFORMATION:
NAME: Muthard, David A
REGISTRATION NUMBER: 35,297
REFERENCE/DOCKET NUMBER: 18856
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-3903
TELEFAX: (908) 544-4703
INFORMATION FOR SEQ ID NO: 8:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 40.2%;
Best Local Similarity 66.7%;
Matches 6; Conservative
                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Power Mac
OPERATING SYSTEM: SYSTEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 379 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein
HYPOTHETICAL: NO
FRAGMENT TYPE: N-termin
              CORRESPONDENCE ADDRESS:
ADDRESSEE: Merck & Co
                                                        P.O.Box 2000
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ||| ::|||
94 DKFRDVYDY 102
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US-08-429-964-5
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Sequence 8, Application US/08424268

Sequence 8, Application US/08424268

Patent No. 5821118

GENERAL INFORMATION:
APPLICANT: Omer, Charles A
APPLICANT: Omer, Charles A
APPLICANT: Gibbs, Jackson B
APPLICANT: Kohl, Nancy E
APPLICANT: Kohl, Nancy E
TITLE OF INVENTION: Assay for Inhibitors of Farnesyl-Protein
TITLE OF INVENTION: Transferase
                APPLICANT: Brown, Michael S.
APPLICANT: Brown, Michael S.
APPLICANT: Goldstein, Joseph L.
APPLICANT: Reiss, Yuval
TITLE OF INVENTION: Tetrapeptide-Based Inhibitors of Farnesyl
TITLE OF INVENTION: Transferase
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: B.O. Box 4433
CITY: Houston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1; Length 379; 72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Indels
                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPATION SYSTEM: PC-DOS/MS-DOS/ASCII
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 03-APR-1992
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. 72; ; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Parker, David L.
REGISTRATION UNBER: 32,165
REFERENCE/DOCKET NUMBER: UTSD:297/PAR
RELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
PILING DATE: 19-7an-1992
CLASSIPECATION: 530
APPLICATION WIMBER: US 07/937,893
FILING DATE: 18-APR-1991
CLASSIPECATION: 530
APPLICATION NUMBER: US 615,715
FILING DATE: 20-NOV-1990
CLASSIPICATION: 530
APPLICATION: 530
APPLICATION: 530
ATTORNEY/AGENT INFORMATION:
ANAMER: US 510,706
FILING DATE: 18-APR-1990
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
ANAMER: US 510,706
ATTORNEY/AGENT INFORMATION:
ANAMER: US 510,706
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                         United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (713) 789-2679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               379 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEX: 79-0924
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 379 amino acida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 40.2
Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS: single
                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
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US-07-863-169A-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ||| ::|||
| 94 DKFRDVYDY 102
            GENERAL INFORMATION:
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                                                                                                                                                                                                                                   Texas
                                                                                                                                                                                                                                                                  ZIP: 77210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX:
                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                          CITY: 1
STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 1.3
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Gaps

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Length 379; 1; Indels US/07/822,011

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Gaps

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Score 39; DB 3; Length 379; Pred. No. 72; 2; Mismatches 1; Indels

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NAME: PARKER, DAVID L.
REGISTRATION NUMBER: 32,165
REFRERENCE/DOCKET NUMBER: UTSD:269/PAR
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-320-7200
meriox: 512-474-7577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Search completed: January 29, 2002, 10:24:01 Job time: 507 sec
                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS: LENGTH: 379 amino acid residues TYPE: amino acid residues aline acid
                                 FILING DATE: 01/16/92
ATTORNEY/AGENT INFORMATION:
NAME: PARKER, DAVID L.
                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 40.2
Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                         ; TOPOLOGY: linear
US-07-935-087-5
               APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | | | | ::|||
94 DKFRDVYDY 102
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ZIP.:
COUNTRY T7210

COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1 (converted to ASCII-DOS)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/935,087
FILING DATE: 1992084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 379;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: BROWN, MICHAEL S.
APPLICANT: GOLDSTEIN, JOSEPH L.
APPLICANT: GOLDSTEIN, JOSEPH L.
APPLICANT: REISS, YUVAL
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
TITLE OF INVENTION: THE IDENTIFICATION,
TITLE OF INVENTION: CHARACTERIZATION,
TITLE OF INVENTION: AND INHIBITION OF FARNESYL
TITLE OF INVENTION: PROTEIN TRANSFERASE
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 39; DB 2;
Pred. No. 72;
2; Mismatches
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/021,625
CLASSIPECATION: 435
CLASSIPECATION: 435
APPLICATION NUMBER: US 07/822,011
FILING DATE: AARNONED
CLASSIPECATION: 435
APPLICATION NUMBER: PCT/US/91/02650
FILING DATE: 18 AAR-1991
CLASSIPECATION: 435
APPLICATION NUMBER: US 07/615,715
FILING DATE: 10 ANO-1990
CLASSIPECATION: 435
APPLICATION NUMBER: US 07/510,706
FILING DATE: 10 ANO-1990
CLASSIPECATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: PARKER, DAVID L.
REGISTRATION NUMBER: US5:432/PAR
TELEPHONE: (713) 789-2679
TELEPHONE: (512) 418-3000
TELERAXION FOR EEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: ARNOLD, WHITE & DURKEE STREET: P.O. BOX 4433 CITY: HOUSTON STATE: TEXAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 5, Application US/07935087 Patent No. 6083917 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  40.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                379 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 379 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |||| ::|||
94 DKFRDVYDY 102
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US-07-935-087-5
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein – protein search, using sw model

Run on:

January 29, 2002, 11:13:36; Search time 80.65 Seconds (without alignments) 7.274 Million cell updates/sec

US-09-763-397A-3 Title: Perfect score: Sequence:

1 KPLDKFGNIYDYHYEH 16 Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

100059 Total number of hits satisfying chosen parameters:

100059 seqs, 36664827 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_39:\* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	,	thermotoga	escherichia	ia angu		la irid	us qall	u	pseudomonas	aquifex aeo	caenorhabdi	saccharomyc	calliphora	saccharomyc	mesocricetu	bacteriopha	methanococc	haemophilus	aquifex aeo	butyrivibri	saccharomyc	saccharomyc	a porce	a porce	cavia porce	schizosacch	schizosacch	autographa	llus su	llus su	chlamydia t	homo sapien	llus su	mays (m
	tion	ther	esch	pichia	sacc	tipula	qailus	arab	psen	aqui	caen	sacc	call	sacc	meso	bact	meth	haem	adui	buty	sacc	sacc	cavia	cavia	cavi	schi	schi	auto	bacillus	bacillus	chla	рошо	bacillus	zea
	Description	005651	P78258	P30263	P00175	P22856	P26007	P34881	005489	066893	P41999	P47054	P28514	P26754	064148	P04531	058648	P15446	066607	P22541	P39008	P25381	064417	064406	064409	P36587	010313	P41452	034623	P40746	084538	935	86	P48190
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SUMMARIES		THEMA	LECOLI	CATA_PICAN	CYB2_YEAST	VL96_IRV1	ITA6_CHICK	MTDM_ARATH	LIP_PSEGL	TOP1_AQUAE	NH10_CAEEL	YJD9_YEAST	ARY2_CALVI	RFA2_YEAST	CP3A_MESAU	KDNM_BPT4	YC52_METJA	MTH2_HAEPA	LEU3_AQUAE	GUNA_BUTFI	POP2_YEAST	YCT5_YEAST	CP3E_CAVPO	CP3F_CAVPO	CP3H_CAVPO	NCPR_SCHPO	YD5A_SCHPO	RPOB_NPVAC	DP3A_BACSU	TGL_BACSU	CHLT	PFTA_HUMAN	YWJE_BACSU	_MAIZE
U)	ID	PORA	TALA_I	CATA	CYB2	VL96	ITAE	MTDN	LIP	TOP	NHI	YJD	ARY?	RFA	CP3/	KDN	XC52	MTH	LEU	GUN/	POP	YCT	CP3E	CP3F	CP3F	NCPF	XD54	RPOE	DP34	TGL	LPXC_C	PFT	YWJE	MATK
	DB	-	Н	Н	Н	Н	Н	Н	Н		Н	-	٦	,-	-	-	٦	-	Н		Н	-	7	-	Н	Н	-		٦	П	-	-	Н	-
	Length	392	316	207	591	867	1072	1534	358	540	395	1683	759	273	503	241	251	358	364	429	433	491	503	503	503	678	787	876	1115	245	286	379	398	544
de	Query		45.9	45.9	45.4	45.4	45.4	45.4	٠		•	•		42.3	•		41.2	•	•	41.2	٠	•	٠	•	•	•	•	•	٠	٠	40.2		。	
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	Score	4	₹.				₹	4	₹	7	4	4	41.	4	₹	₹	4	4	₹	40	₹	₹	₹	₹	₹	₹	₹	₹	₹	m	m	m'	ώ,	3,
	Result No.	-	7	m	4	Ŋ	9	7	œ	σ	10	11	12		14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29	30	31	32	33

Q47861 erwinia her P42846 saccharomyc	P43573 saccharomyc O51124 borrelia bu P25178 helicobacte	~ ~		P79217 oryctolagus P50391 homo sapien	062762 rattus norv
TR2M_ERWHE	YFC3_YEAST Y097_BORBU LSPA_HELPY	LSPA_HELPJ Y011_BORBU	ACP2_ENTHI CPP2_ENTHI	NY6R_RABIT NY4R_HUMAN	KC12_RAT
					1
562 591	796 128 157	163 279	310 315	371 375	414
40.2	40.2 39.2 39.2	39.2 39.2	39.2 39.2	39.5 39.2	39.2
36 8	6 8 8 6 8 8	38 38	38	388	38
34 35	36 37 38	39 40	41 42	4 4 4	45

## ALIGNMENTS

RESU!	RESULT 1 PORA THEMA	
1 1 1 1 1 1	·	
DT DT	15-DEC-1998 (Rel. 37, Created) 15-DEC-1998 (Rel. 37, Last sequence update)	
DT		ŭ.
DE		- 1 - 1 - 1
N C		
88		
N OX	NCBI_TaxID=2336;	
RP.	SEQUENCE FROM N.A., AND SEQUENCE OF 1-43.	
Z X		
RA.		•
RT F		ø
RT	and pyruvate ferredoxin oxidoreductase from Thermotoga mari	a
RL		
RN C		
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R R	n hair D.H., hickey E.N., Ferenson J.D., Neison W.C., Aelchum A.A., McDonald L., Otterback T.R., Malek J.A., Linher K.D., Garrett M.M.,	
RA		. :
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RL	Nature	
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7 P	SEQUENCE OF 1-43, AND CHARACTERIZATION.	
Z X		
RA	Blamey J.M., Adams M.W.W.A.;	
RT		
Z Z	oxidoreductase from the hyperthermophilic maritims.":	
RL		
ဗ္ဗ	-!- CATALYTIC ACTIVITY: PYRUVATE + COA + OXIDIZED FERREDOXIN -	
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Construction of a contiguous 874-kb sequence of the Escherichia coli-
- K12 genome corresponding to 50.0-68.8 min on the linkage map and
analysis of its sequence features.";
DNA Res. 4:91-113(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Yamamoto Y., Alba H., Baba T., Hayashi K., Inada T., Isono K., Itoh T., Kimura S., Kitagawa M., Makino K., Miki T., Mitsuhashi N., Mizobuchi K., Mori H., Nakade S., Nakamura Y., Nashimoto H., Oshima T., Oshima T., Oshima T., Sampei G., Satoh Y., Sivasuharam S., Tagami H., Takahashi H., Takeda J., Takemoto K., Uehara K., Wada C., Yamagata S., Horiuchi T.;
                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN=KIZ / MG1655
MEDLINE=97426617; Pubmed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-0157:H7 / EDL933 / ATCC 700927;
STRAIN-0157:H7 / EDL933 / ATCC 700927;
STRAIN-0157:H7 / EDL933 / ATCC 700927;
STRAIN-0157:H7 / EDL933 / ATCC 700927;
PEDLINE-21074935; PubMed=11206551;
Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
Posfa1 G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
Posfa1 G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
Welch R.A., Blattner F.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Proteobacteria; gamma subdivision; Enterobacterlaceae; Escherichia.
                                                                                                                                                                                   4;
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"The complete genome sequence of Escherichia coli K-12.";
Science 277:1453-1474(1997).
                                                                                                                                                      46.4%; Score 45; DB 1; Length 392; 53.3%; Pred. No. 8.2; tive 3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN=K12 / W3110,
Iida A., Fashiba S., Mizobuchi K.;
Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                              SEQUENCE 392 AA; 44111 MW; ACEF0E34C9EC1818 CRC64;
                                                                                                                                                                                                                                                                                                               TALA_ECOLI STANDARD; PRT; 316 AA. P78258; P80218; 26. Created) 01-UUL-1993 (Rel. 35, Last sequence update) 20-AUG-2001 (Rel. 40, Last annotation update) TALA OR E2464 OR 23720 OR ECS3326.
                                                                                                      POLY - ALA
                 EMBL; X85171; CAA59457.1; ALT_INIT.
EMBL; AE001690; AAD35111.1; ALT_INIT.
TIGR; TM0017; -.
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MEDLINE=97349980; PubMed=9205837;
                                                                                        Oxidoreductase; Complete proteome.
DOMAIN 72 79 POLY-
                                                            Interpro; IPR002880; POR_N. Pfam; PF01855; POR_N; 1.
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Best Local Similarity
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                                                                                                                                                 Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K., Hanakin T., Makino K., Ohnishi M., Kurokawa K., Tanaka M., Tobe T., Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T., Kuhara S., Shiba T., Hattori M., Shinagawa H., Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genomic comparison with a laboratory strain K-12.";
                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
"Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";
Nature 409:529-533(2001).
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Eukaryota, Fungi, Ascomycota, Saccharomycotina, Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Pichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS01058; TRANSALDOLASE 2; 1.
PROSITE; PS01054; TRANSALDOLASE 1; 1.
Transferase; Pentose shunt; Multigene family; Complete proteome.
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Best Local Similarity 33.3%; Pred. No. 7.8;
Matches 9; Conservative 4; Mismatches 3; Indels 1:
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990B00ED7937CF19 CRC64;
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01-APR-1993 (Rel. 25, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
PXP9 OR PXP-9.
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                                                                                                                                                                                                                                                                                                                                                                             [6] PRESENCE OF TWO TRANSALDOLASES IN E.COLI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL, D13159; BAA21821.1; -.
EMBL, AE000333; AAC75517.1; -.
EMBL, D90875; BAA16339.1; -.
EMBL, AE006475; AAG57573.1; -.
EMBL, AE0065475; AAG57573.1; -.
EMBL, AP002561; BAB36749.1; -.
HSSP; P30148; 1UCW.
ECOGENE; EG11797; talA.
InterPro, IPR001585; Transaldolase.
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                                                                                                               STRAIN=0157:H7 / RIMD 0509952;
MEDLINE=21156231; PubMed=11258796;
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  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ij
                                                   yeast Hansenula polymorpha.";
FEBS Lett. 303:113-116(1992).
-!- FUNCTION: OCCURS IN ALMOST ALL AEROBICALLY RESPIRING ORGANISMS AND
SERVES TO PROTECT CELLS FROM THE TOXIC EFFECTS OF HYDROGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BY SIMILARITY.
PROXIMAL HEME LICAND (BY SIMILARITY).
MICROBODY TARGETING SIGNAL (POTENTIAL).
3536ED0A49539CC3 CRC64;
           MEDLINE-92299073; PubMed-1607006;
Didion T., Roggenkamp R.O.;
"Targeting signal of the peroxisomal catalase in the methylotrophic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11-JUL-1986 (Rel. 01, Created)
01-APR-1988 (Rel. 07, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
cytochrome B2 PRECURSOR (EC 1.1.2.3) (L-LACTATE DEHYDROGENASE
[CYTOCHROME]) (L-LACTATE FERRICYTOCHROME C OXIDOREDUCTASE) (L-LCR).
CYB2 OR YML054C OR YM9958.08C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Structure, expression and regulation of a nuclear gene encoding a mitochondrial protein: the yeast L(+)-lactate cytochrome c oxidoreductase (cytochrome b2)."; EMBO J. 4:3265-3272(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   45.9%; Score 44.5; DB 1; Length 507; 47.1%; Pred. No. 13;
                                                                                                                                                                                                                                                                                                                EMBL: X56501; CAA39856.1; -.
HSSP: 923422; S33422.
HSSP: P00432; 7CAT.
InterPro: IPR002226; Catalase.
Priny: PF00199; catalase: 1.
PRINTS: PR00067; CATALASE.
PROSTIE: PS00342; MICROBODIES_CTER; 1.
PROSTIE: PS00343; CATALASE_1.
PROSTIE: PS00439; CATALASE_2.1; 1.
PROSTIE: PS00439; CATALASE_2.2; 1.
PROSTIE: PS00439; CATALASE_2.2; 1.
PROSTIE: PS00439; CATALASE_2.2; 1.
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MEDLINE-86135959; PubMed-3004948;
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415 KPDEKYTGEVVPYHWEH 431
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138 1
348 3
505 5
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Matches 8; Conserv
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P00175;
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                                                                                                                                                                                                                                                                                                                                                                                 Ghrir R., Becam A.-M., Lederer F.; "Primary structure of flavocytochrome b2 from baker's yeast. Purification by reverse-phase high-pressure liquid chromatography and sequencing of fragment alpha cyanogen bromide peptides."; Eur. J. Blochem. 139:59-74(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=75156546; PubMed=165435; Guiard B., Lederer F., Jacq C.; Guiard B., Lederer F., Jacq C.; More similarity between bakers'yeast L-(+)-lactate dehydrogenase and liver microsomal sytochrome B5.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -:- SUBCELLULAR LOCATION: MITOCHONDRIAL INTERMEMBRANE SPACE.
-:- INDUCTION: BY L-LACTATE. INDUCED DURING RESPIRATORY ADAPTATION.
-:- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE CYTOCHROME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           J. Mol. Biol. 212:837-863(1990).
-: - CATALYTIC ACTIVITY: L-LACTATE + 2 FERRICYTOCHROME C = PYRUVATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P.PUTIDA S-MANDELATE DEHYDROGENASE, AND TO M.SMEGMATIS LACTATE 2-MONOOXYGENASE.
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MEDILINE-20230330315, PubMed-2329585;
Xia Z.-X., Mathews F.S.
"Molecular structure of flavocytochrome b2 at 2.4-A resolution.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 395-591.
MEDLINE-86030284; PubMed=3902473;
Lederer F., Cortial S., Becam A.M., Haumont P.-Y., Perez L.;
"Complete amino acid sequence of flavocytochrome b2 from baker's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         core in bakers'
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STRAIN-S288C / AB972;
Devlin K., Churcher C., Barrell B.G., Rajandream M.A.;
Submitted (NOV-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-76206228; Pubmed-776230;
Guiard B., Lederer F.;
Complete amino acid sequence of the heme-binding of yeast cytochrome b2 (L-(+)-lactate dehydrogenase).
Blochinie 58:305-316(1976).
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SGD; S0004518; CYB2.
InterPro; IPR001199; Cyt_B5.
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PIR; A23095; A23095.
PDB; 1FCB; 15-JUL-92.
PDB; 1LTD; 31-AUG-94.
PDB; 1LCO; 15-SEP-95.
                                                                                                                                                                                                                                                                 SEQUENCE OF 81-394.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gene 94:243-248(1990).
-i- FUNCTION: MAY BE INVOLVED IN TIV GENOMIC DNA PACKAGING IN A MANNER RELATED TO THE GAG POLYPROTEINS OF THE MAMMALIAN VIRUSES.
-i- SIMILARITY: CONTAINS 1 OTU DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE=91078646; PubMed=1701750;
Home W.A., Tajbakhsh S., Seligy V.L.;
"Molecular cloning and characterization of a late Tipula iridescent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tipula iridescent virus (TIV) (Insect iridescent virus type 1).
Viruses; dsDNA viruses, no RNA stage; Iridoviridae; Iridovirus.
                                                                                                                                                                                                                                                                                                                                                                                                  Length 591;
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Last annotation update)
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Pred. No.
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PIR, JH0225; JH0225.
InterPro; IFR003123; OTU.
Pfam; PF02338; OTU.
Teat; DNA packaging; DNA-binding.
DOMAIN 606 745
SEQUENCE 867 AA; 96011 MW; F19DBDE
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20-AUG-2001 (Rel. 40, Last anno
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Best Local Similarity 53.8
Matches 7; Conservative
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198 PLDNIINLYDFEY 210
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HEME LIGAND (BY SIMILARITY).
HEME LIGAND (BY SIMILARITY).
REMOVES THE SUBSTRATE ALPHA-PROTON AS THE FIRST STEP IN CATALXSIS.
SUBSTRATE BINDING.
Q -> E (IN REF. 4).
E -> Q (IN REF. 4).
IN InterPro; IPR003009; FMN_enzyme.

IN InterPro; IPR000262; FMN_hydroxy_acid_dh.

IN Fram; PF001073; heme_l: 1.

IN PROSITE; PS00191; CYTOCHROME_B5_l: 1.

IN PROSITE; PS00557; FMN_HYDROXY_ACID_DH: 1.

IN PROSITE; PS00557; FMN_HYDROXY_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_H
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-!- SIMILARITY: CONTAINS 2 BAH DOMAINS
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INTEGRIN ALPHA-6 HEAVY CHAIN (POTENTIAL).
INTEGRIN ALPHA-6 LIGHT CHAIN (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                   Gaps
                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN-WHITE LEGHORN; TISSUE-Retina;

MEDLINE-91185416; PubMed-1826298;

de Curtis I., Quaranta V., Tamura R.N., Reichardt L.F.;

de Curtis I., Quaranta V., Tamura R.N., Reichardt L.F.;

Laminin receptors in the retina: sequence analysis of the chick integrin alpha 6 subunit. Evidence for transcriptional and posttranslational requlation.";

J. Cell Biol. 113:405-416(1991).

T. FUNCTION: INTEGRIN ALPHA-6/BETA-1 IS A RECEPTOR FOR LAMININ ON PLATELETS. INTEGRIN ALPHA-6/BETA-4 IS A RECEPTOR FOR LAMININ IN EPITELETAL CELLS. IT PLAYS A CRITICAL STRUCTURAL ROLE IN THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BY A
BETA-4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIR: A38457; A38457.

HSSP: P11215; 1A8X.

Interro: IPR000413; Integrin_alpha.

Pfam: PF01839; FG-GAP: 5.

Pfam: PF01839; FG-GAP: 5.

PRO185; INTEGRINA.

SMART: SM00191; INT_A1Pha: 1.

PROSTIE: PS00242; INTEGRINA.

Integrin: Cell adhesion: Receptor; Glycoprotein; Transmembrane; Signal; Extracellular matrix; Cytoskeleton; Phosphorylation; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA SUBUNIT. THE ALPHA SUBUNIT IS COMPOSED OF AN HEAVY AND A LIGHT CHAIN LINKED BY A DISULEIDE BOND. ALPHA-6 ASSOCIATES WITH EITHER BETA-1 OR BETA-9 SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
                                   ·.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-!- DEVELOPMENTAL STAGE: ALPHA-6 LEVELS DECREASE WITH AGE.
-!- PTM: PHOSPHORYLATED IN VIVO.
-!- SIMILARITY: BELONGS TO THE INTEGRIN ALPHA CHAIN FAMILY.
            Length 867;
                                   5; Indels
           DB 1;
                                                                                                                                                                                  Last sequence update)
Last annotation update)
                                   Mismatches.
           Score 44; DB Pred. No. 27;
                                                                                                                                                                                                        INTEGRIN ALPHA-6 PRECURSOR (VLA-6).
                                                                                                                                                                    01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequ
20-AUG-2001 (Rel. 40, Last anno
          45.4%;
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      Query Match
Best Local Similarity 64.3
Matches 9; Conservative
                                                                                                                                              STANDARD;
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726 KPLIPLGFIDDYHY 739
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"Isolation and identification by sequence homology of a putative cytosine methyltransferase from Arabidopsis thaliana.";
Nucleic Acids Res. 21:2383-2388(1993).
-i FUNCTION: METHYLATES CG RESIDUBS.
-i CATALYTIC ACTIVITY: S-ADENOSYL-L-METHIONINE + DNA = S-ADENOSYL-L-HOMOCYSTEINE + DNA CONTAINING 5-METHYLCYTOSINE.
-i SIMILARITY: LOW, TO OTHER EUKARYOTIC DNA METASE.
-i SIMILARITY: SOME TO BACTERIAL RESTRICTION SYSTEMS
METHYLFRANSFERASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                       (POTENTIAL)
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C0-AUG-2001 (Rel. 40, Last annotation update)
DNA (CYTOSINE-9)-METHITRANSFERASE ATHI (EC 2.1.1.37) (DNA
METHYLTRANSFERASE ATHI) (DNA METASE ATHI).
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N LINKED (GLCNAC. . .) (POTEN N-LINKED (GLCNAC. . .) (POTEN
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1; Mismatches
                                                                                                                                                                                  POTENTIAL.
GFFKR MOTIF
FG-GAP 1.
FG-GAP 2.
FG-GAP 3.
FG-GAP 4.
FG-GAP 5.
FG-GAP 6.
FG-GAP 7.
POTENTIAL.
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MEDLINE=93281384; Pubmed=8389441;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-FEB-1994 (Rel. 28, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   45.48;
58.38;
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Best Local Similarity 58.3.
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1043
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ACT_SITE
DISULFID
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                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its was by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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MEDLINE=94009622; PubMed=8405390;
Noble M.E.M., Cleasby A., Johnson L.N., Egmond M.R., Frenken L.G.J.;
"The crystal structure of triacylglycerol lipase from Pseudomonas
glumae reveals a partially redundant catalytic aspartate.";
FEBS Lett. 331:123-128(1993).
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MEDLINE=95306500; PubMed=7786905;
Taipa M.A., Liebeton K., Costa J.V., Cabral J.M.S., Jaeger K.-E.;
"Lipase from Chromobacterium viscosum: biochemical characterization indicating homology to the lipase from Pseudomonas glumae.";
Biochim. Biophys. Acta 1256:396-402(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Verrips C.T.; "Cloning of the Pseudomonas glumae lipase gene and determination of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Frenken L.G.J., Egmond M.R., Batenburg A.M., Bos J.W., Visser C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Proteobacteria; beta subdivision; Burkholderia group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                           REBASE; 2839; MATAIL.

RILGEPTO; IPR001025; BAH.

RICHEPTO; IPR00155; C5_DNA_meth.

R Pfam; PF01426; BAH; 2.

R Pfam; PF00145; DNA_methylase; 3.

R PRINTS; PR00105; C5MTRFRASE.

R SMART; SM00439; BAH; C5_MTASE_1; 1.

R PROSITE; PS00094; C5_MTASE_1; 1.

R PROSITE; PS00095; C5_MTASE_2; 1.

R PROSITE; PS00096; C5_MTASE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 1534;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A., SEQUENCE OF 40-61, AND MUTAGENESIS. SPECIES-P.glumae; STRAIN-PG1 / CBS 322.89; MEDLINE-93119130; PubMed-1476423;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-OCT-1994 (Rel. 30, Created)
01-OCT-1994 (Rel. 30, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
LIPASE PRECURSOR (EC 3.1.1.3) (TRIACYLGIXCEROL LIPASE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pseudomonas glumae, and Chromobacterium viscosum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the active site residues.";
Appl. Environ. Microbiol. 58:3787-3791(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            358 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 40-54, AND CHARACTERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 44;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             [4]
x-ray crystallography (1.6 angstroms).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        45.48;
                                                                                                                                                                                                          EMBL; L10692; AAA32829.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            166 KPAASYRKVYDYFYE 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 KPLDKFGNIYDYHYE 15
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Best Local Similarity
'..hog 7; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Burkholderia.
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Q05489;
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30-MAY-2000 (Rel. 39, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
DNA TOPOISOMERASE I (EC 5.99.1.2) (OMEGA-PROTEIN) (RELAXING ENZYME)
SPECIES-C.viscosum; STRAIN=ATCC 6918;
MEDLINE=96275656; PubMed-8683577;
Lang D., Hofmann B., Haalck L., Hecht H.-J., Spener F., Schmid R.D.,
                                                                           -i- SUBUNIT: MONOMER.
-i- SUBCELLULAR LOCATION: SECRETED.
-i- SIMILARITY: STRONG TO OTHER PSEUDOMONAS LIPASES.
-i- SIMILARITY: PARTIAL MITH OTHER LIPASES (PANCREATIC, GASTRIC, HEPATIC, LINGUAL, LIPOPROTEIN, BACTERIAL, ETC.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
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COMPLETE LOSS OF ACTIVITY.
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H->A: COMPLETE LOSS OF ACTIVITY.
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PROSITE; PS00120; LIPASE_SER; 1.
Hydrolase; Lipid degradation; Signal; Calcium; 3D-structure.
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CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
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EMBL; A16323; CAA01279.1; -.
EMBL; A32021; CAA02073.1; -.
PIR; A48952; A48952.
PIR; 37291; S37291.
PDB; ITAH; 31-MAY-94.
InterPro; IPR000073; Abhydrolase.
InterPro; IPR000739; Est_lip_thioest_actsite.
InterPro; IPR000739; Lipase.
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1; Mismatches
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D->A:
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D->E:
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                                                                                                                                                                                       A FATTY ACID ANION.
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Best Local Similarity
Matches 7; Conserv
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                                                                   Schomburg D.;
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                                                                                                                                                                                                                                                                                                                                                  between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00104; hormone_rec; 1.
Pfam; PF00105; zf-C4; 1.
PRINTS; PR00047; STROIDFINGER.
SMART; SM00430; hoLI; 1.
SMART; SM0039; ZnF_C4; 1.
PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
Receptor; Transcription regulation; DNA-binding; Nuclear protein;
                                                                                                                                                                                                                       -!- SUBCELLULAR LOCATION: NUCLEAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pohl T.M., Aljinovic G.:
Submitted (SEP-1995) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
HYPOTHETICAL 191.5 KDA PROTEIN IN NSP1-TAD2 INTERGENIC REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 42; DB 1; Length 395;
Pred. No. 24;
1; Mismatches 4; Indels
                                                                                                                              Fulton L., Waterston R.;
Submitted (JUN-1994) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: ORPHAN NUCLEAR RECEPTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                44899 MW; AFDB075D989EEBEA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUCLEAR RECEPTOR-TYPE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT; 1683 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wormpep, 10280.8; CE00815.
InterPro; IPR000536; Hormone_rec_lig.
InterPro; IPR001628; zf-C4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C4-TYPE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                43.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; U10438; AAA19086.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match
Best Local Similarity 58.30,
Enc. 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          83
38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       188 RFANOSDYHYWH 199
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18
54
395 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5 KFGNIYDYHYEH
                                                                                                STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KJL039C OR J1216.
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Zinc-finger.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YJD9_YEAST
P47054;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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ZN_FING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YJD9_YEAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its muse by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                         NATURE 392:353-358(1998).

-I FUNCTION: THE REACTION CATALYZED BY TOPOISOMERASES LEADS TO THE CONVERSION OF ONE TOPOLOGICAL ISOMER OF DNA TO ANOTHER.

-I CATALYTIC ACTIVITY: ATP-INDEPENDENT BREAKAGE OF SINGLE-STRANDED DNA, FOLLOWED BY PASSAGE AND REJOINING.
-I SUBUNIT: MONOMER (BY SIMILARITY).
-I SUBUNIT: MONOMER (BY SIMILARITY).
-I MISCELLANEOUS: WHEN A TOPOISOMERASE TRANSIENTLY BREAKS A DNA WHICH A TYROSYL OXYGEN IN THE ENZYME IS JOINED TO A DNA PHOSPHORUS AT ONE END OF THE ENZYME SADIND.

AT ONE END OF THE ENZYME-SEVERED DNA STRAND.
-I SIMILARITY: BELONGS TO PROKARYOTIC TYPE I/III TOPOISOMERASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                 MEDLINE-98196666, PubMed-9537320;
Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L., Graham D.E., Overbeek R., Snead M.A., Keller M., Aujay M., Huber R., Feldman R.A., Short J.M., Olson G.J., Swanson R.V.;
"The complete genome of the hyperthermophilic bacterium Aquifex aeolicus";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSTICE: PS00396; TOPOISOMERASE_I_PROK; 1.
ISOMERASE: TOPOLSOMERASE; DNA-binding; Complete proteome.
ACT_SITE 281 281 DNA CLEAVAGE (BY SIMILARITY).
SEQUENCE 540 AA; 63427 MW; 89C0604DFF5B042E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
NUCLEAR HORMONE RECEPTOR FAMILY MEMBER NHR-10.
NHR-10 OR B0280.8.
Caenorhabditis elegans.
                                                                                             Bacteria; Aquificales; Aquificaceae; Aquifex.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     395 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro: IPR003601; DNAtopI_ATP_bind.
InterPro: IPR003601; DNAtopI_DNA_bind.
InterPro: IPR0003802; DNAtopI_DNA_bind.
InterPro: IPR002936; Toprim.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF01131; Topolsom_bac; 1.
Pfam; PF01751; Toprim; 1.
SMRINTS; PR00417; PRPTSMRASEI.
SWART; SM00437; TOPLAC; 1.
SWART; SM00436; TOPLBC; 1.
SWART; SM00493; TOPRIM; 1.
(UNTWISTING ENZYME) (SWIVELASE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AE000700; AAC06848.1; -.
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50.0%;
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197 KGSEEFWAIYDYRYEN 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8; Conservative
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                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                          NCBI_TaxID-63363;
                                                           Aquifex aeolicus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NH10_CAEEL
P41999;
                                                                                                                                                                                                                           STRAIN-VF5
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RESULT 10 NH10\_CAEEL

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Matches

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Gaps

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InterPro; IPR000896; Hemocyanin.
          hemocyanin;
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        Pfam; PF00372;
                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cooper
                                                                                                                                                                                                                      RESULT 13
RFA2_YEAST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           proteins and arthropod hemocyanins.";
Proteins and arthropod hemocyanins.";
Plochem. Biophys. Res. Commun. 177:963-972(1991).
SERVE AS A STORAGE PROTEIN USED PRIMARILIS.
AMINO ACIDS FOR PROTEIN SYNTHESIS DURING METAMORPHOSIS. IT IS A CONSTITUTENT OF THE SCLEROTIZING SYSTEM OF THE CUTICLE, AND SERVES AS A CARRIER FOR ECDYSTEROID HORMONE.
                                                                                                                                                                                                                                                                                                                                                                                                 ARYLEHORIN SUBBURT C223 PRECURSOR.
Calliphora vicina (Blue blowfly) (Calliphora erythrocephala).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Oestroidea; Calliphoridae; Calliphora
                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Complete cDNA and gene sequence of the developmentally regulated arylphorin of Calliphora vicina and its homology to insect hemolymph
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- SIMILARITY: TO OTHER ARYLPHORINS AND TO ARTHROPOD HEMOCYANINS.
                                                                                                                                                                                                                                             5;
                                                                                                                                                                                                                        Length 1683;
                                                                                                                                                                                                               Score 42; DB 1; Length 100
Pred. No. 1.1e+02;
                                                                                                                                                                                        FD2D61FDEA5451C4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                               (Rel. 24, Last sequence update)
(Rel. 35, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBUNIT: HETEROHEXAMER.
SUBCELLULAR LOCATION: EXTRACELLULAR.
TISSUE SPECIFICITY: FAT BODY.
                                                                              POTENTIAL.
POTENTIAL.
POTENTIAL.
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EMBL, X59390; CAA42233.1; -.
PIR; JQ1044; JQ1044
HSSP; P04253; ILLI.
                           Transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Fat body;
MEDLINE=91282793; PubMed=1711849;
                                                                                                                                                                                                                                                                                                                                                                  01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last seq
01-NOV-1997 (Rel. 35, Last anno
                                                                                                                                                                                                                           43.3%;
61.5%;
                                                                                                                                                                                          1683 AA; 191534
    CAA89330.1;
                                                                                                                                                                                                                           Query Match 43.3
Best Local Similarity 61.5
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Naumann U., Scheller K.;
                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                         1228 LNKYCSGNIYDFH 1240
                                                                                                                          932
1042
1315
1363
1526
1615
                                                                                                                                                                                                                                                                     3 LDKF--GNIYDYH 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=7373;
     Z49314; C
S0003576;
                           Hypothetical
                                                                                                                                                                                                                                                                                                                                                ARY 2_CALVI
P28514;
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TRANSMEM
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                                                                                                                                                                                            SEQUENCE
                                       RANSMEM
                                                FRANSMEM
                                                             TRANSMEM
                                                                      LRANSMEM
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DENCEMBER FROM N.A.

SUBJULET C.T.C., Urbanus J.H.M., Planta R.J.;

Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.

-! FUNCTION: BRINDS TO SINGLE-STRANDED SEQUENCES PARTICIPATING IN DNA

-! FUNCTION: BRINDS TO SINGLE-STRANDED SEQUENCES PARTICIPATING IN DNA

REPLICATION IN ADDITION TO THOSE MEDIATING TRANSCRIPTIONAL

REPRESSION (URS1) AND ACTIVATION (CAR1). STIMULATES THE ACTIVITY

OF A COGNARTE STRAND EXCHANGE PROPEIN (SEP1). IT COOPERATES WITH

T-AG AND DNA TOPOISOMERASE I TO UNWIND TEMPLATE DNA CONTAINING THE

SIMIAN VIRUS 40 ORIGIN OF DNA REPLICATION.

-! SUBUNIT: HETEROPATHER OF 69, 36, AND 13 KDA CHAINS. THE

DNA-BINDING ACTIVITY MAY RESIDE EXCLUSIVELY ON THE 69 KDA SUBUNIT.
                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MATAIN=2288C / FY1676;
MEDLINE=9606632; PubMed=7502583;
Maftahl M., Nicaud J.-M., Levesque H., Gaillardin C.;
"Sequencing analysis of a 24.7 kb fragment of yeast chromosome XIV identifies six known genes, a new member of the hexose transporter family and ten new open reading frames.";
yeast 11:1077-1085(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Brill S.J., Stillman B.;
"Replication factor-A from Saccharomyces cerevisiae is encoded by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A., AND SEQUENCE OF 100-118; 150-172 AND 184-196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REAZ_YEAST STANDARD; PRT; 273 AA.
P26754; p88905;
01-AUG-1992 (Rel. 23, Last sequence update)
01-NV-1997 (Rel. 35, Last annotation update)
01-NV-1997 (Rel. 35, Last annotation update)
REPLICATION FACTOR-A PROTEIN 2 (RF-A) (DNA BINDING PROTEIN BUF1)
RFA2 OR BUF1 OR YNL312W OR N0368.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Saccharomyces cerevisiae BUF protein binds to sequences participating in DNA replication in addition to those mediating transcriptional repression (URS1) and activation."; Mol. Cell. Biol. 13:5749-5761(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                 ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Luche R.M., Smart W.C., Marion T., Tillman M., Sumrada R.A.,
                                                                                                                                                                                                                                                                                                         1; Length 759;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     genes coordinately expressed at S phase."
                                                                                                                                                                                                                                                                                                                                                                                    1; Indels
                                                                                             Signal; Storage protein; Glycoprotein; Multigene family SIGNAL
                                                                                                                                                                    ARYLPHORIN SUBUNIT C223.
BE66CC7A2D71352D CRC64;
                                                                                                                                                                                                                                                                                                                    DΒ
                                                                                                                                                                                                                                                                                                             Score 41.5; DE
Pred. No. 59;
4; Mismatches
PRINTS; PR00187; HARMOCYANIN.
PROSITE; PS00209; HEMOCYANIN_1; FALSE_NEG.
PROSITE; PS00210; HEMOCYANIN_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A., AND SEQUENCE OF 5-16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=93361008; PubMed=8355713;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=91357474; PubMed=1885001;
                                                                                                                                                                                                        759 AA; 92525 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genes Dev. 5:1589-1600(1991).
                                                                                                                                                                                                                                                                                                                    42.8%;
                                                                                                                                                                                                                                                                                                                       Query Match 42.8
Best Local Similarity 53.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                :|||::||:| |
748 EKFGH-FDYNYHH 759
                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 DKFGNIYDYHYEH 16
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TISSUES BY VARIOUS FOREIGN COMPOUNDS, INCLUDING DRUGS, PESTICIDES.
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                                                                                                                                                                                                                                                                                                                                                                       EMBL; M73992; -; NOT_ANNOTATED_CDS.
EMBL; S79317; AAB35091.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE-86037230; Pubmed-4057254;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 148-241 FROM N.A. MEDLINE-82150240; Pubmed-7063418;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               bacteriophage T4 tRNA region.";
J. Mol. Biol. 185:545-563(1985)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 KPLDKFGNIYDYH 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ||| || || || 42 KPLPFFGTILGYH 54
                                   CARCINGGENS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  503 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          T4-like phages.
NCBI_TaxID=10665;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteriophage T4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KDNM_BPT4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15
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                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
CYTOCHROME P450 3A10 (EC 1.14.14.1) (CYPIIA10) (6 BETA-HYDROXYLASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Subramanian A., Teixeira J., Wang J., Gil G.;
"A STAT factor mediates the sexually dimorphic regulation of hepatic cytochrome P450 340/Jihocholic acid 6 beta-hydroxylase gene expression by growth hormone.";
Mol. Cell. Biol. 15:4672-4682(1995).
-i- FUNCTION: CATALYZES THE 6 BETA-HYDROXYLATION OF LITHOCHOLIC ACID AND STEROID HORMONES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OXIDIZED FLAVOPROTEIN + H(2)0.
-1- SUBCELLULAR LOCATION: MEMBRANE-BOUND. ENDOPLASMIC RETICULUM.
-1- DEVELOPMENTAL STAGE: EXPRESSED ONLY IN MALE HAMSTERS.
-1- INDUCTION: P450 CAN BE INDUCED TO HIGH LEVELS IN LIVER AND OTHER
-! - PTM: PHOSPHORYLATED IN A CELL-CYCLE-DEPENDENT MANNER (FROM THE S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -! - CATALYTIC ACTIVITY: RH + REDUCED FLAVOPROTEIN + O(2) - ROH
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"Cloning, expression and regulation of lithocholic acid 6beta-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            42.3%; Score 41; DB 1; Length 273; 40.0%; Pred. No. 24;
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; F6087501E4E28CC1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA replication; Phosphorylation; Nuclear protein. MOD_RES ?1 ?1 BLOCKED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             503 AA.
                             PHASE UNTIL MITOSIS).
-!- SIMILARITY: TO OTHER SPECIES RFA2/RPA2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Biol. Chem. 266:21030-21036(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; Z46259; -; NOT_ANNOTATED_CDS.
EMBL; Z71588; CAA96241.1; -.
PIR; B37281; B37281.
PIR; S17021; S17021.
TRANSFAC; T01249; -.
SGD; S0005256; RFA2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR002309; tRNA-synt_2. Pfam; PF01336; tRNA_anti; 1.
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29936 MW;
                                                                                                                                                                                                                                                                                                                                                                    EMBL; X59749; CAA42421.1; -. EMBL; S64861; AAB27888.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6; Conservative
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SEQUENCE 273 AA;
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Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mesocricetus.
NCBI_TaxID=10036;
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Q64148;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oxidoreductase; Monooxygenase; Electron transport; Membrane; Heme; Microsome; Endoplasmic reticulum.

BINDING 442 442 HEME (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleotide sequence of the bacteriophage T4 gene 57 and a deduced
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 41; DB 1; Length 503;
Pred. No. 45;
0; Mismatches 5; Indels
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13-AUG-1987 (Rel. 05, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
BEOXXNUCLECTIDE MONOPHOSPHATE KINASE (EC 2.7.4.13) (DNK).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        142 HEME (BY SIMILARITY).
57693 MW; D4D24FEE87FD7F51 CRC64;
-1- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              241 AA
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MEDLINE=89296504; PubMed=2740234;
Koch T., Lamm N., Rueger W.;
"Sequencing, cloning and overexpression of between map positions 74.325 and 77.184.";
Nucleic Acids Res. 17:4392-4392(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      42.3%; Score 41;
                                                                                                                                                                                                                                                                                                                                                                                                             Incerpro; IPR001128; Cyt_P450.
Pfam; PF00607; p450; 1.
PRINTS; PR00359; BP450.
PRINTS; PR00463; EP450.
PRINTS; PR00464; EP450I.
PRINTS; PR00464; EP450I.
PRINTS; PR00464; EP450I.
PRINTS; PR00465; EP450I.
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Nucleic Acids Res. 10:1105-1112(1982).
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41.2%; Score 40; DB 1; Length 241;
Best Local Similarity 63.6%; Pred. No. 30;
Matches 7; Conservative 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                       EMBL; X03016; CAA26800.1; -.
EMBL, X14845; CAA32953.1; -.
EMBL, 202516; AAA32497.1; -.
PIR; A04309; KIBPD4.
PIR; S04612; S04612.
PDB; IDEK; 11-JAN-97.
PDB; IDEK; 11-JAN-97.
Transférase; Kinase; 3D-structure.
SEQUENCE 241 AA; 27329 MW; 61AD2375CC94BDE8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Search completed: January 29, 2002, 11:13:37 Job time: 813 sec
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Sequence of an imm Synthetic peptide Malaria antigen fo

Non-immunogenic am Resin-bound Plasmo fdMal protein N-te

fdMal protein

full and 2 half

Perfect score:

Sequence:

OM protein

Run on:

Scoring table:

Searched:

Minimum DB Maximum DB

Database

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Anino acid sequence
P. falciparum circ
Synthetic immunoge
Plasmodium sporozo
Malaria parasite p
Synthetic NaNP pep
Amino acid sequence
Modified CDR3 of t
Sequence of mutage
Sequence of mutage
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Malarial TIB seque
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Anti-malarial pept
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Plasmodium falcipanium immunodominant epitope.
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AABB4362
AAB49997
AAP60804
AAR49980
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AAR70039
AAY03673
AAB15523
AAR22907
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AAW69278
AAB08105
AAR59808
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AAP82566
AAG63514
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AAR14261
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AAR14262
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AAB73754
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Verdini AS,
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 RESULT
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Malarial B-cell ep
Plasmodium falcipa
Plasmodium falcipa
Plasmodium falcipa
Plasmodium falcipa
Plasmodium falcipa
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Plasmodium falcipa
Synthetic peptide
Plasmodium falcipa
                                                                                                                                   (without alignments)
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              GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Listing first 45 summaries
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AAW61556
AAW29731
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hybrid surface proteins are claimed in which an active polypeptide (e.g. a surface antigen from a mammalian tumnour cell, sperm or an allergen, bacterium, virus, parasite or fungus) is fused to an anchor region from a surface antigen normally expressed on the cell surface of gram positive bacteria. The anchor segment is pref. derived from a streptococcal M protein (see AAR41780). Sequence AAR41783 is a peptide sequence from the cs protein of p. falciparum (Nature 314.111-114) suitable for development of a vaccine against malaria.
                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gene encoding hybrid surface protein of gram positive bacteria useful for preparing vaccine compsn. for protecting animals from bacterial infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0
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The sequence NANP can be repeated 3-40 times. When conjugated to a tuberculin protein derivative, the product is useful as an anti-malaria vaccine and provides a high antibody response.
                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.0%; Pred. No. 0.00016; Matches 12; Conservative 0; Mismatches 0;
                                                                              100.0%; Score 69; DB 11;
100.0%; Pred. No. 0.00016;
Live 0; Mismatches 0;
                                                                                                                                                                                                                                                   Plasmodium falciparum cs protein antigen.
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                                                                                                                                                                                           AAR41783 standard; protein; 12 AA.
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                                                                                                      Conservative
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Best Local Similarity
Matches 12; Conserv
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AAR41783
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Synthetic peptide antigen analogues of native peptide antigens which are either (1) retro modified, (2) inverso modified or (3) retronances modified with respect to the native antigen can be used to raise antibodies which recognise the native antigen and hence can be used in the treatment and/or prophylaxis of diseases and therapy of disease states. They can be used in the production of vaccines and in assays for antibodies specific for the native antigen. They can have increased stability to degredation after administration and they can immunodominant epitope of the circumsporcozoite coat protein of plasmodium falciparum. The retro-inverso versionof this sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                           Peptide; retro; inverso; retro-inverso; therapy; disease; vaccine; immunogen; antibody; antibodies; assay; treatment; prophylaxis; plasmodium falciparum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New retro, inverso and retro-inverso peptide analogues - used as immunogens for the prodn. of antibodies and in diagnosis, therapy and prophylaxis of diseases
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                                                                                                                                            Synthetic peptide analogue of P. falciparum used as immunogen.
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iive 0; Mismatches 0;
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AAR49981 standard; peptide; 12 AA.
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is described in AAR60483.
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Best Local Similarity
Matches 12; Conserv
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The malaria circumsporozoite protein repeat region is used in an immunogenic composition along with the T-cell epitope derived from malaria. The T-cell epitope elicits an anti-malarial T-cell response in mammals of diverse genetic backgrounds. The composition can be used as a vaccine to confer prophylactic or therapeutic immunity against malaria. They may also be used to inhibit the propagation of a malarial organism in a susceptible animal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence is a peptide comprising a malarial B-cell epitope, which is contained in the COOH-terminal repeat region of the Plasmodium falciparum circumsporzoite (CS) protein. It is this epitope that stimulates the production of antibodies that specifically recognise and bind to the malarial CS protein. This epitope can be incorporated into a polyoxime with T-cell epitopes to produce a vacche that is packgrounds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Immunogenic composition containing T cell epitope of malaria-derived peptide - incorporated into a poly:oxime and optionally B cell epitope, used in vaccines to protect against malaria in subjects of differing genetic background(s)
                                           New immunogenic compositions for malaria – comprise malaria derived peptide comprising universal T-cell epitope which elicits anti-malarial T-cell response
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Circumsporozoite protein; CS; antibody; polyoxime; T-cell epitope;
                                                                                                                                                                                                                                                                                       Score 69; DB 19;
Pred. No. 0.00016;
Mismatches 0;
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                                                                                                  Disclosure; Page 2; 38pp; English.
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Best Local Similarity 100.
Matches 12; Conservative
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                                                                                                                                                                                                                                                                                                                                                                       The protein represents 12 amino acid units of the P. falciparum circumsporozoite protein repeat region (AAR70034), which are sufficient for the production of antibodies reactive against the whole protein. Insertion of the coding sequence into the major coat protein gene VIII of bacteriophage Fd in a region of the protein known to be exposed on the virus surface results in expression of the P. falciparum antigen on the phage surface. Thus, the phage is useful in a vaccine composition against malarla, or as a therapeutic/diagnostic product.
                                                                                                                                                                                                                                                                                    Filamentous bacteriophage engineered to display T- and B-cell epitopes and/or a peptide eliciting HIV neutralising antibodies - useful in vaccines and as a therapeutic/diagnostic prod.
Bacteriophage Fd; phage display; malaria; vaccine; therapeutic;
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                                                                                                                                                                                                                 Veronese F, Willis AE;
                                                                                                                                                                                   (CAMB-) CAMBRIDGE BACTERIOPHAGE TECHNOLOGIES.
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Matches 12; Conserv
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              diagnostic
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  Matches
                                                                                         AAY29734
                                                                               RESULT
                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δy
                                             QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention describes a hybrid protein (H1) comprising at least a portion of a particle forming protein and one or more polypeptides having at least one epitope of interest such as an epitopic site of a pathogen or toxin. Also describes is a method of the interest of pathogen or toxin. Also describes is a method of the interest of pathogen or toxin. Also describes of interest of for inducing an immune response to one or more epitopes of interest of patholic site is immunologically reactive. The patholic site is immunologically reactive. The particles can be used as vaccines or for the production of antibodies of the proposition in vitro diagnostics. Which can be used for passive immunisation, in vitro diagnostics, which can be used for passive immunisation. The particles can also be expected on a says for detecting the presence of antibodies to the antigen of interest. The present sequence represents a peptide used in the complification of the present invention.
                                                                      0
                                                                                                                                                                                                                                                           Immunogenic composition; viral particle; hybrid protein; expression; immunogen; diagnosis; passive immunisation; vaccination; vaccine; immune response; epitopic site; pathogen; toxin.
                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New hybrid protein comprising a particle forming protein and a polypeptide having epitopes, useful as a vaccine
                                                                        0;
                                                Score 69; DB 19; Length 12; Pred. No. 0.00016;
                                                                        0; Indels
                                                                                                                                                                                                                                          Plasmodium falciparum circumsporozoite core peptide.
                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Column 20; 13pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Barr PJ, Kuo G, Valenzuela PDT;
                                                                                                                                                                           AAY41790 standard; peptide; 12 AA.
                                                  udery Match
Best Local Similarity 100.0%;
Matches 12; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                   85US-0777976.
87US-0128639.
92US-0966291.
93US-0126115.
94US-0352989.
                                                                                                                                                                                                                                                                                                                                                                                98US-0132079
                                                                                                                                                                                                                                                                                                                                                                                                                                                              84US-0650323
                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                              Plasmodium falciparum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1999-579892/49.
                                                                                                             1 NANPNANPNANP 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (CHIR ) CHIRON CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAZ25062
                      12 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12
                                                                                                                                                                                                                                                                                                                                                                                                                           26-OCT-1992;
23-SEP-1993;
09-DEC-1994;
12-SEP-1984;
                                                                                                                                                                                                                                                                                                                                                                                10-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                      19-SEP-1985;
04-DEC-1987;
                                                                                                                                                                                                                          08-DEC-1999
                                                                                                                                                                                                                                                                                                                                      US5965140-A.
                                                                                                                                                                                                                                                                                                                                                           12-OCT-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                    AAY41790;
                       Sednence
                                                                                                                                                         7
                                                                                                                                                                   AAY41790
                                                                                                                                                           RESULT
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Length 12;

Score 69; DB 20; Pred. No. 0.00016;

100.0%;

Query Match Best Local Similarity

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The present invention describes a conjugate (A) comprising a catrategically modified hepatitis B core (HBC) protein (I) attached to a trategically modified hepatitis B core (HBC) protein (I) attached to a hapten, where (I) includes amino acids (aas 10-140 of the wild type (II) in the 183 as sequence (given in ANZ29674) and additionally has an insert (II) in the region corresponding to aa's 50-100, where the insert is corresponding to a protective antibody response against corporations from which the hapten is derived, in humans or other corporation of (II) correcomes the low reactivity of aa side chains in native HBC protein, increasing the reactivity with hapten corporating in conjugates of improved immunogenicity. Modified HBC can be derivatised in the form of particles by well-defined chemical corporations and is unlikely to cause immunological side-effects. ANX29675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conjugate of hepatitis B core protein, modified to increase reactivity with hapten, used to raise antibodies against the hapten, e.g. in vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                    Human hepatitis B core protein; HBC; modified; immunodominant; nucleocapsid protein; vaccine; T cell epitope.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 69; DB 20;
ilarity 100.0%; Pred. No. 0.00016;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                       Plasmodium falciparum polypeptide hapten.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 3; Page 39; 128pp; English.
                                                                                                                                                                                                               AA.
                                                                                                                                                                                                           AAY29734 standard; Protein; 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99WO-US03055.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (IMMU-) IMMUNE COMPLEX CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98US-0074537
                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 NANPNANPNANP 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1999-527340/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
                                                  1 nanphanphanp 12
1 NANPNANPNANP 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19-AUG-1999.
                                                                                                                                                                                                                                                                                                                                 08-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Birkett AJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                           AAY29734;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT
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Lal AA, Shi YP, Hasnain SE;
                                                                                                                                                                                                                         (NAIM-) NAT INST IMMUNOLOGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                        Plasmodium falciparum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 nanpnanpnanp 12
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                                                                                                                                                                                                                                                                                  WPI; 2000-237654/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12 AA;
                                                                                                                             WO200011179-A1.
                                                                                                                                                                           19-AUG-1999;
                                                                                                                                                                                                  21-AUG-1998;
                                                                                                                                                    02-MAR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB73753;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB73753
   ö
                                                                                           Activated T helper cell; CD4+; cytotoxic T cell; CD8+; liposome; epitope; peripheral blood lymphocyte; antigen-presenting cell; APC; virus; tumour; bacterium; parasite; cytokine; vaccine; cancer; malaria; HIV; hepatitis; tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hepatitis, tuberculosis). The activated T-cells can be used to treat the same conditions by adoptive T-cell transfer therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                Peptides AAW67583-W67611 are used to produce activated T helper (CD4+) and cytotoxic (CD8+) T-cells. The activated T cells are produced by treating peripheral blood lymphocytes with liposome-enospaulated peptide antigen to generate Ag-loaded antigen-presenting cells (APC), contacting naive or anergic T-cells with these APC, and isolating the resulting partivalarly one derived from a temour, but also those from viruses, bacteria and other parasites. It can also be used to identify antigens and epitopes able to generate an Ag-specific T-cell response (by assessing proliferation and cytokine release). Also the Ag-loaded APC can be used as cellular vaccines for treating cancer (claimed) or other diseases (e.g. malaria, human immune deficiency virus infection,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                Method of activation of T cells - by exposure to antigen-presenting cells loaded with antigen in liposome, used for, e.g. treating
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                  Longenecker BM, Reddish MA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Plasmodium falciparum CSP antigenic epitope, P519.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 69; DB 20;
100.0%; Pred. No. 0.00016;
ive 0; Mismatches 0;
                                                                             Plasmodium falciparum T-cell activation peptide.
                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 24; 75pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY70280 standard; peptide; 12 AA.
         AAW67599 standard; peptide; 12 AA.
                                                                                                                                                                                                                                                                                                                                                                                       cancer and microbial infections
                                                                                                                                                                                                                                               98WO-US09288.
                                                      02-MAR-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         06-JUN-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 100.
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                  Agrawal B, Krantz MJ,
                                                                                                                                                                       Plasmodium falciparum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 NANPNANPNANP 12
                                                                                                                                                                                                                                                                                            (BIOM-) BIOMIRA INC.
                                                                                                                                                                                                                                                                                                                                       WPI; 1999-034715/03.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12 AA;
                                                                                                                                                                                               WO9850527-A1.
                                                                                                                                                                                                                                              07-MAY-1998;
                                                                                                                                                                                                                                                                     08-MAY-1997;
                                                                                                                                                                                                                      12-NOV-1998
                                                                                                                                                               Synthetic.
                                  AAW67599;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY70280;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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AAW67599
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Recombinant protein; CDC/NIIMALVAC-1; multivalent; malaria; vaccine; real-patiope; treatment; recall epitope; treatment; circumsporozoite protein; CSP: sporozoite surface protein-2; SSP-2; liver stage antigen-1; LSA-1; merozoite surface protein-1; MSP-1; MSP-2; apical membrane antigen-1; AMA-1; erythrocyte binding antigen-175; EBA-175; rhoptry associated protein-1; RAP-1; gamete specific antigen; Pfg27; antiparasitic; prevention; anti-CDC/NIIMALVAC-1 antibody.
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monoclonal antibody; affinity chromatography; DEAE-Sephadex A50 resin;
diethylamine-ethyl group.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel recombinant protein as vaccine for treating malarial infection comprises antigenic peptides obtained from different stages of plasmodium falciparum life cycle \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 69; DB 21; 100.0%; Pred. No. 0.00016;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 falciparum in biological samples.
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                                                                                                                                                                                                                                                                                             The invention relates to the use of the anion exchange resin DEAE-sephadex A50 as a solid support for solid phase peptide synthesis and affinity chromatography. The present sequence represents a repetitive plasmodium falciparum circumsporozoite peptide epitope which was used to raise monochonal antibodies. The affinity between the antibodies and free recombinant antigen was determined via competition affinity chromatography using a DEAE-Sephadex A50 column comprising a resin-bound form of the peptide epitope (AAB73754).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                       Use of an anion exchange resin (EPM-7) as solid support for peptide, e.g. angiotensin II, synthesis and affinity chromatography .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Amino acid sequence of MAL1, which is displayed on E2 core surface.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E2 core protein; 2-oxo acid dehydrogenase; multienzyme complex;
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 69; DB 22;
100.0%; Pred. No. 0.00016;
ive 0; Mismatches 0;
                                                                                                                                                                                            Rodrigues MM;
                                                                                                                                                                   (CNPQ-) CNPQ CONSELHO NACIONAL DESENVOLVIMENTO.
                                                   /note= "Optionally acetylated"
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                      Location/Qualifiers
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                                                                                                                                                                                            Cilli EM,
                                                                                                                                                                                                                                                                             Disclosure; Page 6; 17pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08-DEC-2000; 2000WO-GB04720.
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                                                                                                                         20-DEC-2000; 2000WO-BR00160.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                99BR-0006091
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Domingo GJ;
                                                                                                                                                                                                Ianzer DA,
        Plasmodium falciparum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 NANPNANPNANP 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-475830/51.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                12 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        vaccine; MAL1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unidentified.
                                                                               WO200146216-A2
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                                   Key
Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14-JUN-2001
                                                                                                                                                 22-DEC-1999;
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                                                                                                    28-JUN-2001
                                                                                                                                                                                                Nakale CR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB84362;
                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
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                                                                                                                 The specification describes a truncated E2 core protein of a 2-oxo acid dehydrogenase multienzyme complex, where the protein assembles into a core structure of the complex. The E2 core protein has an ability to display a variety of different numbers of peptides or polypeptides on a single complex, and the ability to display a variety of different peptides or polypeptides on the same complex. The E2 core protein is perides or polypeptides or polypeptides or polypeptides or polypeptides or polypeptides or polypeptides or polypeptides, and for the elicitation of immune responses, e.g. for vaccination. It is also useful for obtaining and/or raising antibodies to the peptides or polypeptides, for evoking an immune response, and in pharmaceutical compositions. The present sequence response, and in pharmaceutical compositions. The present sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention provides a novel method of immunisation involving
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Immunization by administering ex vivo a transgene having a hematopoletic cell-specific expression element operationally linked to a polynucleotide encoding one or more heterologous epitopes to a
                          Novel truncated E2 core protein of 2-oxo acid dehydrogenase multienzyme complex, which assembles into a core structure of the complex, useful in screening for polypeptides which bind target proteins of interest \cdot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Somatic transgene immunisation; immune response; haematopoietic cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                       ő
                                                                                                                                                                                                                                                                                                                                                                                                         Length 12;
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                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 69; DB 22; 100.0%; Pred. No. 0.00016;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  immunity; disease treatment; disease prevention.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tumour antigen MUC-1 epitope peptide #1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB49997 standard; Peptide; 12 AA.
                                                                                                Disclosure; Page 27; 53pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 NANPNANPNANP 12
        WPI; 2001-381670/40.
                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
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Peptide; retro; inverso; retro-inverso; therapy; disease; vaccine; immunogen; antibody; antibodies; assay; treatment; prophylaxis; Plasmodium falciparum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New retro, inverso and retro-inverso peptide analogues - used as immunogens for the prodn. of antibodies and in diagnosis, therapy and prophylaxis of diseases
                                                                                                                                         Synthetic peptide analogue of P. falciparum used as immunogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 6; Page 21; 87pp; English.
                                     AAR49980 standard; peptide; 13 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fischer P, Tyler MI;
                                                                                                         10-OCT-1994 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                    (DEAK-) DEAKIN RES LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1994-100849/12
                                                                                                                                                                                                                                                                                                                                                27-AUG-1993;
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                                                                                                                                                                                                                                             Synthetic.
                                                                       AAR49980;
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the administration of a haematopoietic cell specific expression element to a lymphoid cell. The method is known as somatic transgene immunisation. It is particularly useful in the treatment and prevention of tunours, autofimmune diseases, allergy, metabolic disorders, endocrine disorders, pain, blood disorders and dental disorders.
                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The patentors claim a novel conjugate which comprises AAP60804 and a carier protein. The conjugates are useful for providing protective immunity against malaria. The conjugates are effective in raising high titres of antibodies in vivo. These antibodies recognise sporozoites and neutralise sporozoite infectivity in vitro by a vigorous CSP reaction. The epitope of the P.falciparum CS protein is
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conjugate of immunogenic peptide - having amino acid sequence corresp. to immuno-dominant epitope of P.falciparum circumsporozoite protein
                                                                                                                                                         Length 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ch 100.0%; Score 69; DB 7; Length 13; 1 Similarity 100.0%; Pred. No. 0.00018; 12; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence of an immunodominant epitope of P.falciparum
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                                                                                                                                                         100.0%; Score 69; DB 22; 100.0%; Pred. No. 0.00016;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      circumsporozoite (CS) protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (UYNY-) NEW YORK UNIVERSITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Zavala FP;
                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                           12; Conservative
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                                                                                                                                                         Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27-MAR-1986;
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93WO-AU00441. 92AU-0004374.

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Synthetic peptide antigen analogues of native peptide antigens which are either (1) retro modified, (2) inverso modified or (3) retro-inverso modified with respect to the native antigen can be used to raise antibodies which recognise the native antigen and hence can be used in the treatment and/or prophylaxis of diseases and therapy of disease states. They can be used in the production of vaccines and in assays for antibodies specific for the native antigen. They can have increased stability to degredation after administration and they can be administrated orally. This sequence is based on the immunodominant epitope of the circumsporcozoite coat protein of plasmodium falciparum. The retro-inverso version of this peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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Pred. No. 0.00018;
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Job time: 417 sec
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Matches 12; Conserv
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Best Local Similarity Matches 12; Conserv

8, Appli 27, Appli 27, Appli 10, Appli 10, Appli 11, Appl 14, Appl 12, Appl 50, Appl

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Sequence Sequence

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Sequence 105, Application US/09248588
Sequence 105, Application US/09248588
Patent No. 6231864
APPLICANT: BIrkett, Ashley J.
TITLE OF INVENTION: Strategically Modified Hepatitis B Core Proteins and TITLE OF INVENTION: their Derivatives
TITLE OF INVENTION: their Derivatives
FILE REPERENCE: SYN-101 4564/69529
CURRENT APPLICATION NUMBER: US/09/248,588
CURRENT FILING DATE: 1999-02-11
SARLIER RPLING DATE: 1999-02-12
NUMBER OF SEQ ID NOS: 113
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 105
LENGTH: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: Description of Artificial Sequence: Cytochrome OTHER INFORMATION: P-450 fragment PUBLICATION INFORMATION: JOURNAL: Science
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 12;
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Sequence 4, Application US/08909551
Sequence 5.261569
GENERAL INFORMATION:
APPLICANT: COMIS, ALFIO
APPLICANT: FISCHER, PETER
APPLICANT: TYLER, MARGARET I
ATILE OF INVENTION: Retro-, Inverso-
TITLE OF INVENTION: Setro-, Inverso-
TITLE OF INVENTION: Synthetic Peptide Analogues
NUMBER OF SEQUENCES: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 69; DB 4; L
Pred. No. 8.3e-05;
Mismatches 0;
US-08-822-324-23
US-08-570-311-29
US-08-8318-818-13
US-08-894-818B-1
US-08-894-818B-1
US-08-353-485-8
US-08-570-311-27
US-08-353-384-10
US-08-350-311-10
US-08-350-311-10
US-08-350-311-10
US-08-350-311-14
US-08-570-311-14
US-08-570-311-14
US-08-770-312-40
US-08-346-856A-12
US-08-346-856A-12
US-08-346-856A-12
US-08-346-856A-12
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Best Local Similarity 100.0%; Pi
Matches 12; Conservative 0;
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PAGES: 1436-1440
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     TYPE: PRT
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Sequence 3, Appli
Sequence 8, Appli
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Sequence 35, Appl
Sequence 35, Appl
Sequence 13, Appl
Sequence 13, Appl
Sequence 11, Appl
Sequence 12, Appl
Sequence 14, Appli
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2.028 Million cell updates/sec
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                                                                                                                   Search time 133.18 Seconds
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Compugen Ltd
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US-08-909-551-4
US-08-909-551-3
US-08-614-626-8
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5219987-4
US-08-614-626-8
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US-08-614-626-8
US-08-614-35-625-35
US-08-143-3654-13
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US-08-143-36-14
US-08-
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                                                                                                                                                                                                                                                                                                  212252 seqs, 22503292 residues
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                 GenCore version
Copyright (c) 1993 - 2000
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                 January 29, 2002, 10:24:01
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Gapop 10.0 , Gapext 0.5
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Sequence:
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Minimum DB Maximum DB

Database

Result

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Searched:

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Gaps

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LOCATION: 1..2
COTHER INFORMATION: /label= A
OTHER INFORMATION: /note= "RESIDUE 1 IS AN EXTRA CYSTEINE
OTHER INFORMATION: PESTIDUE ADDED TO THE N-TERMINUS OF THE
OTHER INFORMATION: PEPTIDE"
DUBLICATION: PEPTIDE"
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                                                                        COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Vers. #1.25
SOFTWARE: Patentin Release #1.0, Vers. #1.25
CURREWT APPLICATION DATA:
FILING DATE: 12-AUG-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/387,932
FILING DATE: 27-FEB-1995
APPLICATION NUMBER: PCT/AU93/00441
FILING DATE: 27-AUG-1993
PRICH APPLICATION NUMBER: AU 4374
FILING DATE: 27-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
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US-07-987-286-8

US-07-987-286

Sequence 8, Application 07/987286

Patent No. 550036

CENERAL INFORMATION:
APPLICANT: RUSSELL-JONES, GREGORY JAPLICANT: GECZY, ANDREW F

TITLE OF INVENTION:
UNMBER OF SEQUENCES: 26

CORRESPONDENCE ADDRESS:
         Pennsylvania
: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                    GHC2USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Plasmodium falciparum
DEVELOPMENTAL STAGE: SPOROZOITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-540-9200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27-AUG-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ANTI-SENSE: NO FRAGMENT TYPE: internal ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: 215-540-920
TELEFAX: 215-540-5818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DEVELOPMENTAL STAGE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 NANPNANPNANP 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 NANPNANPNANP 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 12; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOCUMENT NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
US-08-909-551-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HYPOTHETICAL:
                                     19477
         STATE: Pe
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APPLICANT: FISCHER, PETER
APPLICANT: TYLER, MARGARET
TITLE OF INVENTION: Retro., inverso., and Retro-Inverso
TITLE OF INVENTION: Synthetic Peptide Analogues
NUMBER OF SEQUENCES: 16
CORRESONDE ADDRESS:
ADDRESSE: Howson and Howson
STREET: Spring House Corporate Cntr., P.O. Box 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
CORRESPONDENCE ADDRESS:
ADDRESSEE: Howson and Howson
STREET: Spring House Corporate Cntr., P.O. Box 457
                                                                                                                                      100.0%; Score 69; DB 4; I
100.0%; Pred. No. 8.3e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Plasmodium falciparum
DBVELCPMENTAL STAGE: SPOROZOITE
PUBLICATION INFORMATION:
COCUMENT NUMBER: AU PL4374
FILING DATE: 27-AUG-1992
US-08-909-551-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
REFRENCE/POCKEY NUMBER: GHC2USA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-540-5818
                                                                          STATE: Pennsylvania
COUNTRY: United States of America
ZIP: 19477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 %3-08-909-551-3
; Sequence 3, Application US/08909551
; Patent No. 651569
; GENERAL INPORMATION:
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SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
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Best Local Similarity 100.
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
                                                                                                                                 COMPUTER READABLE FORM:
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                                                          Spring House
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Gaps

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Sequence 35, Application US/08455625
Patent No. 593218
GENERAL INFORMATION:
APPLICANT: Berzofsky, Jay A.
APPLICANT: Ahlers, Jeffrey D.
APPLICANT: Nara, Peter
APPLICANT: Nara, Peter
TITLE OF INVENTION: COMPOSITE SYMTHETIC PEPTIDE CONSTRUCT
TITLE OF INVENTION: LYMPHOCYTES AGAINST HIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 6
5219987-4
; Patent No. 5219987
; APPLICANT: VERDINI, ANTONIO S.; PESSI, ANTONELLO; BONELLI,
                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 69; DB 2; I 100.0%; Pred. No. 0.00012;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 69; DB 6; 100.0%; Pred. No. 0.00017;
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STREET: P.O. Box 747
                            FILING DATE: 17-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 40 PK2361
FILING DATE: 18-SEP-1990
ATOMNEY/AGENT INFORMATION:
NAME: BENY. STEPHEN A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 16786/175/CHAC
TELEPHONE: 202 672 5399
TELEPHONE: 202 672 5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
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        MBER: PCT/AU91/00429
17-SEP-1991
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NUMBER OF SEQUENCES: 7

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/227,364

FILING DATE: 02-AUG-1988
                                                                                                                                                                                                                        TELEFAX: 202 672 5399
TELEX: 904136
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 100.
Matches 12; Conservative
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Best Local Similarity 100.

Matches 12; Conservative
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ADDRESSEE: Birch, St
              APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 NANPNANPNANP 12
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                                                                                                                                                                                                                                                                                                                           amino acid
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5219987-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: FLORPY disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-FOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/614,626
                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATUS SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 07/987,286
FILING DATE: 16-MAR-1993
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                               16786/175/CHAC
                                                                                                                                                                                                                                                                         PRIOR APPLICATION 19.434
PRIOR APPLICATION 10.424
APPLICATION NUMBER: PCT/AU91/00429
FILING DATE: 17.5EP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PK2361
FILING DATE: 18-5EP-1990
ATTORNEY/AGENT INFORMATION:
NAME: BENT, STEPHEN A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 16786/175/CH
TELECHONE: 202 672 5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence B, Application US/08614626
Patent No. 5928644
GENERAL INFORMATION:
APPLICANT: RUSSELL-JONES, GREGORY J
APPLICANT: GECZY, ANDREW F
TITLE OF INVENTION: T-CELL EPITOPES
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY & LARDNER
STREET: 3000 K STREET, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/987,286
FILING DATE: 16-MAR-1993
ADDRESSEE: FOLET & CARRET, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEX: 904136
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 17 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match 100.
Best Local Similarity 100.
Matches 12; Conservative
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                                              WASHINTON, D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 NANPNANPNANP 15
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                                                                                    20007-5109
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                                                                  COUNTRY:
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HELPBR T-LYMPHOCYTE, CYTOTOXIC T LYMPHOCYTE AND NEUTRALIZING ANTIBODY RESPONSES AGAINST HIV-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 69; DB 4;
100.0%; Pred. No. 0.00052;
iive 0; Mismatches 0;
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THAT ELICIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: Windows95
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/060,988A
FILING DATE: 14-MAY-1993
PRIOR APPLICATION DATE:
FILING DATE: 06-MAR-1992
FILING DATE: 06-MAR-1992
                                                                                                                                                                                                                                                                                                                                                 08830/022003
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/455,685
FILING DATE: 31-MAY-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/060,988
FILING DATE: 14-MAY-1993
APPLICATION NUMBER: 07/847,311
FILING DATE: 06-MAR-1992
APPLICATION NUMBER: 07/751,998
FILING DATE: 29-AUG-1991
APPLICATION NUMBER: 07/148,692
FILING DATE: 26-JAN-1988
ATTORNEY/AGENT INFORMATION:
NAME: Beattie, Ingrid A.
RECISTRATION NUMBER: P-42,306
RECISTRATION NUMBER: P-42,306
RECISTRATION NUMBER: 08030/022(
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: 617/542-8906
TELEFAX: 200154
TILERAX: 200154
TILERAX: 200154
TILERAX: 200154
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ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 35, Application US/08060988A Patent No. 6294322 GENERAL INFORMATION: APPLICANT: Berzofsky, Jay A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Berzofsky, Jay A.
APPLICANT: Ahlers, Jeffrey D.
APPLICANT: Pendleton, C. David
APPLICANT: Nara, Peter
APPLICANT: Shirai, Mutsunori
TITLE OF INVENTION: MULTIDETERNIN
TITLE OF INVENTION: THAT ELICIT
TITLE OF INVENTION: HELPER T-LIMP
TITLE OF INVENTION: NEUTRALIZING
NUMBER OF SEQUENCES: 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 06-MAR-1992
APPLICATION NUMBER: 07/751,998
FILING DATE: 29-AUG-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 66 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 100.
Best Local Similarity 100.
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             , MOLECULE TYPE: peptide US-08-455-685-35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE:
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APPLICANT: Ahlers, Jeffrey D.
APPLICANT: Applers, Jeffrey D.
APPLICANT: Pendleton, C. David
APPLICANT: Pendleton, C. David
APPLICANT: Pendleton, C. David
APPLICANT: Shirai, Mutsunori
TITLE OF INVENTION: MULTIDETERMINANT PEPTIDES THAT ELICIT
TITLE OF INVENTION: HELPER T.LYMPHOCYTE, CYTOTOXIC T LYMPHOCYTE
TITLE OF INVENTION: NEUTRALIZING ANTIBODY RESPONSES AGAINST HIV-1
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 2.25 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: 1..66; Jabel= peptide; OTHER INFORMATION: /note= "peptide from P. falciparum CS antigen" US-08-455-625-35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.0%; Score 69; DB 2; Length 66;
Best Local Similarity 100.0%; Pred. No. 0.00052;
Matches 12; Conservative 0; Mismatches 0; Indels
                                                                                                          COMPUTER FAUGUS TO COMPUTER FAUGUS TO COMPUTER FAUGUS TO COMPUTER FAUGUS TO COMPUTE FAUGUS SOFTWARE FAUGUS SOFTWARE FAUGUS SOFTWARE FAUGUS TO CORRENT APPLICATION NUMBER: US/08/455,625
FILING DATE: US/08/455,625
FILING RAPPLICATION 1435
PRICATION NUMBER: US 08/060,988
FILING DATE: 14-MAY-1993
ATTONEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSEQ for Windows Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 35, Application US/08455685 Patent No. 6214347 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Svensson, Leonard R.
REGISTRATION NUMBER: 30330
REGISCOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: 703-205-8000
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGIH: 66 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Clrr
STATE: Mr
COUNTRY: US
TD 02110-2804
                        Falls Church
Virginia
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22 NANPNANPNANP 33
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             amino acid
GY: linear
                                                                                           22040-0747
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                                                                          COUNTRY:
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                                                                                                                                         Gaps
/label= peptide
/note= "peptide from P. falciparum CS antigen"
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                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: LOWell, George H
TITLE OF INVENTION: IMMUNO-POTENTIATING SYSTEMS FOR
TITLE OF INVENTION: DREPARATION OF IMMUNOGENIC MATERIALS
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hendricks and Assoc.
STREET: 9669 A Main Street
                                                                                                 Length 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floopy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION NATE: APPLICATION NAMBER: US/08/143,365A FILING DATE: 29-OCT-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 69; DB 1; I
Pred. No. 0.00053;
                                                                                               100.0%; Score 69; DB 5;
100.0%; Pred. No. 0.00052;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 100.0%; Score 69; DB Best Local Similarity 100.0%; Pred. No. 0.0 Matches 12; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Hendricks, Glenna M
REGISTRATION NUMBER: 32,535
REFERENCE/DOCKET NUMBER: Lowell-2
TELECOMMUNICATION INFORMATION:
TELECHONE: (703) 425-4250
TELECHONE: (703) 425-2767
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 68 amino acids
                                                                                                                                                                                                                                                                                                                   Sequence 13, Application US/08143365A Patent No. 5726292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-268-348A-12; Sequence 12, Application US/08268348A; Patent No. 5750374; GENERAL INFORMATION:
                                                                                                 Query Match 100.
Best Local Similarity 100.
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sss: single
unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; FRAGMENT TYPE: internal US-08-143-365A-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: unknown
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
; OTHER INFORMATION:
; OTHER INFORMATION:
PCT-US94-05142-35
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22 NANPNANPNANP 33
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COUNTRY: US
ZIP: 22031
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US-08-143-365A-13
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TITLE OF INVENTION: ELICITING NEUTRALIZING ANTIBODIES AND CYTOTOXIC T
TITLE OF INVENTION: LYMPHOCYTES AGAINST HIV
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: BLTCh, Stewart, Kolasch & Birch
STREET: P.O. Box 747
CITY: Falls Church
STATE: VIrginia
COUNTRY: USA
ZIP: 22040-0747
COMPUTER FRADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIBLE
COMPUTER: STATE: NOTATE DOSMS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
              FILING DATE: 26-JAN-1988
ATTORNEY/AGENT INFORMATION:
NAME: BEALLE, Ingrid A.
REGISTRATION NUMBER: P-42,306
REFERENCE/DOCKET NUMBER: 08830/022001
TELEPHONE: 617/542-6070
TELEFAX: 617/542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Svensson, Leonard R.
REGISTRATION NUMBER: 30330
REFERCE/DOCKET NUMBER: 1173-434P
TELECOMMUNICATION:
TELEPHONE: 703-205-8000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: PCT/US94/05142
FILING DATE: 13-MAY-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/060,988
FILING DATE: 14-MAY-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PCT-US94-05142-35; Sequence 35, Application PC/TUS9405142
GENERAL INFORMATION:
APPLICANT:
  07/148,692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 35: SEQUENCE CHARACTERISTICS:
                                                                                                                                                       TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 66 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : 66 amino acids
amino acid
GY: linear
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Best Local Similarity 100.
Matches 12; Conservative
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                                                                                                                                                                                                                                                                                            , MOLECULE TYPE: peptide US-08-060-988A-35
  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 NANPNANPNANP 12
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                                                                                                                                                                                                                                                                                TOPOLOGY: linear
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APPLICANT: Ding, Zhi-Ming
TITLE OF INVENTION: Targeted Nucleic Acid Delivery into
TITLE OF INVENTION: Liver Cells
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WEDION TYPE: CIPOPY disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPARE: PATENTIN PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/021,625D
FILING DATE: 16-FEB-1993
CLASS! FILCATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Highlander, Steven L.
REGISTRATION NUMBER: 37,642
REFERENCE/DOCKET NUMBER: UTSC:410/HYL
TELECOMMUNICATION INFORMATION:
SYSTEM: PC-DOS/MS-DÖS
PatentIn Release #1.0, Version #1.30
                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Highlander, Steven L.
REGISTRATION NUMBER: 37,642
REFERENCE/DOCKET NUMBER: UTSC:410/HYL
TELECOMMUNICATION INFORMATION:
                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/395,602A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Arnold, White & Durkee STREET: P.O. Box 4433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 4, Application US/08021625D Patent No. 5976851 GENERAL INFORMATION:
                                                                                                                                                                                                                             TELEPHONE: (512) 418-3000
TELEFAX: (713) 789-2679
TELEX: 79-0924
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 126 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (512) 418-3000
(713) 789-2679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEX: 79-0924
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 126 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 100.
Best Local Similarity 100.
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: United State ZIP: 77210
COMPUTER READABLE FORM: MEDIUM TYPE: Floppy (
                                                                                   FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 NANPNANPNANP 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TOPOLOGY: linear
US-08-021-625D-4
                                                                                                                                                                                                                                                                                                                                                                                                     linear
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TOPOLOGY:
US-08-395-602A-4
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STATE:
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                                                                                                         Process for Producing Hydrophobic
Polypeptides and Proteins, and Fusion Proteins for Use in
Producing Same
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Kuo, M. Tien
APPLICANT: Ding, Zhi-Ming
TITLE OF INVENTION: Targeted Nucleic Acid Delivery into
TITLE OF INVENTION: Liver Cells
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSE: Arnold, White & Durkee
                                                                                                                                                                                                                                                                                                                                                                                                                       SOUTHWARE: Patentin Release #1.0, Version #1.25
SOUTHWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/268,348A
FILING DATE: 29-JUN-1994
CLASSIFICATION PATA:
APPLICATION DATA:
APPLICATION NUMBER: EP 93110755.1
FILING DATE: 06-JUL-1993
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Parise, John P. REGISTRATION NUMBER: 34,403
REFERENCE/DOCKET NUMBER: 4105/157
                                                                                                                                                                                                                      Hoffmann-La Roche Inc.
                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 4, Application US/08395602A Patent No. 5766899 GENERAL_INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
        APPLICANT: Dobeli, Heinz
APPLICANT: Draeger, Nicholas
APPLICANT: Trottman, Gerda H
APPLICANT: Jakob, Peter
APPLICANT: Stuber, Dietrich
TITLE OF INVENTION: Process for
TITLE OF INVENTION: Polypeptid
TITLE OF INVENTION: Producing shumber of SEQUENCES: 12
                                                                                                                                                                                                                  ADDRESSEE: HOIIMann ---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
TELEPHONE: (201) 235-6326
TELEFAX: (201) 235-3500
INFORMATION FOR SEQ ID NO: 12:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 126 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein
                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                 STREE1.
CITY: Nutley
STATE: New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 NANPNANPNANP 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Houston
STATE: Texas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: Ur
                                                                                                                                                                                                                                                                                                         COUNTRY: U. ZIP: 07110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-268-348A-12
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US-08-395-602A-4
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Query Match 100.0%; Score 69; DB 2; Length 126; Best Local Similarity 100.0%; Pred. No. 0.001; Matches 12; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CAPPUTER TRADABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/268,348A
FLING DATE: 09-JUN 1994
FLING APPLICATION DATA:
APPLICATION NUMBER: EP 93110755.1
FILING DATE: 06-JUL-1993
ATYONREY/AGENT INFORMATION:
NAME: PATISE, John P:
REGISTRATION NUMBER: 34,403
REFRENCE/DOCKET NUMBER: 34,403
REFRENCE/DOCKET NUMBER: 201,235-6326
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 18FORMATION:
TELECOMMUNICATION 00 8:
SECURECE EMRACTERISTICS:
TENGTH 133 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Search completed: January 29, 2002, 10:24:02
Job time: 508 sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; MOLECULE TYPE: protein US-08-268-348A-8
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## ALIGNMENTS

망 QY A;Cross-references: GB:M60972; NID:g160228; PIDN:AAA29561.1; PID:g160229 C;Superfamily: circumsporozoite protein; thrombospondin type 1 repeat homeology <THR1> C;Accession: A39756
R;Lal, A.A.; Goldman, I.F.
J. Biol. Chem. 266, 6686-6689, 1991
A;Title: Circumsporozoite protein gene from Plasmodium A;Reference number: A39756; MUID:91201303
A;Accession: A39756 C;Species: Plasmodium reichenowi
C;Date: 14-Feb-1992 #sequence\_revision 14-Feb-1992 #text\_change 20-Aug-1999 A; Molecule type: DNA A; Residues: 1-388 <LAL> A; Status: preliminary circumsporozoite protein - Plasmodium reichenowi A39756 Matches Query Match 196 Local 1 NANPNANPNANP 12 NANPNANPNANP l Similarity 12; Conserva Conservative 207 100.0%; 0 Score 69; DB 2; Pred. No. 0.002; Mismatches <u>ب</u> 0; Length 388, Indels reichenowi, a repeat homology 0, Gaps chimpanzee malar 0

RESULT 2
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Clarcumsporozoite protein - malaria parasite (Plasmodium falciparum) (isolate NF54)
Clarcumsporozoite protein - malaria parasite (Plasmodium falciparum) (isolate NF54)
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Clarcumsporozoite protein 07-Jun-1990 #text\_change 09-Jun-2000
Clarcumsporozoite protein 07-Jun-1990 #text\_change 09-Jun-2000
Clarcumsporozoite protein 07-Jun-1990 #text\_change 09-Jun-2000
Clarcumsporozoite protein 98 application not shown
All Title: DNA sequence of the gene encoding a Plasmodium falciparum malaria candidate
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C;Species: Plasmodium falciparum
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C;Date: 15-Nov-1984 #sequence_revision 15-Nov-1984 #text_change 09-Jun-2000
C;Date: 15-Nov-1984 #sequence_revision 15-Nov-1984 #text_change 09-Jun-2000
C;Accession: A03388
R;Dame, J.B.; Williams, J.L.; McCutchan, T.F.; Weber, J.L.; Wirtz, R.A.; Hochmeyer, W.T.
Science 225, 593-599, 1984
A;Title: Structure of the gene encoding the immunodominant surface antigen on the sporoz
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A;Teference number: A03388; MUID:84250215
A;Accession: A03388; MUID:84250215
A;Accession: A03388
A;Molecule type: DNA
A;Residues: 1-412 <DAM>
A;Residues: 1-412 <DAM>
A;Residues: 1-412 <DAM>
A;Coss-references: GB:K02194; NID:g160160; PIDN:AAA29524.1; PID:g160161
A;Experimental source: clone 7G8
C;Comment: There are 41 copies of a 4-residue repeating unit in the middle domain of the C;Superfamily: circumsporozoite protein; thrombospondin type 1 repeat homology
F;336-390/Domain: thrombospondin type 1 repeat homology <THRI>
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Mol. Biochem. Parasitol. 37, 275-280, 1989
A;Title: Wild isolates of Plasmodium falciparum show extensive polymorphism in A:Reference number: A60657; MUID:90114334
A;Accession: I60657
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A;Residues: 319-336,354-373 <LOC>
A;Residues: 319-336,354-373 <LOC>
C;Superfamily: circumsporozoite protein; thrombospondin
F;329-383/Domain: thrombospondin type 1 repeat homology
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                                                                                                                                                                                                                                                                                                                                                                                             circumsporozoite protein - malaria parasite (Plasmodium falciparum) (strain T4, C;Species: Plasmodium falciparum C;Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 09-Jun-2000
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                                                                                                                   A;Cross-references: GB:M19752; NID:g160216; PIDN:AAA29555.1; PID:g160217 C;Superfamily: circumsporozoite protein; thrombospondin type 1 repeat how F;348-402/Domain: thrombospondin type 1 repeat homology <THR1>
                                                                                                                                                                                                                                                           A;Title: Circumsporozoite gene of a Plasmodium falciparum A;Reference number: A54533; MUID:87315205 A;Accession: A54533
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A; Residues: 1-424 <DEL>
                                                                                                                                                                                                                                                                                                                              R;del Portillo, H.A.; Nussenzweig, R.S.; Enea, V. Mol. Biochem. Parasitol. 24, 289-294, 1987
                                                                                                                                                                                                                                                                                                                                                                            C; Accession:
                                                                                                                                                                                                                                      A; Status: preliminary
                                                                                                                                                                                                                                                                                                                            Mol. Biochem. Parasitol. 24, 289-
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Best Local
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Best Local
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12; Conser
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Pred. No. 0.0
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Pred. No. 0.0021;
Mismatches 0
                                 Score 69;
Pred. No.
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                                                       Length 424;
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R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Aloc Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, A.; Liu, S.X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzi, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzi, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Talk, Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A; Reference and analysis of chromosome 1 of the plant Arabidopsis.
A; Accession: A86132
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Mol. Biochem. Parasitol. 22, 101-108, 1987

A;Title: Strain variation in the circumsporozoite protein gene of A;Reference number: A54529; MUID:87115616

A;Accession: A54529

A;Accession: A54529
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Superfamily: circumsporozoite protein; thrombospondin type 1 C;Keywords: tandem repeat F;366-420/Domain: thrombospondin type 1 repeat homology <THR1>
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A; Residues: 1-442 <LOC>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein AAF27098.1 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: GB:M15505; NID:g160214; PIDN:AAA29554.1;
                                                                                                                                                                                                                                                                              A;Cross-references: GB:AE005172; NID:g6730703; PIDN:AAF27098.1;
                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-387 <STO>
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9; Conserv
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95
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75.0%;
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                                                                                                                             Score 54; DB 2; Pred. No. 0.35;
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Pred. No.
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0.0023;
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Porphyromonas

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C:Species: Plasmodium falciparum
C:Species: Plasmodium falciparum
C:Species: Plasmodium falciparum
C:Species: Plasmodium falciparum
C:Date: 18-OCt-1989 #sequence_revision 21-Jul-1995 #tex
C:Accession: B29795; A60657
R:de la Cruz, V.F.; Lal, A.A.; McCutchan, T.F.
J. Biol. Chem. 262, 11935-11939, 1987
A:F1tle: Sequence variation in putative functional doma
A:Reference number: A92609; MUID:87308186
A:Accession: B29795
A:McCession: B29795
A:Residues: 1-161 <DEL>
A:Cross-references: GB:M17802; GB:M17803; GB:M17806
D:Frorver M.T.: Marsh. K.: Newbold, C.I.
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                                         R:Lockyer, M.J.; Marsh, K.; Newbold, C.I.
Mol. Biochem. Parasitol. 37, 275-280, 1989
A;Title: Wild isolates of Plasmodium falciparum show
A;Reference number: A60657; MUID:90114334
A;Accession: A60657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Accession: A29795
R;de la Cruz, V.F.; Lal, A.A.; McCutchan,
J. Biol. Chem. 262, 11935-11939, 1987
A;Title: Sequence variation in putative fi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   circumsporozoite protein - malaria parasite (Plasmodium falciparum) (strain C;Species: Plasmodium falciparum C;Date: 28-Aug-1989 #sequence_revision 28-Aug-1989 #text_change 09-Jun-2000
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A; Residues: 1-171 <DELA>
C; Superfamily: circumsporozoite
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C;Keywords: c
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                           A; Status: preliminary; not compared
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A; Residues: 1-1526 <ADU>
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                A; Molecule
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Date: 05-Mar-1995 #sequence_revision 12-May-1995 #text_change 31-Mar-1997
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Best Local
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Best Local
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 type: DNA
: 152-189
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9; Conser
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75.0%;
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Pred. No. 0.41
0; Mismatches
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Pred. No.
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                             with conceptual translation
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A;Gene: ypjA
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R; Perna, N.T.; Plun
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Neuron 21, 225-234,
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C;Species: Drosophila melanogaster
C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999
C;Accession: T13065
                                                                                                                                                           A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1528 <STO>
                                                                                                                                                                                                                                                          R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasiiller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, Nature 409, 529-533, 2001
                                                                                                                                                                                                                                                                                                                                     hypothetical protein ypjA [imported] - Escherichia coli (strain 0157:H7) C;Species: Escherichia coli C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 31-Mar-2001
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A; Residues: 1-1171 <SUR>
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                                                                                                                          A;Cross-references: GB:AE005174; NID:g12517083; PIDN:AAG57760.1; GSPDB:GN00145; UWGP:A;Experimental source: strain 0157:H7, substrain EDL933
                                                                                                                                                                                                                                A; Title: Genome sequence of enterohemorrhagic Escherichia A; Reference number: A85480; MUID: 21074935; PMID: 11206551
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lanta, E.;
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A; Molecule type: DNA
A; Residues: 1-1704 <-PAV>
A; Residues: 1-1704 <-PAV>
A; Cross-references: GB:U15282; NID:g557067; PIDN:AAA69539.1; PID:g557068
A; Pike, R.; McGraw, W.; Potempa, J.; Travis, J.
J. Biol. Chem. 269, 406-411, 1994
A; Title: Lysine- and arginine-specific proteinases from Porphyromonas gi A; Reference number: A53113; MUID:94103245
A; Accession: D53113.
A; Accession: D53113.
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                                                          A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-1350,'N',1352-1363,'Y',1365-1447,'H',1449-1732 <L
A; Cross-references: EMBL:AF017059; NID:g2738802; PID:g2738803;
A; Cross-references: EMBL:AF017059; Travis, J.
R:Pike, R.; McGraw, W.; Potempa, J.; Travis, J.
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A;Cross references: EMBL:U42210; NID:g1314325; PID:g1314326;
R;Slakeski, N.; Cleal, S.M.; Reynolds, E.C.
submitted to the EMBL Data Library, October 1996
A;Reference number: Z20896
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A;Title: Molecular cloning and structural characterization of the Arg-gingipa A;Reference number: A55426; MUID:95138080
A;Accession: A55426
                                                                                                                                                                                                                               A;Title: IS195, an insertion sequence-like element associated with A;Reference number: Z20844; MUID:98298016
A;Accession: T30526
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A;Molecule type: DNA
A;Residues: 1-795,'I',797-1389,'N',1391-1478,'Y',1480-1732 <SLA>
A;Residues: 1-795,'I',797-1389,'N',1391-1478,'Y',1480-1732 <SLA>
A;Cross-references: EMBL:075366; NID:92182811; PID:92182812; PIDN:AAB60809.1
R;Lewis, J.P.; Macrina, F.L.
Infect. Immun. 66, 3035-3042, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  lysine-specific cysteine proteinase porphypain (EC 3.4.22.-) - Porphyromonas gingivalis N.Alternate names: lysine-specific cysteine proteinase 1, 60K
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                        R;Pike, R.; McGraw, W.; Potempa, J. Biol. Chem. 269, 406-411, 1994
A;Title: Lysine- and arginine-spe
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A; Residues: 1-1732 <
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and arginine-specific proteinases er: A53113; MUID:94103245
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3; PIDN:AAC26523
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RESULT
T28651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues; 1-2628 <HANN
A;Cross-references: EMBL:U41807; NID:g1552410; PID:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hemagglutinin A - Porphyromonas gingivalis
C;Species: Porphyromonas gingivalis
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Gene: prtP; prtK
C;Keywords: cysteine
                                                                                                                                                                                                                                                                                                                                      transcription factor Vpl - common ice plant
C;Species: Mesembryanthemum crystallinum (common ice plant)
C;Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 20-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Title: The hemagglutinin gene A (hagA) of Porphyromonas A; Reference number: Z20494; MUID:96406248 A; Accession: T28651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Note: sequence extracted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: protein A; Residues: 229-249 < PIK>
                                                                                                                 A; Gene:
                                                                                                                                                    A; Cross-references: EMBL: AB015183
                                                                                                                                                                     A; Molecule type: mRNA
A; Residues: 1-790 <FUK>
                                                                                                                                                                                                                              A; Accession: T12203
                                                                                                                                                                                                                                              A;Description: Expression of Vp1
A;Reference number: Z17452
                                                                                                                                                                                                                                                                                   submitted to the EMBL Data Library, June 1998
                                                                                                                                                                                                                                                                                                    C; Accession: T12203
R; Fukuhara, T.; Bohnert, H.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Gene: hagA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Han, N.; Whitlock, J.; Progulske-Fox, A. Infect. Immun. 64, 4000-4007, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C; Accession: T28651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Experimental source: H66
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                                                                                                                                                                                                         A;Status: preliminary; translated from GB/EMBL/DDBJ
Query Match
Best Local Similarity
                                                                                           Superfamily: rice transcription factor VP1
                                                                                                                                  Genetics:
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Best Local
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Matches 8; Conserv
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                                                                          DNA binding; transcription regulation
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Pred. No.
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Pred. No.
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Pred. No. 6
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                   Length 790;
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Conservative

Mismatches

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0,

Qy 2 ANPNANPANP 12
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Db 377 ADPNPNPNP 387

Search completed: January 29, 2002, 10:26:35
Job time: 646 sec

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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

January 29, 2002, 11:13:37; Search time 80.65 Seconds (Without alignments) 5.455 Million cell updates/sec Run on:

US-09-763-397A-4 69 1 NANPNANPNANP 12 Title: Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

100059 segs, 36664827 residues Searched:

100059 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_39:\* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

	CSP	Length DB ID  315 I CSP  317 I CSP  412 I CSP  424 I CSP  425 I CSP  426 I PRO  436 I PRO  436 I PRO  436 I PRO  436 I PRO  437 I SGR  431 I SGR  441 I SGR  451 I SG	DB CSSP CSSP CSSP CSSP CSSP CSSP CSSP CSS	Length DB ID 315 1 CSP 338 1 CSP 3497 1 CSP 424 1 CSP 424 1 CSP 441 1 GUN 441 1 GUN 641 1 DEX 651 1 PRO 756 1 PRO 75	SUMMARIES	Descr Therein	LAFL P05691 plasmodium	P26694	P19597	P02893	P13814	P08307	I Q51845	P26222	P04923	P04926	042713	P09547	P30404	P38956	P39820	058497	005201	ROVI Q24742 drosophila			93MCQ	09xt18			YEAST P32831 saccharomyc		094916			P07261	P06915	100101
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38         55.1         423         1 YHJ3_YEAST         P40356 saccharomyc           38         55.1         448         1 AAC2_DICDI         P40356 saccharomyc           38         55.1         448         1 AAC2_DICDI         P4196 dictyostell           38         55.1         448         1 CC24_YEAST         P41357 saccharomyc           38         55.1         1 PUR4_YIBCH         Q9ktn2 vibrio chol           37         53.6         19         1 LEP_STAAU         P72365 staphylococ           37         53.6         19         1 LEP_STAAU         Q92030 chlamydomon           37         53.6         198         1 SECG_HELPJ         Q92jx2 helicobacte           37         53.6         199         1 FEG_HELPJ         Q92jx2 helicobacte           37         53.6         241         1 HFBL_HAEIN         P35757 haemophillus	PERULT 1  SP.PLAFL  CSP PLAFL  TO 11-MOV-1988 (Rel. 09, Last sequence update)  TO 11-MOV-1988 (Rel. 09, Last sequence update)  TO 11-MOV-1988 (Rel. 09, Last sequence update)  CIRCUMAPOPOXOTE PROTEIN (CS) (FRACMENT)  SEQUENCE PLAFA ANCOLADAM  TO 11-MOV-1989 (Rel. 28, Last annothina update)  ELGIZO VET. Lal A.A., MCCUTCHAN  NELLAR-GROSSIE PROTEIN (CS) (FRACMENT)  TO 11-MOV-1989 (Rel. 09)  TO 11-MOV-1988 (Rel. 09)  TO 10-MOV-1988 (Rel. 09)  TO 11-MOV-1988 (Rel. 09)  T	PLARE STANDARD; PRT; 388 AA.
40000000000000000000000000000000000000	SSUL P_G	CSP_
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CONFLICT
            REVISIONS
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                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its was by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                    -!- MISCELLANDOUS: THE C-TERMINAL REGION IS PROBABLY USED FOR ANCHORING THE PROTEIN TO THE CELL MEMBRANE. THE REPEAT SEQUENCES WOULD BE THE SUBRACE ANTIGEN OF THE ORGANISM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "DNN sequence of the gene encoding a Plasmodium falciparum malaria candidate vaccine antigen.";
Nucleic Acids Res. 17:5854-5854(1989).
                                                                                                                     DEDINE-91201303; PubMed-2016283;
Lal A.A., Goldman I.F.;

Chimpanzee malaria parasite evolutionarily related to the human malaria parasite Plasmodium falciparum.";
J. Biol. Chem. 266:6686-6689(1991).

- : FUNCTION: THE CIRCUMSPOROZOITE PROFEIN IS THE IMMUNODOMINANT SURFACE ANTIGEN ON THE SPOROZOITE (THE INFECTIVE STAGE OF THE MALARIA PARASITE THAT IS TRANSMITTED FROM THE MOSQUITO TO THE MALARIA PARASITE THAT IS TRANSMITTED FROM THE MOSQUITO TO THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SWART; SMULLUY; ISEL, A.
Malaria; Sporozoite; Repeat; Signal.
SIGNAL 17 388 CIRCUMSPOROZOITE PROTEIN.
CHAIN 120 267 62 X 4 AA TANDEM REPEATS OF N-A-N-P.
COMAIN 120 267 W; C031EEFBEZE35604 CRC64;
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0
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P19597; Q25798;
01-FEB-1991 (Rel. 17, Created)
01-KEB-1991 (Rel. 39, Last sequence update)
20-MAY -2000 (Rel. 39, Last sequence update)
20-MG-2001 (Rel. 40, Last annotation update)
CIRCUMSPOROZOITE PROTEIN PRECURSOR (CS).
Plasmodium falciparum (isolate NF94).
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
                                                                  Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBL_TaxID=5854;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 69; DB 1; Length 388; 100.0%; Pred. No. 0.0016; Live 0; Mismatches 0; Indels
     01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
01-AUG-2001 (Rel. 40, Last annotation update)
CIRCUMSPOROZOITE PROTEIN PRECURSOR (CS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-89345189; PubMed=2668895; Campbell J.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIR; A39756; A39756.
InterPro; IPR003067; Crcmsprzoite.
InterPro; IPR000884; TSP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00090; tsp_1; 1.
PRINTS; PR01303; CRCMSPRZOITE.
SMART; SM00209; TSP1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; M60972; AAA29561.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 100.
Matches 12; Conservative
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                                                                                                                 SEQUENCE FROM N.A.
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE=89364998; PubMed=2671723;
Caspers P., Gentz R., Matile H., Pink J.R., Sinigaglia F.;
"The circumsporozoite protein gene from NF54, a Plasmodium falciparum "The circumsporozoite protein gene from SF4, a Plasmodium falciparum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -:- MISCELLANEOUS: THE C-TERMINAL REGION IS PROBABLY USED FOR ANCHORING THE PROTEIN TO THE CELL MEMBRANE. THE REPEAT SEQUENCES WOULD BE THE SURFACE ANTIGEN OF THE ORGANISM.
-:- SIMILARITY: CONTAINS 1 TSP TYPE-1 DOMAIN.
                                                   [3]
SEQUENCE FROM N.A.
MEDLINE-92155298; PubMed-1346766;
Davis J.R., Cortese J.F., Herrington D.A., Murphy J.R., Clyde D.F.,
Thomas A.W., Baqar S., Cochran M.A., Thanassi J., Levine M.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CIRCUMSPOROZOITE PROTEIN.
43 X 4 AA TANDEM REPEKTS OF N-A-N-P.
A -> ANPHANDHA (IN REF. 4).
9E81146FS9EBCEA3 CRC64;
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                                                                                                                                                                                        Hackett C.S.;
"Plasmodium falciparum: in vitro characterization and human "Plasmodium falciparum: a cloned line.";
Exp. Parasitol. 74:159-168(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
  Campbell J.R.; Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
ENCHARDAROROZOITE PROTEIN PRECURSOR (CS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AA
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SIGNAL 1 16 PROBABI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR003067; Crcmsprzoite.
InterPro; IPR00884; TSP1.
InterPro; IPR00884; TSP1.
PRIMTS; PR01303; CRCMSPRZOITE.
SMART; SM00209; TSP1; 1.
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EMBL; M83886; AAA29521.1; -.
EMBL; M22982; AAA29527.1; -.
PIR; S05428; S05428.
PIR; A45527; A45527.
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Best Local Similarity 100.
Matches 12; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VERTEBRATE HOST)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  397 AA;
                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
J.R.;
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- Mon Feb

THE REPEAT SEQUENCES

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MISCELLANEOUS: THE C-TERMINAL REGION IS PROBABLY USED FOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                 CHAIN
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Inter
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                                                                                                                                                                                                                                                                                    MISCELLANEOUS: THE C-TERMINAL REGION IS PROBABLY USED FOR MACHORING THE PROTEIN TO THE CELL MEMBRANE. THE REPEAT SEQUENCES WOULD BE THE SURFACE ANTIGEN OF THE ORGANISM.
SIMILARITY: CONTAINS I TSP TYPE-1 DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOI. Blochem. Parasitoí. 24:289-294(1987).
-!- FUNCTION: THE CIRCUMSPORZOZITE PROTEIN IS THE IMMUNDDOMINANT
SURFACE AWTIGEN ON THE SPORZOZITE (THE INFECTIVE STAGE OF THE
MALARIA PARASITE THAT IS TRANSMITTED FROM THE MOSQUITO TO THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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MEDLINE-87315205; Pubmed-3306373;
del Portillo H.A., Nussenzweig R.S., Enea V.;
"Circumsporozoite gene of a Plasmodium falciparum strain from Thailand.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Plasmodium falciparum (isolate t4 / Thailand).
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 69; DB 1; Length 412; 100.0%; Pred. No. 0.0017; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
02-JAG-2001 (Rel. 40, Last annotation update)
CIRCUMSPOROZOITE PROTEIN PRECURSOR (CS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    424 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PIR; A03388; OZZQAF.
InterPro; IPR003067; Crcmsprzoite.
InterPro; IPR000884; TSP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; K02194; AAA29524.1; -.
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Matches 12; Conserv
                                                  SEQUENCE FROM N.A.
                  NCBI_TaxID=5833;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=5846;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CSP_PLAFT
P13814;
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CSP_PLAFT
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                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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-!- FUNCTION: THE CIRCUMSPOROZOITE PROTEIN IS THE IMMUNODOMINANT
SURFACE ANTIGEN ON THE SPOROZOITE (THE INFECTIVE STAGE OF THE
MALARIA PARASITE THAT IS TRANSMITTED FROM THE MOSQUITO TO THE
VERTEBRATE HOST).

-!- MISCELLANBOUS: THE C-TERMINAL REGION IS PROBABLY USED FOR
ANCHORING THE PROTEIN TO THE CELL MEMBRANE. THE REPEAT SEQUENCES
WOULD BE THE SURFACE ANTIGEN OF THE ORGANISM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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SEQUENCE FROM N.A.
MEDLINE-87115616; Pubmed-3543671;
Lockyer M.J., Schwarz R.T.;
"Strain variation in the circumsporozoite protein gene of Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CIRCUMSPOROZOITE PROTEIN.
45 X 4 AA TANDEM REPEATS OF N-A-N-P.
710AB14238786CD9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Plasmodium falciparum (isolate Wellcome).
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBL_TaxID=5848;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 424;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
ANCHORING THE PROTEIN TO THE CELL MEMBRANE. TH WOULD BE THE SURFACE ANTIGEN OF THE ORGANISM. SIMILARITY: CONTAINS 1 TSP TYPE-1 DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Score 69; DB 1;
; Pred. No. 0.0017;
0; Mismatches 0;
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20-AUG-2001 (Rel. 40, Last annotation update)
CIRCUMSPOROZOITE PROTEIN PRECURSOR (CS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              442 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Malaria; Sporozoite; Repeat; Signal.
SIGNAL 1 16 PROBABLE.
                                                                                                                                                                                                                                                                                                                                                                                                            PIR; A54533; A54533.
InterPro; IPR003067; Crcmsprzoite.
InterPro; IPR00084; TSP1.
Pfam; PF00090; Lsp_1; 1.
PRINTS; PR01303; CRCMSPRZOITE.
SMART; SM00209; TSP1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-AUG-1988 (Rel. 08, Created)
01-AUG-1988 (Rel. 08, Last sequ
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                                                                                                                                                                                                                                                                                                                                                                                  EMBL; M19752; AAA29555.1; -.
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Best Local Similarity 100.
Matches 12; Conservative
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P08307;
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Wilson D.B.;
                                                                 01-MAY-1992
                                                                                                                                                                                                                                                                                                                               STRAIN-YX;
Jung E.D.,
                                          GUN2_THEFU
                                                                                                                                                                                                                                STRAIN=YX;
                                                       P26222;
                               GUN2_THEFU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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Pfam; PF01364; Peptidase_C25; 5.
Hemagglutinin; Virulence; Hydrolase; Thiol protease; Signal; Repeat.
SIGNAL 1 24 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           CIRCUMSPOROZOITE PROTEIN.
47 X 4 AA TANDEM REPEATS OF N-A-N-P.
BD57A9A152B85E03 CRC64;
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Pred. No. 8.6;
                                                                                                                                           100.0%; Score 69; DB 1; Length 442; 100.0%; Pred. No. 0.0018; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HEMAGGLUTININ A.
PEPTIDASE C25-LIKE 1.
PEPTIDASE C25-LIKE 2.
PEPTIDASE C25-LIKE 3.
PEPTIDASE C25-LIKE 4.
PEPTIDASE C25-LIKE 5.
MW; 61C4DE32540C99DA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                      Porphyromonas gingivalis (Bacteroides gingivalis).
Bacteria; CFB group; Bacteroidaceae; Porphyromonas.
                                                                                                                                                                                                                                                                                                                       (Rel. 39, Last sequence update)
(Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                     PRT; 2628 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
      Pfam; PF00090; tsp_1; 1. PRINTS; PR01030; CRCMSPRZOITE. SMART; SM00209; TSP1; 1. Malaria; Sporozoite; Repeat; Signal. SIGNAL
InterPro; IPR003067; Crcmsprzoite.
InterPro; IPR000884; TSP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=97047672; PubMed=8926061;
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                                                                                                           442 AA; 47402 MW;
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66.7%;
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HEMAGGLUTININ A PRECURSOR
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                                                                                                                                                                        Conservative
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Best Local Similarity
Matches 12; Conserv
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                                                                                                                                                                                                                                                                                                                          30-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-381;
                                                                                                                                                                                                                                                                                      HAGA_PORGI
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                                                                               01-FEB-1996 (Rel. 33, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
ENDOGLUCANASE E-2 PRECURSOR (EC 3.2.1.4) (ENDO-1,4-BETA-GLUCANASE E-2) (CELLULASE E-2) (CELLULASE E-2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cellulose degradation; Hydrolase; Glycosidase; Signal; 3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- SIMILARITY: BELONGS TO CELLULASE FAMILY B (FAMILY 6 OF GLYCOSYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Biochemistry 32:9906-9916(1993).
-!- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF 1,4-BETA-D-GLUCOSIDIC
-!- CATALACES IN CELLULOSE.
-!- PATHWAY: CELLULOSE DEGRADATION.
-!- SIMILARITY: CONTAINS 1 BACTERIAL-TYPE CELLULOSE-BINDING DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Jung E.D., Lao G., Irwin D., Barr B., Benjamin A., Wilson D.B., submitted (MAX-1993) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "FAX CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF 32-317.
MEDLINE=94002001; PubMed=8399160;
Spezio M., Wilson D.B., Karplus P.A.;
"Crystal structure of the catalytic domain of a thermophilic endocellulase.";
                                                                                                                                                                                                                                                                               Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptosporangineae; Thermomonosporaceae;
Thermobifida.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-91258320; PubMed=1904434;
Lao G., Ghangas G.S., Jung E.D., Wilson D.B.;
"DNA sequences of three beta-1,4-endoglucanase genes from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ENDOGLUCANASE E-2
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PDB; 1TML; 31-JAN-94.
InterPro; 1FR001349; CBD_2.
InterPro; 1FR001349; CBD_2.
Pfam; PF00553; CBD_2: 1.
Pfam; PF00553; GBD_2: 1.
PRINTS; PR00733; GLHYDRLASE6.
ProDom; PD003733; GLHYDRLASE6.
PROSITE; PS00565; GLYCOSYL_HYDROL_F6-1.
PROSITE; PS00655; GLYCOSYL_HYDROL_F6-1; I.
PROSITE; PS00655; GLYCOSYL_HYDROL_F6-1; I.
441 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Cellulases of Thermomonospora fusca.";
Meth. Enzymol. 160:314-323(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              J. Bacteriol. 173:3397-3407(1991)
                                                                 (Rel. 22, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REVISIONS, SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; M73321; AAC06388.1; -.
STANDARD;
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                                                                                                                                                                                                                                                              Thermomonospora fusca.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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                                           CIRCUMSPOROZOITE-PROTEIN RELATED ANTIGEN FB60C8250BC0B589 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-85215483; PubMed-2582354;
MEDLINE-85215483; PubMed-2582354;
Hope I.A., McKay M., Hyde J.E., Goman M., Scalfe J.;
Hope I.A., McKay M., Hyde J.E., Goman M., Scalfe J.;
Hope i.A., McKay M., Hyde J.E., Goman M., Scalfe J.;
Hope i.A., McKay M., Hyde J.E., Goman M., Scalfe J.;

Mucleic Acids Res. 13:369-379(1985).

-!- MISCELLANEOUS: THIS PROTHEIN IS ADDRESSED TO A NEW COMPARTMENT
WITHIN THE CYTOPLASM OF THE INFECTED RED CELL. IT ALSO SURROUNDS
THE PARASITE, PROBABLY IN THE PARASITOPHOROUS VACUOLE MEMBRANE.
-!- MISCELLANEOUS: THIS ANTIGEN AND THE CIRCUMSPOROZOITE PROTEIN
                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-87218504; Pubmed-2438130; Simmons D., Woollett G., Bergin-Cartwright M., Kay D., Scalfe J.; "A malaria protein exported into a new compartment within the host
                                                                                                                                                                                                                                                                                                                                 . 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Plasmodium falciparum.
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
           Alveolata; Apicomplexa; Haemosporida; Plasmodium
                                                                                                                                                                                                                                                                                                               Score 41; DB 1; Length 162;
Pred. No. 8.1;
                                                                                                                                                                                                                                                                                                                                                                                                               EXPI_PLAFA STANDARD; PRT; 162 AA.
P04926; P06718;
13-AUG-1997 (Rel. 05, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
MALARIA PROTEIN EXP-1 PRECURSOR (EXPORTED ANTIGEN AG 5.1).
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                                                                                                                                                                                                                                                                                   17349 MW;
                                                                                                                                                                                                                                                                                                               59.4%;
                                                                                                                                                                                                                                      EMBL; M11145; AAA29523.1; -. PIR; A25780; A25780.
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Best Local Similarity 50.ur
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                                                                                                                                                                                                                                                                   16
162
  Plasmodium falciparum.
                                                                                                                                                                                                                                                                                     162 AA;
                                     SEQUENCE FROM N.A.
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           Eukaryota; Alveo
NCBI_TaxID=5833;
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NCBI_TaxID=5833;
                                                                                                                                                                                                                                                          Signal; Malaria
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01-NOV-1990 (Rel. 16, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
CIRCUMSPOROZOITE-PROTEIN RELATED ANTIGEN PRECURSOR (CRA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3; Indels
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                  CELLULOSE-BINDING
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 CATALYTIC.
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Pred. No.
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70.0%;
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                                     321 NPNPNPNPTP 330
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Matches 7; Conserv
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CRA_PLAFA
P04923;
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15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
16-DEC-1998 (Rel. 37, Last annotation update)
16-DEC-1998 (Rel. 37, Last annotation update)
16-DEC-1998 (Rel. 37, Last annotation update)
17-DEC-1998 (Rel. 37, Last annotation u
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EPITOPE (DEDUCED).

D -> G (IN 5.1 NEGATIVE STRAINS).

P -> T (IN STRAINS PALO ALTO17 & 3D7).

V -> A (IN REF. 2).

AFGB57446E4AA212 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Transmembrane; Signal.
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TISSUE-Cotyledon;
MEDLINE-95148760; PubMed=7846182;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1;
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                                                                                                                                                                                                                                                                                                                                                                                              EMBL; X05074; CAA28735.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          59.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; A04553; CAA00366.1; -. PIR; A23052; YAZQ51. PIR; A26769; A26769.
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                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; X01745; CAA25881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Malaria; Sporozoite;
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Best Local Similarity
Matches 9; Conserv
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                                                                                                                                                                                  91 CHLOROPLAST (POTENTIAL).
463 GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE.
50834 MW; 5792E933068A534D CRC64;
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"Characterization of the yeast SWII, SWI2, and SWI3 genes, which
encode a global activor of transcription.";
cell 68:573-583(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAR-1989 (Rel. 10, Created)
01-MAR-1989 (Rel. 10, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
TRANSCRIPTION REGULATORY PROTEIN ADR6 (SWI/SNF COMPLEX COMPONENT ADR6) (REGULATORY PROTEIN (REGULATORY PROTEIN SWI1) (REGULATORY PROTEIN GAM3).
ADR6 OR SWI1 OR GAM3 OR YPL016W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Indels
                                InterPro; IPR002123; Acyltransferase.
Phospholipid biosynthesis; Transferase; Acyltransferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1;
23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 41; DB 1
Pred. No. 23;
4; Mismatches
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MEDLINE-92154671; Pubmed-1339306;
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EMBL, X12493; CAA31013.1; -.
PIR, S05728; TNBYR6.
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TRANSFAC; T01279; -.
SGD; S0005937; SWII.
InterPro; IPR001606; ARID.
                                                                                                                                            Transit peptide; Chloroplast.
TRANSIT 1 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      59.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 50.00
EMBL; L33841; AAA74319.1;
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                                                                                                                                                                                                                                                                                                         SEQUENCE 463 AA;
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us-09-763-397a-4.rsp

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1 NANPNANPNAN 11
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Best Local Similarity
Matches 8; Conserv
                                                                    SEQUENCE FROM N.A.
                                                                                                                      CHARACTERIZATION.
                                                   NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                   Transcription
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PROB_BACSU
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                                                                                        Gaps
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                                                                                                                                                                                                                                                           Bos taurus (Bovine).
Sukaryota: Metazoa; Chordata; Cranlata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
TRANSCRIPTION REGULATORY PROTEIN SNF11 (SWI/SNF COMPLEX COMPONENT
                                                                                                                                                                                                                                                                                                                                               Inoue T., Yoshida Y., Isaka Y., Tagawa K.;
Isolation of mitochondrial cyclophilin from bovine heart.";
Blochem. Blophys. Res. Commun. 190:857-863(1993).
-!- FUNCTION: PETAESE ACCELERATE THE FOLDING OF PROTEINS.
-!- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC PETILE BONDS IN OLIGOPEPTIDES.
-!- SUBCELLULAR LOCATION: MITOCHONDRIAL MATRIX.
-!- SIMILARIY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
PIR; PC1237; PC1237.
                                                                                                                                                                                              01-APR-1993 (Rel. 25, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
PEPTIDYL-PROLYL CIS-TRANS ISOMERASE, MITOCHONDRIAL (EC 5.2.1.8)
PPIFSD; (ROTAMASE) (CYCLOPHILIN F) (FRAGMENTS).
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                                        F442D5A82013CDBD CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 40; DB 1;
Pred. No. 4.5;
                                                                    Score 41; DB J
Pred. No. 64;
1; Mismatches
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                                                                                                                                                                              64 AA
            ASN/THR-RICH.
GLN-RICH.
C4-TYPE.
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PROSITE; PS00170; CSA_PPIASE_1; PARTIAL.
PROSITE; PS50072; CSA_PPIASE_2; PARTIAL.
                                                                                                                                                                              PRT;
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MEDLINE-93176190; PubMed-7679902;
                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR002130; CSA_PPIase.
           5 65
337 385
1241 1258
1314 AA; 147938 M
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63.6%;
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Best Local Similarity 63.6
Matches 7; Conservative
                                                                                       Conservative
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                                                                    Query Match
Best Local Similarity
Matches 7; Conserv
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Zinc-finger.
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DOMAIN
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ZN_FING
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SEQUENCE
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P38956;
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P30404;
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SEQUENCE
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SNFB_YEAST
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28 31 1-1.
32 35 1-2.
36 39 1-3.
40 43 1-4.
41 47 1-5.
76 165 2 X 5 AA REPEATS OF L-L-A-R-V.
                                                                                                                                                                                                                                                                                                                                                                        Treich I., Cairns B.R., de Los Santos T., Brewster E., Carlson M.;
"Srelich I., Cairns B.R., de Los Santos T., Brewster E., Carlson M.;
"Srelil, a new component of the yeast SNF-SWI complex that interacts
with a conserved region of SNF2.",
Mol. Cell. Biol. 15:4240-4248(1995)
-!- FUNCTION: INVOLVED IN TRANSCRIPTIONAL ACTIVATION. THE SWI/SNF
COMPLEX IS REQUIRED FOR THE INDUCED EXPRESSION OF A LARGE NUMBER
OF GENES. THIS COMPLEX ALTERS CHROMATIN STRUCTURE TO FACILITATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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SNF11 OR YDR073W OR D4411.
Saccharomyces cerevisiae (Baker's yeast).
Eukaryota: Fungi; Ascomycota: Saccharomycotina: Saccharomycetes; Saccharomycetales; Saccharomycetales; Saccharomycetales;
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P39820: 034562;
01-FEB-1995 (Rel. 31, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
GLUTAMATE 5-KINASE (EC 2.7.2.11) (GAMMA-GLUTAMYL KINASE) (GK).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BINDING OF GENE-SPECIFIC DEDICATED TRANSCRIPTION FACTORS
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                                                                                                                                                                                                                     STRAIN=S288C / FY1679;
Coster F., Jonniaux J.-L., Goffeau A.;
Submitted (OCT-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FC626E373C32C2C7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SUBCELLULAR LOCATION: NUCLEAR (PROBABLE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
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EMBL, 274369; CAA9891.1; --
EMBL, X82086; CAA57601.1; --
EMBL, X82086; CAA57600.1; --
PIR, S48760; S48760.
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ilarity 72.7%;
Conservative
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                                                                                                                                                                                                           Devine K.M.;
"Sequence of the Bacillus subtilis genome between xlyA and ykoR.";
Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: ATP + L-GLUTAMATE = ADP + L-GLUTAMATE
5-PHOSPHATE (PRODUCT RAPIDLY CYCLIZES TO 5-OXOPROLINE AND ORTHOPHOSPHATE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 58.0%; Score 40; DB 1; Length 365; Best Local Similarity 70.0%; Pred. No. 25; Matches 7; Conservative 1; Mismatches 2; Indels
                                                                                                      Ogura M., Kawata Mukai M., Itaya M., Takio K., Tanaka T.;
"Multiple copies of the proB gene enhance degS-dependent
extracellular protease production in Bacillus subtilis.",
123 Bacteriol. 176:5673-5680(1994).
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                             -i- PATHWAY: FIRST STEP IN PROLINE BIOSYNTHESIS PATHWAY.
-i- SUBCELLULAR LOCATION: CYTOPLASMIC.
-i- SIMILARITY: BELONGS TO THE GLUTAMATE 5-KINASE FAMILY.
       Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillus/Staphylococcus group; Bacillus.
NCBL_TaxID=1423;
                                                                  SEQUENCE FROM N.A., AND SEQUENCE OF 1-20.
                                                                                             MEDLINE=94364946; PubMed=8083159;
Bacillus subtilis.
                                                                                    STRAIN=168
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Search completed: January 29, 2002, 11:13:38 Job time: 814 sec

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Gaps

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Q9m9v1 arabidopsis
Q9z2u3 mus musculu
Q9r9b7 porphyromon
Q51838 porphyromon
Q9v9y2 drosophila
Q9v709 drosophila
Q9v3e2 drosophila
Q9v3e2 drosophila
Q9v3e2 drosophila
Q9v4q0 drosophila
Q9l157 arabidopsis
Q9v4q0 drosophila
Q9v4q0 drosophila
Q9157 porphyromon
Q9znb5 porphyromon
Q52050 porphyromon
Q52191 porphyromon
Q52191 porphyromon
Q52191 porphyromon
Q52181 porphyromon
                      arabidopsis
mus musculu
mus musculu
Q9dh26 meleagrid h
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A Zheng C., Xie P., Chen Y.;
A Zheng C., Xie P., Chen Y.;
Twolecular cloning and expression of circumsporozoite protein gene from Plasmodium falciparum FCC-1/HN strain in mycobacterium.";
Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.

IN EMBL, AF13469; ARG37074.1;
InterPro; IPR000804; TSP1.
R InterPro; IPR00080804; TSP1.
R InterPro; IPR00090; tsp_1; 1.
R Pfam; PF00090; tsp_1; 1.
R Pfam; PF00190; tsp_1; 1.
TWON_TER 383 383
C SEQUENCE 383 AA; 40893 MW; 503C5DFDF61A9E27 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CIRCUMSPOROZOITE PROTEIN (FRAGMENT).
Plasmodium falciparum.
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 383;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9GPN1;
01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 69; DB 5; L
Pred. No. 0.0018;
Mismatches 0;
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01-NOV-1996 (TrEMBLrel. 01, Created)
  Q9DH26
Q9FY84
O54817
O88933
Q9M9V1
Q9Z2U3
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09LJ57
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Q51839
Q9V9Y2
Q9W0C9
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Local Similarity 100.0%;
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6.151 Million cell updates/sec
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Copyright (c) 1993 - 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUMMARIES
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MEDLINE=84250215; PubMed=6204383; McCutchan T.F., Weber J.L., Wirtz R.A., Hockmeyer W.T., Malloy W.L., Haynes J.D., Schneider I., Roberts D., Sanders G.S., Reddy P.E., Diggs C.L., Miller L.H.; "Structure of the gene encoding the immunodominant surface antigen on the sporozoite of the human malaria parasite Plasmodium falciparum."; Science 225:593-599(1984).
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MEDLINE=B4250215; PubMed=6204383;
Dame J.B., Williams J.L., McCutchan T.F., Weber J.L., Wirtz R.A.,
Hockmeyer W.T., Maloy W.L., Haynes J.D., Schneider I., Roberts D.,
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5839;
                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5833;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      la Cruz V.F.;
Submitted (MAR-1992) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              L; I.
44829 MW; D3EF560B2D368DE9 CRC64;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                      01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
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Mol. Biochem. Parasitol. 0:0-0(0).
EMBL; M83172; AAA29550.1; -.
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InterPro; IPR03067; Crcmsprzoite.
Pfam; PF00090; tsp_1; 1.
PRINTS; PR01303; CROMSPRZOITE.
SMART; SM00209; TSP1: 1.
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1 NANPNANPNANP 12
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-1- MISCELLANEOUS: THE C-TERMINAL REGION IS PROBABLY USED FOR ANCHORING THE PROTEIN TO THE CELL MEMBRANE. THE REPEAT SEQUENCES WOULD BE THE SURFACE ANTIGEN OF THE ORGANISM.

EMBL, M57484, AAA63421.1;

InterPro, IPR000384; TSP1.

InterPro, IPR003067; Cromsprzoite.
                                                                                                                                                                                                                                                                                                                                              MOI. BIOCHOM. PARASITCI. 45:179-182(1991).
-!- FUNCTION: THE CIRCUMSPOROZOITE PROTEIN IS THE IMMUNODOMINANT
SURFACE ANTIGEN ON THE SPOROZOITE (THE INFECTIVE STAGE OF THE
MALARIA PARASITE THAT IS TRANSMITTED FROM THE MOSQUITO TO THE
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
CIRCUMSPOROZOITE PROTEIN (CS) PRECURSOR, VARIANT 1 (FRAGMENT).
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NCBL_TaxID=5833;
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN-SANTA LUGIA, SAL1;
Oari S.H., Lal A.A.; Lal A.A.;
Submitted (FEB-1995) to the EMBL/GenBank/DDBJ databases.
EMBL; U20969; AAA63153.1;
TherPro: IPR00084; TSP1;
Pfam; PF00090; tSp_1; 1.
Pfam; PF00090; tSp_1; 1.
PRINTS; PR01303; CRCMSPRZOITE.
SMART; SM00209; TSP1; 1.
SEQUENCE 408 AA; 43871 MW; A545BE517822515C CRC64;
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                                                                                           Plasmodium falciparum.
Eukaryota: Alveolata; Apicomplexa; Haemosporida; Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 69; DB 5; Length 393; 100.0%; Pred. No. 0.0018; Pred. No. 0.0018; ive 0; Mismatches 0; Indels
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4-RESIDUE TANDEM REPEATS.
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Last sequence update)
Last annotation update)
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SIGNAL 1 16 POTENTIAL.
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PRINTS; PR01303; CRCMSPRZOITE.
SMART; SM00209; TSP1; 1.
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Best Local Similarity 100.
Matches 12; Conservative
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393 AA;
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Matches 12; Conserv
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                                                                                                                                                       NCBI_TaxID=5833;
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Best Local Similarity 100.0%;
Matches 12; Conservative 0;
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Best Local Similarity 100.
Matches 12; Conservative
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SEQUENCE FROM N.A.
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MEDLINE-84250215; PubMed-6204383;
Dame J.B., Williams J.L., Mcoutchan T.F., Weber J.L., Wirtz R.A.,
Hockmeyer W.T., Maloy W.L., Haynes J.D., Schneider I., Roberts D.,
Sanders G.S., Reddy P.E., Diggs C.L., Miller L.H.;
"Structure of the gene encoding the immunodominant surface antigen on
the sporozoite of the human malaria parasite Plasmodium falciparum.";
Sanders G.S., Reddy P.E., Diggs C.L., Miller L.H.; "Structure of the gene encoding the immunodominant surface antigen on the sporozoite of the human malaria parasite Plasmodium falciparum."; Science 225:593-599(1984).
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                                                                                                                                                                                                                                                                         100.0%; Score 69; DB 5; Length 420; 100.0%; Pred. No. 0.0019; Ive 0; Mismatches 0; Indels
                                                                             la Cruz V.F.;
Submitted (MAR-1992) to the EMBL/GenBank/DDBJ databases.
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Mol. Blochem. Parasitol. 0:0-0(0).
BMBL; M03161; AAA29574.1; -.
InterPro; IPR000804; TSP1.
InterPro; IPR003067; Crcmsprzoite.
Pfam; PF00090; tsp_1; 1.
PRINTS: PR01303; CRCMSPRZOITE.
SWART; SM00209; TSP1; 1.
SEQUENCE 420 AA; 45155 MW; 3A85B92432C2893C CRC64;
                                                                                                                                                                                                                              SMART; SM00209; TSP1; 1.
SEQUENCE 420 AA; 45318 MW; F7F70F1C4939DEA7 CRC64;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                       420 AA
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Mol. Biochem. Parasitol. 0:0-0(0).
EMBL; M83174; AAA29552.1;
InterPro: IPR000884; TSP1.
InterPro: IPR03067; Crcmsprzoite.
PRIMTS: PR01303; CRCMSPRZOITE.
PROSITE: PS50092: TSP1; 1.
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Best Local Similarity 100.
Matches 12; Conservative
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
CIRCUMSPOROZOITE PROTEIN (CS) PRECURSOR, VARIANT 2 (FRAGMENT).
Plasmodium falciparum.
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5833;
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NCBI_TaxID=5833;
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  Length 420;
                                                  0; Indels
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Submitted (MAR-1992) to the EMBL/GenBank/DDBJ databases.
EMBL, M83169; AAA29547.1;
EMBL: M83149; AAA29562.1;
InterPro; IPR000884; TSP1.
InterPro; IPR003067; Cromsprzoite.
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PRINTS; PR01303; CRCMSPRZOITE.
SMART; SM00209; TSP1; 1.
SEQUENCE 424 AA; 45592 MW; F20CEB60636DB9BE CRC64;
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Last annotation update)
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Pred. No. 0.0019;
; Mismatches 0;
Score 69; DB 5;
Pred. No. 0.0019;
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100.0%; Pred. No. v.
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EMBL; M83168; AAA29546.1; -.
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NCBI_TaxID=5833;
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01-NOV-1996 (
01-JUN-2001 (
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                                                                                                                    -I VELIENTE HOSI).

NEXTERIAL HOSI).

NEXTERIAL HOSI).

NUSCELLANEOUS THE C-TERMINAL REGION IS PROBABLY USED FOR ANCHORING THE PROTEIN TO THE CELL MEMBRANE. THE REPEAT SEQUENCES WOULD BE THE SURFACE ANTIGEN OF THE ORGANISM.

EMBL, M57499; AAA63422.1; -
INTERPO, IPRO00884; TSP1.
INTERPO; IPRO00884; TSP1.
INTERPO; IPRO0090; LSP_1: 1.
PRINTS; PRO1303; CRCMSPEXCITE.
SMART; SM00209; TSP1; 1.
MAIATIA; Repeat; Sporozoite; Signal.

ASIGNAL

17 > 424 CIRCUMSPOROZOITE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                   protein gene.";
Mol. Biochem. Parasitol. 45:179-182(1991).
-!- FUNCTION: THE CIRCUMSPOROZOITE PROTEIN IS THE IMMUNODOWINANT
SURFACE ANTIGEN ON THE SPOROZOITE (THE INFECTIVE STAGE OF THE
MALARIA PARASITE THAT IS TRANSMITTED FROM THE MOSQUITO TO THE
                                        variation in the Plasmodium falciparum circumsporozoite
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NCBL_TaxID=5833;
                                                                                                                                                                                                                                                                                                                        100.0%; Score 69; DB 5; Length 424; 100.0%; Pred. No. 0.0019; Live 0; Mismatches 0; Indels
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Submitted (MAR-1992) to the EMBL/GenBank/DDBJ databases.
Submitted (MAR-1992) to the EMBL/GenBank/DDBJ databases.
EMBL; M83155; AAA29568.1; -
EMBL; M83152; AAA29565.1; -
EMBL; M83158; AAA29571.1; -
EMBL; M83166; AAA29544.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (MAR-1992) to the EMBL/GenBank/DDBJ databases
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Last annotation update)
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               MEDLINE-91270295; PubMed-2052038;
                                                                                                                                                                                                                                                                                          45609 MW;
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Q27246;
01-NOV-1996 (TEMBLEEL. 01,
01-NOV-2001 (TEMBLEEL. 01,
01-JUN-2001 (TEMBLEEL. 17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CIRCUMSPOROZOITE PROTEIN.
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Best Local Similarity 100.
Matches 12; Conservative
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                                                                                                               VERTEBRATE HOST)
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SEQUENCE FROM N.A.
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
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                                                                                                                                                                            Length 432;
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InterPro; IPR000884; TSP1.
InterPro; IPR003067; Crcmsprzoite.
Pfam; PF00090; tsp_1; 1.
PRINTS; PR01303; CRCMSPRZOITE.
SMART; SM00209; TSP1; 1.
SEQUENCE 432 AA; 46414 MW; 8787E6005578873A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (TrEMBLrel. 01, Created)
(TrEMBLrel. 01, Last sequence update)
(TrEMBLrel. 17, Last annotation update)
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0
                                                                                                                                                                            100.0%; Score 69; DB 5; 100.0%; Pred. No. 0.002;
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Mol. Biochem. Parasitol. 0:0-0(0).
EMBL; M813165; AAA29543.1; -
InterPro: IPR000884; TSP1.
InterPro: IPR003067; Crcmsprzoite.
Pfam; PF00090; LSP_1; 1.
PRINTS; PR01303; CRCMSPRZOITE.
SMARY; SM00209; TSP1; 1.
SEQUENCE 432 AA; 46385 MW; 2CE8D9A681
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                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
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Best Local Similarity
Matches 12; Conserv
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Best Local Similarity
Matches 12; Conserv
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MEDLINE=84250215; PubMed=6204383;
Dame J.B., Williams J.L., McCutchan T.F., Weber J.L., Wirtz R.A.,
Dame J.B., Williams J.L., Haynes J.D., Schneider I., Roberts D.,
Sanders G.S., Reddy P.E., Diggs C.L., Miller L.H.;
"Structure of the gene encoding the immunodominant surface antigen the sporozoite of the human malaria parasite Plasmodium falciparum. Science 225:593-599(1984).
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5833;
                                                                                                                                                                                                                                                                                             Length 436;
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     Submitted (MAR-1992) to the EMBL/GenBank/DDBJ databases
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                                                                      Jongwittwes S., Tanabe K., Kanbara H.;
Mol. Blochem. Parasitol. 0:0-0(0).
EMBL; M83167; AAA39545.1;
InterPro; IPR000884; TSP1.
InterPro; IPR003067; Crcmsprzoite.
Pfam: PF00090; tsp1.1; PR01313; CRCMSPRZOITE.
PROSITE: PS50092; TSP1; 1.
SWART; SM0209; TSP1; 1.
SWART; SM0209; TSP1; 1.
SEQUENCE A36 AA; 46875 MW; P102683C5CIDC85A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SMART; SM00209; TSP1; 1.
SEQUENCE 442 AA; 47414 MW; BFAF9D939D7862FF CRC64;
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                                                                                                                                                                                                                                                                                           Score 69; DB 5;
Pred. No. 0.002;
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Mol. Biochem. Parasitol. 0:0-0(0).
EMBL. M83173, AAA29551.1; -.
InterPro; IPRO00884; TSP1.
InterPro; IPRO03067; Cromsprzoite.
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100.0%; Pr
tive 0;
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PRINTS; PR01303; CRCMSPRZOITE.
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Best Local Similarity 100.

Matches 12; Conservative
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Best Local Similarity 100.
Matches 12; Conservative
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01-JUN-2001
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                                                            STRAIN-842;
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MEDLINE-84250215; PubMed-6204383;
MEDLINE-84250215; PubMed-6204383;
Dame J.B., Williams J.L., McCutchan T.F., Weber J.L., Wirtz R.A., Hockmeyer W.T., Maloy W.L., Haynes J.D., Schneider I., Roberts D., Sanders G.S., Reddy P.E., Diggs C.L., Miller L.H.;
"Structure of the gene encoding the immunodominant surface antigen on the sporozoite of the human malaria parasite Plasmodium falciparum.";
                                                                                                                                                                                                    Dame J.B., Williams J.L., McCutchan T.F., Weber J.L., Wirtz R.A., Hockmeyer W.T., Maloy W.L., Haynes J.D., Schneider I., Roberts D., Sanders G.S., Reddy P.E., Diggs C.L., Miller L.H.; "Structure of the gene encoding the immunodominant surface antigen on the sporezotte of the human malaria parasite Plasmodium falciparum."; Science 225:593-599(1984).
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                                                                Plasmodium falciparum.
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBL_TaxID=5833;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 436;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Jongwitiwes S., Tanabe K., Kanbara H.;
Submitted (MAR-1992) to the EMBL/GenBank/DDBJ databases.
EMBL; M83164; AAA295421;
EMBL; M83163; AAA295576.1;
EMBL; M83163; AAA29576.1;
                                                                                                                                                                                                                                                                                                                                                                 la Cruz V.F.;
Submitted (MAR-1992) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            436 AA; 46688 MW; 5B42FF3348B68655 CRC64;
01-NOV-1996 (TrEMBLrel. 01, Last sequence update) 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
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Last annotation update)
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InterPro; IPR03067; Crcmsprzoite.
Pfam; FR00090; tsp_1; I.
PRINTS; PR01303; CRCMSPRZOITE.
SMART; SM00209; TSP1; I.
                                                                                                                                                                                 MEDLINE-84250215; PubMed-6204383;
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                                     CIRCUMSPOROZOITE PROTEIN.
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Best Local Similarity 100.
Matches 12; Conservative
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SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
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Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Pterygoto; Drosophilidae; Drosophila.
                                                                                                                                                                                                           Dame J.B., Williams J.L., McCutchan T.F., Weber J.L., Wirtz R.A., Hockmeyer W.T., Maloy W.L., Haynes J.D., Schneider I., Roberts D., Sanders G.S., Reddy P.E., Diggs C.L., Miller L.H.; "Structure of the gene encoding the immunodominant surface antigen on the sporozoite of the human malaria parasite Plasmodium falciparum.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-BERKELEY;
MEDILINE-20196006; PubMed-10731132;
Adam M.D., Cellniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
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                                                                                                                                        Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
                                                                                                                                                                                                                                                                                                                               Submitted (MAR-1992) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  452 AA; 48431 MW; 6E739D6C53223805 CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                               Last sequence update)
Last annotation update)
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                                               452 AA
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EMBL, M83156; AAA29569.1; -.
InterPro; IPR000884; TSP1.
InterPro; IPR003067; Crcmsprzoite.
                                                                       Created)
                                               PRT;
                                                                                                                                                                                        STRAIN=827;
MEDLINE-84250215; PubMed=6204383;
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PROSITE; PS50092; TSP1; 1.
                                                                      01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1996 (TrEMBLrel. 01, 01-JUN-2001 (TrEMBLrel. 17,
                                                                                                                                                                                                                                                                       Science 225:593-599(1984).
                                                                                             01-JUN-2001 (TrEMBLrel. 1 CIRCUMSPOROZOITE PROTEIN.
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                                                 PRELIMINARY;
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                                                                                                                               Plasmodium falciparum.
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Matches 12; Conserv
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Q9V650;
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                                                            025834;
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                            RESULT 14
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George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X.,
Bradion R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
R.A. Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
R.A. Beson R.Y., Basu A., Baxendale J., Bayraktaroglu L., Baldwin D.,
Bankova D., Botchan M.R., Bouck J., Brokstein P., Bolshakov S.,
Burtis R.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I.,
R.A. Burtis R.C., Busam D.A., Lauler H., Cadieu E., Center A., Chandra I.,
R.A. Dodgon K., Doup L.E., Downess M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
R.A. Cong F. Gorrell J.H., Gu Z., Gana P., Dav I., Dietz S.M.,
R.A. Gong F. Gorrell J.H., Gu Z., Gana P., Harris M.,
R. Alaris M.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
R.A. Hostin D., Houston K.A., Helman T.J., Wel M.-H., Ibogwam C.,
Jalali M., Kalush F., Karpen G.H., Re Z., Kennisson J.A., Ketchum K.A.
Jalali M., Kalush F., Karpen G.H., Re Z., Kennisson J.A., Ketchum K.A.
Jalali M., Kalush F., Karpen G.H., Re Z., Kennisson J.A., Ketchum K.A.
Jalali M., Mushina N.V., Mobarry C., Morris J., Moshrefi A.,
Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
R.A. Reinert K., Remington K., Stapheton M., Strong R., Sun E.,
Spradiling A.C., Stapheton M., Strong R., Sun E.,
Spradiling A.C., Ztapheton M., Strong R., Sun E.,
Syriskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
R. Wang Z.-Y., Warsarman D.A., Weiter E., Wang A.H., Wang X.,
R. Wang Z.-Y., Warsarman D.A., Weiter K., Wang A.H., Wang X.,
R. Wang Z.-Y., Warsarman D.A., Weiter K., Wang A.H., Wang X.,
R. Wang Z.-Y., Weiter E., Zhan M., Zhang G., Zhao Q., Zhao G., Zhao G
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Pfam; PF02017; CIDE-N; 1.
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Sequence encoded b CS protein of mala Sequence encoded b CS Region I mimeti

Recombinant vaccin

Sequence corresp. PAGE1 polypeptide. PAGE-4 polypeptide

Human secreted pro

Sequence encoded b Sequence of R prot SIVmac239 vpr gene HIV-2/SIV Vpr prot IDI plasmodium sur Human secreted pro M24-M5-M6-M19-M3-M S. pyogenes octava P. vivax circumspo Circumsporozoite a

Human 5' EST secre Lambda gt10ch2 enc Lambda gt10ch101 e Porcine PAM-8. Su

Sequence encoding Plasmodium vivax c

C-terminal amidati Lambda gt10ch201 e Equine C-terminal

Membrane targeted Human secreted pro

Drosophila gustato H. pylori GHPO 173

terminal amidati

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Perfect score:

Sednence:

OM protein

Run on:

Scoring table:

Searched:

Database

Result Š

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Recombinant protein; CDC/NIIMALVAC-1; multivalent; malaria; vaccine; T-cell epitope; tetanus toxoid; antigenic epitope; treatment; circumsporozoite protein; CSP; sporozoite surface protein-2; SSP-2; liver stage antigen-1; LSA-1; merozoite surface protein-1; MSP-1; MSP-2; apical membrane antigen-1; AMA-1; erythrocyte binding antigen-175; EBA-175; rhoptry associated protein-1; RAP-1; gamete specific antigen; Pfg27; antiparasitic; prevention; anti-CDC/NIIMALVAC-1 antibody.
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(USSH ) US DEPT HEALTH & HUMAN SERVICES.
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AAW99813
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AAR51001
AAB03124
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AAR30609
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AAR06400
AAR06379
AAR29770
AAR20026
AAR11113
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AAP61001
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AAR12308
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AAP80835
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AAP80813
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WO200011179-A1.
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Circumsporozoite a
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3.098 Million cell updates/sec
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                                                                                                                                                                                 January 29, 2002, 10:21:41; Search time 310.82 Seconds
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          **SIDSB/gcgdata/geneseq/geneseqp/AA1980 DAT:*

**SIDSB/gcgdata/geneseq/geneseqp/AA1981 DAT:*

**SIDSB/gcgdata/geneseq/geneseqp/AA1991 DAT:*

**SIDSB/gcgdata/geneseq/g
                         GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      522463 seqs, 74073290 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAR07290
AAR07289
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AAR13179

    protein search, using sw model

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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                               1 KHKKLKQPGDGNP 13
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Maximum DB seq length: 2000000000
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Gaps

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P. falciparum in biological samples
                                                                                                                                                                        AAP82541 standard; peptide; 19 AA.
                      Claim 2; Page 16; 52pp; English
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                                                                                                                                                                                           12-DEC-1990 (first entry)
                                                                                                                                13; Conservative
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                                                                                                                                                                                                                                                                     (ENIE ) ENIRICERCHE SPA
                                                                                                                                         1 KHKKLKQPGDGNP 13
                                                                                                                                              WPI; 1988-030026/05.
                                                                                                                      Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                  16-JUL-1987;
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                                                                                                                                                                                                                                DE3723583-A.
                                                                                                                                                                                                                      synthetic.
                                                                                                                                                                                  AAP82541;
                                                                                                         Sequence
                                                                                                                                Matches
                                                                                                                                                                    AAP82541
                                                                                                                                                                RESULT
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The protein was produced by expression of a synthetic gene. The analogue comprises AAs 68-123 of the native P. falciparum CS protein, followed by four repeat sequences (three "B"s, i.e. NANP) and one "A", i.e. NVDP), followed by AAs 289-392 of the native protein. Reduction of the immunological dominance of the repeats relative to the epitopes in the regions flanking the repeats enhances sporozoite neutralising activity.
sequence to a 2nd (C-terminal) sequence comprising tetrapeptide units of CSP. See AAP82542.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 75; DB 11; Length 180; 100.0%; Pred. No. 0.00023; Live 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Recombinant plasmodium circumsporozoite analogues - lacking one or more repeat epitope(s) for use as a malaria sub-unit
                                                                                                                              Length 19;
                                                                                                                                                                      Indels
                                                                                                                              100.0%; Score 75; DB 9; I
100.0%; Pred. No. 2.3e-05;
                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CS protein; plasmodium; malaria; vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Circumsporozoite analogue Falciparum 4.
                                                                                                                                                                                                                                                                                                                                                                AAR07290 standard; protein; 180 AA.
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Best Local Similarity 100.
Matches 13; Conservative
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Best Local Similarity 100.
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Barr PJ, Bathurst IC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 KHKKLKQPGDGNP 13
                                                                                                                                                                                                                                             3 khkklkqpgddgnp 15
                                                                                                                                                                                                                     1 KHKKLKQPGDGNP 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             See also AAR07287-91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1990-314486/42.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (CHIR-) CHIRON CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         180 AA;
                                                                       AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAQ06153
                                                                    19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11-APR-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11-APR-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     28-JAN-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17-0CT-1990.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EP392820-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                        AAR07290,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     vaccine.
                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               46
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AAR07290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                           Qy
                                                                                                                                                                                                                                                               g
        S S S S
                                                                                                                                                    The present sequence is the antigenic epitope P592, derived from circumsporozoite protein (CSP) of the sporozoite stage of plasmodium fallogrum. It is used in the construction of recombinant protein CDC/NIIMALVAC-1, which is a multivalent, multistage malarial vaccine. The recombinant protein comprises, melittin signal peptide, (His)6 tag, Trecal epitope from tetanus toxoid and 21 antigenic epitopes from circumsporozoite protein (CSP), sporozoite surface protein-1 (MSP-1), liver stage antigen-1 (LSA-1), merozoite surface protein-1 (MSP-1), Liver stage antigen-1 (LSA-1), merozoite surface protein-1 (MSP-1), Liver stage antigen-1 (AMA-1), erythrocyte binding antigen-175 (BBA-175), rhoptry associated protein-1 (RAP-1) and gamete specific antigen, Pfg27 These epitopes were obtained at different stages of the circumstant and explese of P. falciparum. CDC/NIIMALVAC-1 vaccine has antiparasitic activity and can used for treatment and prevention of malarial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Region of P.falciparum circumsporozoite protein with linker attached. ^{(}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                            Novel recombinant protein as vaccine for treating malarial infection comprises antigenic peptides obtained from different stages of plasmodium falciparum life cycle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This is the N-terminal of an immunogenic polypeptide useful as a malaria vaccine. It comprises a fragment of the P-falciparum cicumsporozoite protein (CSP) and one copy of a peptide linker, which is pref. present in 3-10 copies, which links the preceding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New immunogenic polypeptide for malaria vaccine - contg.
sequences derived from P. falciparum circumsporozoite protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 75; DB 21; 100.0%; Pred. No. 1.6e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P.falciparum circumsporozoite protein; malaria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pessi A, Verdini AS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            also useful for antibody assay
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 2; 13pp; German.
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Gaps

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AAR07289

**AAR07289** 

Barr PJ,

vaccine.

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The peptides may be synthesised in pure form and used to generate an
                                                                                                                                                                                                                                                                                                                                                   immune response in vaccination against malaria. The featured repeat units are claimed and must be present in copies of 2-1000, in the P.falciparum genome, the first is coded for 37 times.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Immunogenic determinant; circumsporozoite; CS; vaccine; malaria; hybrid; influenza virus; non-structural protein 1; fusion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'note= "Influenza virus nonstructural protein 1"
                                                                                                                                                                                                                                                                     New immunologically active pure synthetic peptide(s) - used for protection against infection by malaria parasite.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /noce= "Region 1 contg. flanking region less
/note= "Region 1 contg. flanking region less
signal sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 250;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                Schneider I;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Score 75; DB 7; Lv; Pred. No. 0.00032; 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label= AAs 297-412 of CS protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1.81
/label= N-terminal of NS1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       82..87
/label= synthetic linker
                                                                                                                                                                                                                Dame JB, Williams JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /label= artifact
/note= "see comments"
 /label= Repeat unit
/note= "of claim 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAR13175 standard; Protein; 309 AA.
                                                                                                                                                                                                                                                                                                              Claim 7; Page 40-41; 49pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Plasmodium falciparum.
Influenza virus (A/PR/8/34/).
                                                                                                 85EP-0107794.
                                                                                                                           84US-0624564.
                                                                                                                                                        OF COMMERCE.
                                                                                                                                                                      GOVERNMENT.
SEC OF THE ARMY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 100.
Best Local Similarity 100.
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 KHKKLKQPGDGNP 13
                                                                                                                                                                                                                                           WPI; 1986-008635/02.
                                                                                                                                                                                                                                                                                                                                                                                                                                250 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NS1_81-RLfdelta9.
                                                                                                                                                        SEC
                                                                                                                                                                                                                McCutchan TF,
                                                                                                 24-JUN-1985;
                                                                                                                           26-JUN-1984;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29-AUG-1991
                                                                                                                                                      (USDC ) US S
(USGO ) US C
(USSA ) US S
                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR13175;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Key
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The protein was produced by expression of a synthetic gene. The analogue comprises AAs 43-123 of the native P. falciparum CS protein, followed by four repeat sequences (three "B"s", i.e. NANP) and one "A", i.e. NVDP), followed by AAS 289-374 of the native protein. Reduction of the immunological dominance of the repeats relative to the epitopes in the regions flanking the repeats enhances sporozoite neutralising activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 184;
                                                                                                                                                                                                                                                                                                                                                                                    Recombinant plasmodium circumsporozoite analogues - lacking one or more repeat epitope(s) for use as a malaria sub-unit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic peptide antigenic for the malaria parasite.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 75; DB 11; 100.0%; Pred. No. 0.00023;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                               plasmodium; malaria; vaccine
                                                                                   Circumsporozoite analogue Falciparum 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18..21
/label- Repeat unit
/note- "of claim 1"
22..26
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                                                                                                                                                                                                                                                                                                              Gibson HL;
AAR07289 standard; protein; 184
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 10; Fig 8; 22pp; English.
                                                                                                                                                                                                                            90EP-0303907
                                                                                                                                                                                                                                                       89US-0336288
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                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 100.
Best Local Similarity 100.
Matches 13; Conservative
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                                                                                                                                                                                                                                                                                                              Bathurst IC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 KHKKLKQPGDGNP 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Plasmoium falciparum.
                                                                                                                                                                                                                                                                                                                                       WPI; 1990-314486/42.
                                                                                                                                                                                                                                                                                 (CHIR-) CHIRON CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   184 AA;
                                                                                                                                                                                                                                                                                                                                                      N-PSDB; AAQ06152.
                                                                                                                                                                                                                            11-APR-1990;
                                                                                                                                                                                                                                                       11-APR-1989;
                                                      28-JAN-1991
                                                                                                               CS protein;
                                                                                                                                                                                                17-0CT-1990
                                                                                                                                                                    EP392820-A.
                                                                                                                                          Synthetic.
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Sequence

AAP60412;

RESULT AAP60412

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N-PSDB; AAQ06580
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                                                                                                                                           01-MAY-1990;
                                                                                                                                                                                                  03-MAY-1989;
                                                                                     22-NOV-1990
                              EP398540-A.
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      Qλ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the polypeptide is prepd. by genetic engineering of genes encoding the P. falciparum circumsporozoite (CS) protein (Dame et al., Science 225: 593 (1984)). and the influenca virus non-structural protein 1 (NSI), [Baez et al., Nucleic Acids Research, 8: 5845 (1980)]. The DNA encoding the 1st 81 AAs of the N-terminal of NSI (NSI_81) is linked via a synthetic sequence to DNA encoding Region I contg. flanking regionless the 18 AA signal region, which in turn is fused to DNA encoding Region II-contg. flanking region less the first nine N-terminal AAs. This CS fusion is designated RLfGelta9. The Pro residue separating the ASP (at the C-terminal of the linker) from RLfGelta9 is an artifact of a filled in BamHI site. The peptide can be used in a vaccine for protection against
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Polypeptide comprising immunogenic determinants from P falciparum for vaccine against malaria infection in humans.
/note= "Region II flanking region minus 9 N-term-
inal AAs"
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100.0%; Pred. No. 0.0004;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 .81
/label= NS181 protein fragment
/note= "from plasmid pMG-1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                See also AAR12306-R12311 and AAR13176-R13179.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Hollingdale MR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 1; Page 7; 18pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NS181RLFAuth plasmid product
                                                                                                                                                                                                                                                                                                                            (SMIK ) SMITHKLINE BEECHAM.
(USSA ) US SEC OF THE ARMY.
(BIOM-) BIOMEDICAL RES INST.
                                                                                                                                                                                                                                                                           89US-0447746
                                                                                                                                                                                                                 90EP-0313257
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Best Local Similarity 100.
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Plasmodium falciparum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1. KHKKLKQPGDGNP 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gross MS, Gordon DM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1991-179771/25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 309 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Malaria; vaccine.
                                                                                                                                                                                                                 06-DEC-1990;
                                                                                                                                                                                                                                                                              08-DEC-1989;
                                                                                                                                                              19-JUN-1991
                                                                                                       EP432965-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           malaria.
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Domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Domain
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Gaps
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/label= N-terminal of NS1
/note= "Influenza virus nonstructural protein 1"
82.87
/label= synthetic linker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Immunogenic determinant; circumsporozoite; CS; vaccine; malaria; hybrid; influenza virus; non-structural protein 1; fusion.
                                                                                                                                                                                                                                     New polypeptide used in malaria vaccine - comprises immunogenic determinants from 1st and 2nd flanking regions of plasmodium surface protein and intermediate repeat domain
                                                                                                                                                                                                                                                                                                                                                                  The product is useful in preparation of vaccines for treatment a prophylaxis of plasmodium sporozite infection. It may be easily produced in large pure quantities from a transformed E.coli expression system.
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89..193
/label= AAs 19-123 of CS protein
/note= "Region 1 contg. flanking region less
signal sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 75; DB 11; Length 319; 100.0%; Pred. No. 0.00041;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /label= artifact
/note="see comments"
195.3319
/label= AAs 288-412 of CS protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "see comments"
                                                                                                                                                                                                                                                                                                                                  Example 2; Page 11-12; 24pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAR13176 standard; Protein; 319 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Plasmodium falciparum.
Influenza virus (A/PR/8/34).
90EP-0304720.
                                            89US-0346863.
                                                                                     (SMIK ) SMITHKLINE BEECHAM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 KHKKLKQPGDGNP 13
                                                                                                                                      Gross MS, Young JF;
                                                                                                                                                                             WPI; 1990-350299/47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        319 AA;
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06-DEC-1990;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gross MS,
        Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 10
AAR13178
                                                Region
                                                                                                             Region
                                                                                                                                                                                                                                                                                                                             Region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The polypeptide is prepd. by genetic engineering of genes encoding the P. falciparum circumsporozoite (CS) protein [Dame et al., Science 225: 593 (1984), and the influenza virus non-structural science 10.53 (1984), and the influenza virus non-structural protein [NSI), [Baez et al., Nucleic Acids Research, 8: 5845 (1980)]. The DNA encoding the 1st 81 AAS of the N-terminal of NSI (1980)]. The DNA encoding the 1st 81 AAS of the N-terminal of NSI contg. flanking regionless the 18 AA signal region, which in turn is fused to DNA encoding Region II-contg. flanking region.

I contg. flanking regionless the 18 AA signal region. The Pro residue separating the ASP (at the C-terminal of the linker) from Rifauth is an artifact of a filled in Bamili site; the Gly separating Region I and CR Region II-contg. CS flanking regions is an artifact of a synthetic PokI/TthIII I linker. The peptide can be used in a vaccine for protection against malaria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                    Polypeptide comprising immunogenic determinants from P falciparum - for vaccine against malaria infection in humans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Immunogenic determinant; circumsporozoite; CS; vaccine; malaria; hybrid; influenza virus; non-structural protein 1; fusion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "Influenza virus nonstructural protein 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 75; DB 12; Length 319; 100.0%; Pred. No. 0.00041; tive 0; Mismatches 0; Indels (
      /note= "Region II flanking region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 See also AAR12306-R12311 and AAR13175-R13179.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1.81
/label- N-terminal of NS1
                                                                                                                                                                                                                                                                                                   Gross MS, Gordon DM, Hollingdale MR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualiflers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Plasmodium falciparum.
Influenza virus (A/PR/8/34/).
                                                                                                                               90EP-0313257.
                                                                                                                                                                        89US-0447746
                                                                                                                                                                                                             (SMIK ) SMITHKLINE BEECHAM.
(USSA ) US SEC OF THE ARMY.
(BIOM-) BIOMEDICAL RES INST.
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                                                                                                                                                                                                                                                                                                                                          WPI; 1991-179771/25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 13; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           319 AA;
                                                                                                                               06-DEC-1990;
                                                                                                                                                                        08-DEC-1989;
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                                                                                       19-JUN-1991.
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Region
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The polypeptide is prepd. by genetic engineering of genes encoding the P. falciparum circumsporozoite (CS) protein [Dame et al., Science 225: 593 (1984)], and the influenza virus non-structural protein 1 (NS1), [Baez et al., Nucleic Acids Research, 8: 5845 (1980)]. The DNA encoding the 1st 81 AAS of the N-terminal of NS1 (NS1_81) is linked via a synthetic sequence to DNA encoding Region I contg. flanking region less the 18 AAS signal region. This is linked to a synthetic sequence encoding two repeat units from the immunodominant region, which in turn is fused to DNA encoding Region II.contg. flanking region. The Pro residue separating the C Region in encoding an artifact of a filled-in BamHI site; the GIS separating the repeat units and the Region II-contg. CS flanking region is an artifact of a filled-in BamHI site; the GIS region is an artifact of a filled-in BamHI site; the GIS region is an artifact of a synthetic FOKI/TthIII I linker. The peptide can be used in a vaccine for protection against malaria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Polypeptide comprising immunogenic determinants from P falciparum - for vaccine against malaria infection in humans.
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                                                                                                                                                                                                                     /note= "Region 1 contg. flanking region less signal sequence"
                                                                                                                                                                                                                                                                                                                  /label- immunodominant repeat region /note= "two tetrapeptide repeat units"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /label= AAS 288-412 of CS protein
/note= "Region II flanking region"
                                                                                                                                                                                           protein
                                                                                                                                                                                     AAs 19-123 of CS
82..87
/label- synthetic linker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hollingdale MR;
                                                                                                                         "see comments"
                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="see comments"
203..327
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                                                                                            /label= artifact
                                                                                                                                                                                                                                                                                                                                                                                                              /label- artifact
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(USSA ) US SEC OF THE ARMY.
(BIOM-) BIOMEDICAL RES INST.
                                                                                                                                                    89..193
/label= #
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                                                                                                                                                                                                                                                                                    194..201
                                                                                                                                /note=
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Best Local Similarity
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Gaps

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1 KHKKLKQPGDGNP 13

335 AA;

Length 335; Indels

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Query Match
Best Local Similarity 100.0%; Pred. No. 0.00043;
Matches 13; Conservative 0; Mismatches 0;
  Sednence
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                                                                                                                                                                                                                                                                                                 1..81
/label- N-terminal of NS1
/note- "Influenza virus nonstructural protein 1"
                                                                                                                                   Immunogenic determinant; circumsporozoite; CS; vaccine; malaria; hybrid; influenza virus; non-structural protein 1; fusion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "see comments"
105.209
/label= AAs 19-123 of CS protein
/note= Region 1 contg. flanking region less signal sequence"
                                                                                                                                                                                                                                                                                                                                                           82.97
/label= immunodominant repeat region
/label= four tetrapeptide repeat units"
98.103
/label= synthetic linker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="see comments"
211..335
1abb== AAs 288-412 of CS protein
/note="Region II flanking region"
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                                                                                                                                                                                                                                                                         Location/Qualifiers
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(USSA ) US SEC OF THE ARMY.
(BIOM-) BIOMEDICAL RES INST.
                                                                                                                                                                                                            Plasmodium falciparum.
Influenza virus (A/PR/8/34).
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                                                      29-AUG-1991 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1991-179771/25.
                                                                                                  NS1_81(NANP)4RLfAuth
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       AAR13178;
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The polypeptide is prepd. by genetic engineering of genes encoding
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/label- N-terminal of NS1
/note= "Influenza virus nonstructural protein 1"
                                                                                                                                          Immunogenic determinant; circumsporozoite; CS; vaccine; malaria; hybrid; influenza virus; non-structural protein 1; fusion.
                                                                                                                                                                                                                                                   82..97
/label= immunodominant repeat region
/note= "four variant tetrapeptide repeat units"
                                                                                                                                                                                                                                                                                                                               /note= ~~~
105...209
/label= AAs 19-123 of CS protein
/note= "Region 1 contg. flanking region less
signal sequence"
                                                                                                                                                                                                                                                                                                                                                                                                             211..335
/label= AAs 288-412 of CS protein
/note= "Region II flanking region"
                                                                                                                                                                                                                                                                                  98.103
/label= synthetic linker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gordon DM, Hollingdale MR;
                                                                                                                                                                                                                                                                                                                  /label= artifact
/note= "see comments"
                                                                                                                                                                                                                                                                                                                                                                                          /label= artifact
/note="see comments"
                                                                                                                                                                                                           Location/Qualifiers
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                                                           AAR13179 standard; Protein; 335 AA.
                                                                                                                                                                           Plasmodium falciparum.
Influenza virus (A/PR/8/34).
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(USSA ) US SEC OF THE ARMY.
(BIOM-) BIOMEDICAL RES INST
                                                                                                    29-AUG-1991 (first entry)
195 khklikqpgdgnp 207
                                                                                                                         NS1_81(NVDP)4RLfAuth.
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Region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Recombinant protein; CDC/NIIMALVAC-1; multivalent; malaria; vaccine; T-cell epitope; tetanus toxoid; antigenic epitope; treatment; circumsporozoite protein; CSP; sporozoite surface protein-1; SSP-2; liver stage antigen-1; LSA-1; merozoite surface protein-1; MSP-1; apical membrane antigen-1; AAA-1; erythrocyte binding antigen-175; EBA-175; rhoptry associated protein-1; RAP-1; gamete specific antigen; profession; anti-CDC/NIIMALVAC-1 antibody;
the P. falciparum circumsporozoite (CS) protein [Dame et al., Science 225: 593 (1984)], and the influenza virus non-structural protein 1 (NSI), [Baez et al., Nucleic Acids Research, 8: 5845 (1980)]. The DNA encoding the 1st 81 AAS of the Nrterminal of NSI (1981) is linked to a synthetic sequence encoding four repeat units (the variant form) from the immunodominant region, which in turn is linked via a synthetic sequence to DNA encoding Region I conty. CIanking region less the 18 AA signal region. This is conty. Cianking region II-conty. Ilanking region II-conty. CIanking region is an artifact of a filled-the Region I-conty. CS flanking region is an artifact of a filled-the Region I-conty. CS flanking region is an artifact of a filled-the Region is the Region I conty. CS flanking region is an artifact of a synthetic Fokl/Tthii I is allowed. The peptide can be used in a vaccine for protection
                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "Recombinant multivalent malarial vaccine"
                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                             Length 335;
                                                                                                                                                                                                                                                                                                                                                                                  Indels
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                                                                                                                                                                                                                                                                                                                                             100.0%; Score 75; DB 12;
100.0%; Pred. No. 0.00043;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1..22
/label= Melittin_signal_peptide
/note= "Derived from Honey bee"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23..350
/label- Mature_CDC/NIIMALVAC-1
                                                                                                                                                                                                                                                             See also AAR12306-R12311 and AAR13175-R13178.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (NAIM-) NAT INST IMMUNOLOGY.
(USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Recombinant vaccine CDC/NIIMALVAC-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY70278 standard; Protein; 350 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chimeric - Apis sp.
Chimeric - Clostridium tetani.
Chimeric - Plasmodium falciparum.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            06-JUN-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 100.
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                      195 khklkqpqdqnp 207
                                                                                                                                                                                                                                                                                                                                                                                                                  1 KHKKLKQPGDGNP 13
                                                                                                                                                                                                                                                                                              335 AA;
                                                                                                                                                                                                                                           against malaria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200011179-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               02-MAR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   honey bee.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY70278;
                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lal AA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Peptide
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The present sequence is that of recombinant protein CDC/NIIMALVAC-1, which is a multivalent, multistage malarial vaccine. The recombinant protein comprises, melittin signal peptide, (His) 6 tag, T-cell epitope from tetanus toxoid and 21 antigenic epitopes from circumsporozoite protein (CSP), sporozoite surface protein-2 (SSP-2), liver stage mantigen-1 (LSA-1), merozoite surface protein-1 (MSP-1), MSP-2, apical membrane antigen-1 (MAA-1), erythrocyte binding antigen-175 (EBA-175), rhoptry associated protein-1 (RAP-1) and gamete specific antigen, Pfg27. These epitopes were obtained at different stages of the life cycle of Plasmodium falciparum. CDC/NIIMALVAC-1 vaccine has antiparasitic activity and can used for treatment and prevention of malarial infections. Anti-CDC/NIIMALVAC-1 antibodies can be used for detecting P. falciparum in biological samples.
                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                        Novel recombinant protein as vaccine for treating malarial infection comprises antigenic peptides obtained from different stages of
                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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                                                                                                                                                                                                                                                                                                                                                                                      ; Score 75; DB 21; Length 350;
; Pred. No. 0.00045;
0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Repeat region, repeat unit = NANP"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence encoded by the circumsporozoite (CS) gene from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Vaccine; antigen; immunogen; probe; hybridisation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAP83144 standard; protein; 411 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 De Wilde M, Harford N;
                                                                                                    Claim 3; Page 43-44; 52pp; English
                                                                        plasmodium falciparum life cycle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Region 1"
                                                                                                                                                                                                                                                                                                                                                                                          100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                           Query Match 100.
Best Local Similarity 100.
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        . . 206
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  immunoassay; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Plasmodium falciparum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 KHKKLKQPGDGNP 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Plasmodium falciparum
                                                                                                                                                                                                                                                                                                                                               350 AA;
               N-PSDB; AAZ51336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20-NOV-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25-JAN-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-JAN-1987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17-AUG-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cabezon T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EP278940-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAP83144;
                                                                                                                                                                                                                                                                                                                                                 Sequence
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Sequence of the CS gene (AAN81108) is from lambda-mpfl. A recombinant DNA molecule is claimed, comprising functional DNA coding sequence fused, in phase, to a portion of the Pre-S2 region of a hepatitis B virus (HBV) Pre-S2-S protein coding sequence. The functional DNA coding sequence comprises the Pre-S2 coding sequence, Pre-S1 coding sequence, pre-S1 coding sequence, the CS protein coding sequence of plasmodium, or a HIV coding sequence such as an HIV coding sequence such as an HIV envelope gene sequence, e.g. HIV C7 protein coding region, HIV Peptide 121 coding region, or HIV Dreesman peptide coding region.
                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The Plasmodium CS gene was used to isolate peptides capable of inducing an immune response to the parasite. Peptide antigens may
                                    DNA encoding hepatitis B virus antigens and hybrids contg. them used for expression in yeast to obtain vaccines and bivalent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             - used for
                                                                                                                                                                                                                                                                                                                                    ;
                                                                                                                                                                                                                                                                                                       100.0%; Score 75; DB 9; Length 411; 100.0%; Pred. No. 0.00053; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New immunologically active pure synthetic peptide(s) protection against infection by malaria parasite.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Schneider I;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            McCutchan TF, Dame JB, Williams JL,
                                                                                               Example; Fig 3Aa-3Af; 101pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     124..127
/label= Repeat unit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAP60416 standard; Protein; 412 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Fig 2; 49pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CS protein of malaria parasite.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (USGO ) US SEC OF COMMERCE.
(USGO ) US GOVERNMENT.
(USSA ) US SEC OF THE ARMY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            84US-0624564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sporozoite; vaccination.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Plasmodium falciparum.
                                                                                                                                                                                                                                                                                                                                                                                    1 KHKKLKQPGDGNP 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1986-008635/02.
N-PSDB; AAN60362.
WPI; 1988-229751/33.
N-PSDB; AAN81108.
                                                                                                                                                                                                                                                                      411 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24-JUN-1985;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-JUN-1984;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13-JUN-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       02-JAN-1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EP166410-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAP60416;
                                                                                                                                                                                                                                                                        Sequence
                                                                         vaccines
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plasmid WR201 was obtained from the Walter Reed Army Institute of Research, and results from insertion of a 2.3 kb EcoRI fragment from lambda mpfl encoding the complete CS protein gene P. falciparum into vector pUC8. A recombinant DNA vector is claimed, which comprises a DNA sequence contg. the coding sequence of the CS P. falciparum operatively linked to an expression control sequence. Prefd. expression control sequences include the yeast glyceraldehyde-3P-dehydrogenase gene (TDH3) promoter and the yeast confithine carbamoyl transferase gene (ARG3) transcription termination region. A suitable coding sequence comprises the 1215bp Stul-Rsal fragment of WR201 contg. the P. falciparum CS protein coding sequence, minus its first 50bp. Also claimed is a
                                                                                                                                        ó
                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                   Circumsporozoite gene; Plasmodium falciparum; lambda mPfl; vaccine; yeast glyceraldehyde-3P-dehydrogenase gene (TDH3) promoter; yeast ornithine carbamoyl transferase gene (ARG3); repeat region.
                                                                                                                                                                                                                                                                                                                                                                 Sequence encoded by the circumsporozoite (CS) gene of Plasmodium falciparum in lambda mPfl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Expression of P. falciparum circumsporozoite protein by yeast using recombinant DNA vector having coding sequence linked to expression control sequence
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0
be synthesised in pure form and used to generate an immune response in vaccination against malaria. The featured repeat units are claimed and must be present in copies of 2-1000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              124..147
/note="repeat region, repeat unit=NANPNVDP"
148..207
                                                                                                          Length 412;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="repeat region, repeat unit=NANP"
212..287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               212.287
/note="repeat region, repeat unit=NANP"
                                                                                                        100.0%; Score 75; DB 7; L
100.0%; Pred. No. 0.00053;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                 AAP80835 standard; protein; 412 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 1; Fig 2a; 44pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       87US-0008791.
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                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   De Wilde M, Gathoye AM;
                                                                                                                                            Conservative
                                                                                                                                                                                            Plasmodium falciparum
                                                                                                                                                                          1 KHKKLKQPGDGNP 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1988-235171/33.
N-PSDB; AAN81781.
                                                                                                                              Best Local Similarity
Matches 13; Conserv
                                                                   412 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-JAN-1987;
                                                                                                                                                                                                                                                                                                                                                 18-SEP-1990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11-SEP-1988
                                                                                                                                                                                                                                                                                                                     AAP80835;
                                                                    Sequence
                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Region
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                                                                                                                                                                                                                                                                         AAP80835
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transformed host cell, a method of culturing the cell to produce CS, the protein, and a vaccine. The vector comprises a 192 bp Sau3A fragment coding for 16 terrapeptide repeats of the P. falciparum CS protein derived from Sau3A digestion of a 1215 bp Stul-Ksaz fragment of WR201 containing the P. falciparum CS protein coding sequence minus approx. Its first 50 bp, or two, three, four or more tandem copies of such 192 bp Sau3A fragment.
88888888
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Sequence 412 AA;

Query Match 100.0%; Score 75; DB 9; Length 412; Best Local Similarity 100.0%; Pred. No. 0.00053; Matches 13; Conservative 0; Mismatches 0; Indels Search completed: January 29, 2002, 10:21:42 Job time: 418 sec ò Q

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Gaps

; 0

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version 4
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GenCore
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 protein search, using sw model OM protein Run on:

January 29, 2002, 10:26:35; Search time 144.96 Seconds (without alignments) 6.831 Million cell updates/sec

Title: Perfect score:

US-09-763-397A-5 75 1 KHKKLKQPGDGNP 13 Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

219241 seqs, 76174552 residues Searched:

219241 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR\_68:\* Database :

pirl:\* pir2:\* pir3:\* pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	circumsporozoite p			circumsporozoite p					vpr protein - simi	ü	hypothetical prote	conserved hypothet	pyruvate dehydroge	circumsporozoite p	circumsporozoite p		V1 protein - tobac	probable membrane	opsin, green-sensi	RH2 opsin - green	circumsporozoite p	ribosomal protein	hypothetical prote	circumsporozoite p	ATP-dependent heli	hypothetical prote	hypothetical prote	peptidylglycine mo	KTAA0645 protein -
SUMMARIES	ID	OZZQAF	A54533	A54529	B29795	S05428	A29795	A39756	203067	ASLJR3	A32993	T18627	B82143	C59237	A29319	A32068	A48571	A42452	H71259	A42347	151319	OZZQAK	H69042	S74326	OZZQAB	T05883	T21431	E81804	URHUAP	T00376
	DB	-	7	7	~	~	~	~	~	Н	7	•	•	~	7	7			•				7	~	П	7	7	~	-	~
	Length	412	424	442	189	405	171	388	97	101	304	944	179	978	343	367	386	102	320	355	355	363	96	97	378	633	739	803	974	1572
ae Ouerv	Match	100.0	100.0	100.0	92.0	92.0	90.7	68.0		61.3	57.3	~	56.0	56.0	55.3	55.3		54.7	54.7	54.7	54.7	•		53.3	53.3	53.3	ω.	•	53.3	53.3
	Score	75	75	75	69	69	99				43	43	42	42				41	41	41	41	41	40	40	40	40			40	40
Result	S.	-	7	3	4	S	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	59

RNA-directed RNA p	vpr protein - numa	cytochrome P450 Rv	hypothetical prote	stress-induced pro	conjugal transfer	lipoxygenase (EC 1	peptidylglycine mo	pregnancy-associat	N-terminus of phag	rRNA (guanine-N1-)	homeotic protein H	circumsporozoite p	hypothetical prote	OXA1 homolog - hum	protein TINI5.19 [
JQ2034	508439	H70921	D64583	T48150	в82606	T10085	URBOAP	S65464	E70446	E82129	A56553	A41156	C84809	138079	D96525
~ ~	7	-	~	7	7	~	-	7	~	7	N	~	N	~	7
478	TOT	400	452	558	685	877	972	1627	195	278	327	395	435	435	455
52.7	0.20	52.0	52.0	52.0	52.0	52.0	52.0	52.0	50.7	50.7	50.7	50.7	50.7	50.7	50.7
39.5	6.	39	39	36	39	39	39	39	38	38	38	38	38	38	38
30	15	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

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Circumsporozoite protein - malaria parasite (Plasmodium falciparum) (isolate IMTM22) Circumsporozoite protein - malaria parasite (Plasmodium falciparum) CiSpecies: Plasmodium falciparum
C;Species: 15-Nov-1984 #sequence_revision 15-Nov-1984 #text_change 09-Jun-2000
C;Accession: A03388
R;Dame, J.B.; Williams, J.L.; McCutchan, T.F.; Weber, J.L.; Wirtz, R.A.; Hochmeyer, W Science 225, 593-599, 1984
A;Title: Structure of the gene encoding the immunodominant surface antigen on the spo A;Reference number: A03388; MUD:84250215
A;Reference number: A03388
A;Molecule type: DNA
A;Residues: 1412 <DAM>A;Residues: 1412 <DAM>A;Residues: clone 768
C;Comment: Residues 1-16 are the probable signal sequence.
C;Comment: Residues 1-16 are the probable signal sequence.
C;Comment: Residues 1-16 are the probable signal sequence.
C;Comment: There are 41 copies of a 4-residue repeating unit in the middle domain of C;Superfamily: circumsporozoite protein; thrombospondin type 1 repeat homology <THRI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 75; DB 1; Length 412; 100.0%; Pred. No. 4.4e-05;
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RESULT
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ö 0; Indels 0; Mismatches Best Local Similarity 100. Matches 13; Conservative

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1 KHKKLKQPGDGNP 13 à

109 KHKKLKQPGDGNP 121

g

7 A54533

circumsporozoite protein - malaria parasite (Plasmodium falciparum) (strain T4, Thail C;Species: Plasmodium falciparum C;Date: 28-Oct-1994 #sequence\_revision 28-Oct-1994 #text\_change 09-Jun-2000

C. Accession: A54533

B.del Portillo, H.A.; Nussenzweig, R.S.; Enea, V.
Mol. Biochem. Parasitol. 24, 289-294, 1987

A. Title: Circumsporozoite gene of a Plasmodium falciparum strain from Thailand. A, Reference number: A54533; MuID:87315205

A, Accession: A54533

A, Status: preliminary

A, Molecule type: DNA

A, Residues: 1-424 CDEL.

A, Cross-references: GB: M19752; NID:9160216; PIDN:AAA29555.1; PID:9160217

C, Superfamily: circumsporozoite protein; thrombospondin type 1 repeat homology

F; 348-402/Domain: thrombospondin type 1 repeat homology

Gaps ó Length 424; Indels 100.0%; Score 75; DB 2; 100.0%; Pred. No. 4.5e-05; Live 0; Mismatches 0; Query Match 100.0 Best Local Similarity 100.0 Matches 13; Conservative

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circumsporozoite protein - malaria parasite (Plasmodium falciparum) (strain B11) (fra circumsporozoite protein - malaria parasite (Plasmodium falciparum) (strain B11) (fra circumsporozoites: Plasmodium falciparum) (2.5pacies: 28-Aug-1989 #sequence_revision 28-Aug-1989 #text_change 09-Jun-2000 (2.5Accession: A29795 Ride la Cruz, V. V.F.; Lal, A.A.; McCutchan, T.F. J. Biol. Chem. 262, 11935-11939, 1987 A.F. A.F. Hitle: Sequence variation in putative functional domains of the circumsporozoite pr A.Reference number: A92609; MUID:87308186
                                                                                                                                                                                                 A;Status: translation not shown
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-405 <CAM>
A;Residues: 1-405 <CAM>
A;Cossosreferences: EMBL: X15363
A;Crossor P.; Gentz, R.; Matile, H.; Pink, J.R.; Sinigaglia, F.
Nol. Biochem. Parasitol. 35, 185-190, 1989
A;Title: The circumsporozoite protein gene from NF54, a Plasmodium falciparum isolate
A;Reference number: A45527; MUID:89364998
A;Accession: A45527.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: GB:M22982; GB:J04650; NID:g160168; PIDN:AAA29527.1; PID:g160169
B;Lockyer, M.J.; Marsh, K.; Newbold, C.I.
Mol. Blochen. Parasitol. 37, 275-280, 1989
A;Title: Wild isolates of Plasmodium falleparum show extensive polymorphism in T cell A;Reference number: A60657; MUID:90114334
                                                                                         Nucleic Acids Res. 17, 5854, 1989
A;Title DNA sequence of the gene encoding a Plasmodium falciparum malaria candidate
A;Reference number: S05428; MUID:89345189
A;Accession: S05428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary; not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 319-336,354-373 <LOC>
C;Superfamily: circumsporozoite protein; thrombospondin type 1 repeat homology
F;329-383/Domain: thrombospondin type 1 repeat homology <THR1>
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C;Superfamily: circumsporozoite protein; thrombospondin type 1 repeat homology
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C;Species: Plasmodium reichenowi
C;Species: Plasmodium reichenowi
C;Date: 14-Feb-1992 #sequence_revision 14-Feb-1992 #text_change 20-Aug-1999
C;Accession: A39756
R;Lal, A.A.; Goldman, I.F.
C;Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 09-Jun-2000 C;Accession: S05428; A45527; I60657 R;Campbell, J.R.
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Pred. No. 0.00028;
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Pred. No. 0.00045;
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92.3%;
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Best Local Similarity 92.3
Matches 12; Conservative
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Best Local Similarity 92.3
Matches 12; Conservative
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A; Residues: 1-171 <DELA>
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A; Residues: 1-405 <CAS>
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Mol. Blochem. Parasitol. 22, 101-108, 1987
A;Title: Strain variation in the circumsporozoite protein gene of Plasmodium falciparum. A;Reference number: A54529; MUID:87115616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          circumsporozoite protein - malaria parasite (Plasmodium falciparum) (isolate NF54) C;Species: Plasmodium falciparum
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A;Molecule type: DNA
A;Residues: 152-189 <LOC>
C;Superfamily: circumsporozoite protein; thrombospondin type 1 repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: GB:M15505; NID:g160214; PIDN:AAA29554.1; PID:g160215 C;Superfamily: circumsporozoite protein; thrombospondin type 1 repeat homology C;Keywords: tandem repeat F;366-420/Domain: thrombospondin type 1 repeat homology <THR1>
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Pred. No. 0.00021;
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92.3%;
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Best Local Similarity 92...
Local 2; Conservative
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Best Local Similarity 100.
Matches 13; Conservative
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A.Molecule type: mRNA
A.Residues: 1-304 < VAVA
A.Residues: 1-304 < VAVA
A.Cross-references: GB:MZ6209; NID:g212628; PIDN:AAA49055.1; PID:g212629
A.Cross-references: GB:MZ6209; NID:g212628; PIDN:AAA49055.1; PID:g212629
C.Superfamily: transcription factor GATA-1; GATA-type zinc finger homology
C.Keywords: DNA binding; nucleus; transcription factor; transcription regulation; zin
F:107-1160/Domain: GATA-type zinc finger homology GZFI>
F:101-134/Region: zinc finger GATA motif
F:161-214/Domain: GATA-type zinc finger homology GZF2>
F:164-188/Region: zinc finger GATA motif
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C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Map position: 4
A;Introns: 18/2; 75/3; 119/2; 350/3; 475/2; 487/3; 521/2; 601/3; 641/3; 749/2; 870/1
                                                                                                                                                                                                                                    M.Alternate names: transcription factor Eryfl
C; Species: Gallus gallus (chicken)
C; Date: 29-Dec-1989 #sequence_revision 29-Dec-1989 #text_change 26-Aug-1999
C; Date: 29-Ber 1989 #sequence_revision 29-Dec-1989 #text_change 26-Aug-1999
C; Accession: A32993
R; Evans, T.: Pelsenfeld, G.
Cell 58, 877-885, 1989
A; Title: The erythroid-specific transcription factor Eryfl: a new finger protein.
A; Reference number: A32993; MUID:89376538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C. Species: Caenorhabditis elegans
C. Species: Caenorhabditis elegans
C. Date: 15-oct-1999 #sequence_revision 15-oct-1999 #text_change 15-oct-1999
C. Accession: T18627
C. Sims, M.
Submitted to the EMBL Data Library, February 1996
A. Reference number: Z18999
A. Accession: T18627
A. Status: preliminary; translated from GB/EMBL/DDBJ
A. Molecule type: DNA
A. Residues: 1-944 <WIL>
A. Residues: 1-944 <WIL>
A. Cross-references: EMBL: Z69634; PIDN: CAA93451.1; GSPDB: GN00022; CESP: B0001.2
A. Streammental source: clone B0001
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61.5%; Pred. No.
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Pred. No.
                                                                                                                                                                                                                         - chicken
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Best Local Similarity 72.7-
اتاتا 8; Conservative
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309 KHRKLFQAGDG 319
                                   HKKLKQPGDGNP 13
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Matches 8; Conserv
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79 HSRIGQPGGGNP
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J. Biol. Chem. 266, 6686-6689, 1991
A;Title: Circumsporozoite protein gene from Plasmodium reichenowi, a chimpanzee malaria
A;Reference number: A39756; MUID:91201303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Guyader, M.; Alizon, M.; Daniel, M.D.; Desrosiers, R.C.; Tiollais, P.
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A;Note: the nucleotide sequence was submitted to the EMBL Data Library, December 1987
C;Superfamily: AIDS vpr protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Chakrabarti, L.; Guyader, M.; Alizon, M.; Daniel, M.D.; Desrosiers, R.C.; Tiollais, Nature 328, 543-547, 1987
A;Title: Sequence of simian immunodeficiency virus from macaque and its relationship A;Reference number: A28887; MUID:87287230
A;Accession: E28887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Hahn, B.H.; Kong, L.I.; Lee, S.W.; Kumar, P.; Taylor, M.E.; Arya, S.K.; Shaw, G.M. Nature 300, 184-186, 1987
A;Title: Relation of HTLV-4 to simian and human immunodeficiency-associated viruses. A;Reference number: S03065
A;Reference number: S03067
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C;Genetics:
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                                                                                                                              A Molecule type: DNA A Readles 1.138 «LAL» A Readles: 1-388 «LAL» A: Cross-references: GB:M60972; NID:g160228; PIDN:AAA29561.1; PID:g160229 C:Superfamily: circumsporozoite protein; thrombospondin type 1 repeat homology F:312-366/Domain: thrombospondin type 1 repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Residues: 1-97 <HAH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gene R protein - human T-cell lymphotropic virus type 4, HTLV-4
C;Species: human T-cell lymphotropic virus type 4, HTLV-4
C;Date: 21-Nov-1993 #sequence_revision 26-May-1995 #text_change 20-Sep-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N;Alternate names: orf-R protein
C;Species: simian immunodeficiency virus, SIV
C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 16-Jul-1999
C;Accession: E28887
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                                                                                                                                                                                                                                                                                                                            Score 51; DB 2; Length 388;
Pred. No. 0.51;
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0.91;
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C,Superfamily: AIDS vpr protein
C,Keywords: AIDS; immunodeficiency
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58.3%;
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75.0%;
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58.3%;
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Best Local Similarity 75.0
Matches 9; Conservative
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Best Local Similarity 58.3
Matches 7; Conservative
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Matches 7; Conservative
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79 HSRIGQPGGGNP 90
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A; Residues: 1-101 <CHA>
                                                                                                        A; Status: preliminary
                                                                                  A; Accession: A39756
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RESULT

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Search completed: January 29, 2002, 10:26:36
Job time: 647 sec
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Best Local Similarity
Matches 9; Conserv
                                                                       A; Molecule type: DNA
A; Residues: 1-98 <MCC>
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C; Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 17-Mar-1999
C; Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 17-Mar-1999
C; Accession. A29319; A44187, Welsh, J.A.; McCutchan, T.F.
J. Biol. Chem. 262, 6464-6467, 1987
A; Title: Evolution of the immunodominant domain of the circumsporozoite protein gene from A; Reference number: A29319; MUID:87194878
A; Accession: A29319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Accession: B82143
A;Status: preliminary
A;Astus: preliminary
A;Cuss.-1-179 <HEI>
A;Cross-references: GB:AE004265; GB:AE003852; NID:g9656424; PIDN:AAF95040.1; GSPDB:GN001
A;Experimental source: serogroup O1; strain N16961; blotype El Tor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Molecule type: DNA
A;Residues: 1-343 <DEL>
R;McCutchan, T.F.; Lal, A.A.; de la Cruz, V.F.; Miller, L.H.; Maloy, W.L.; Charoenvit,
Science 230, 1381-1383, 1985
               R.J.
C; Accession: B02143
R; Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J. chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, L, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Residues: 1-978 <POW>
A; Cross-references: GB:U81808; GB:L75931; NID:q1750277; PIDN:AAB41628.1; PID:g1750280
A; Experimental source: strain ATCC 33020
                                                                                               A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A;Reference number: A82035; MUID:20406833
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Pred. No. 8.1;
2; Mismatches
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Pred. No. 45;
1; Mismatches
                                                                                                                                                                                                                                                                                                                     A;Map position: 1
C;Superfamily: Escherichia coli yafP protein
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70.0%;
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Best Local Similarity 58.3%;
Matches 7; Conservative
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C; Keywords: oxidoreductase
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51 HKAIEQSGDPNP 62
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301 HRKSDQPGDG 310
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Best Local Similarity
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A;Title: Sequence of the immunodominant epitope for the surface protein on sporozoite A;Reference number: A44187; MUID:86070222 A;Accession: A44187 A;Status; preliminary
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Proc. Natl. Acad. Scil U.S.A. 85, 8102-8106, 1988
A;Title: Does biased gene conversion influence polymorphism in the circumsporozoite
A;Reference number: A32068; MUID:89042133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Molecule type: DNA
A;Residues: 1-367 - CARN>
A;Cross-references: GB:M20670; GB:J04090; NID:g160183; PIDN:AAA29534.1; PID:g552194
C;Superfamily: circumsporozoite protein; thrombospondin type 1 repeat homology
E;292-345/Domain: thrombospondin type 1 repeat homology <ffHR1>
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C;Superfamily: circumsporozoite protein; thrombospondin type 1 repeat homology
F;268-321/Domain: thrombospondin type 1 repeat homology <THR1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           circumsporozoite protein - Plasmodium vivax (strain North Korean) (fragment) C;Species: Plasmodium vivax C;Date: 21-May-1990 #sequence_revision 21-May-1990 #text_change 20-Aug-1999 C;Accession: A32068
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56.2%; Pred. No. 20;
:ive 1; Mismatches
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Pred. No. 19;
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56.2%;
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Best Local Similarity 56.2.
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Sequence 4, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 59, Appl 
Sequence 21, Sequence 21, Sequence 21, Sequence 21, Sequence 16, Sequence 16,

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RESULT 1
5178861-5
; Patent No. 5178861
APDLICANT: VERGARA, ULISES; RUIZ, ANDRES; FERREIRA, ARTURO; NUSSENÜMELG, VICTOR N.
; NUSSENÜMELG, VICTOR N.
; TITLE OF INVENTION: CROSS-REACTIVE AND PROTECTIVE EPITOPES
;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 22;
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TITLE OF INVENTION: CLONING, EXPRESSION AND USES OF A
TITLE OF INVENTION: NOVEL SECRETED PROTEIN, F-SPONDIN
NUMBER OF SEQUENCES: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 75; DB 6; I
llarity 100.0%; Pred. No. 2.4e-05;
Conservative 0; Mismatches 0;
US-08-462-679-21
US-08-466-210A-21
US-08-467-147A-21
US-08-469-014-21
PCT-US93-10506A-21
PCT-US93-10506-21
US-08-188-582-16
US-08-646-715-16
US-08-045-806-4
US-08-366-051B-4
US-08-227-536-2
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US-08-450-098-59
US-08-451-233-59
US-08-450-236-59
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STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
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NUMBER OF SEQUENCES: 18
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/370,241
FILING DATE: 22-UNN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 115,634
FILING DATE: 26-OCT-1987
APPLICATION NUMBER: 649,903
FILING DATE: 12-SEP-1984
                                                                                                                                                                                                                                                                                                    5171843-11
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COMPUTER READABLE FORM:
MDDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-313-288B-18

Sequence 18, Application US/08313288B

Patent No. 5750502

GENERAL INFORMATION:
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ADDRESSEE: Cooper &
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Best Local Similarity
Matches 13; Conserv
       4466.7
4466.7
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4466.7
4455.3
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       \begin{matrix} \mathbf{c} & \mathbf{c} 
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       Sequence 3, Appl. Sequence 16, Appl. Sequence 15, Appl. Sequence 15, Appl. Sequence 5, Appl. Sequence 2, Appl. Sequence 2, Appl. Sequence 6, Appl. Sequence 6, Appl. Sequence 6, Appl. Sequence 12, Appl. Sequence 12, Appl. Sequence 12, Appl. Sequence 12, Appl. Sequence 2, Appl. Sequence 446, Appl.
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                                                                                                                                                                                                        (without alignments)
2.197 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 18,
Patent No. 517
Sequence 22,
Patent No. 517
Patent No. 517
Patent No. 517
                                                                                                                                                                            Search time 133.18 Seconds
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Sequence
Sequence
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/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
                              GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-313-288B-18
5178861-17
105-08-937-271-22
5171843-7
5171843-9
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105-08-070-301-3
US-08-070-301-14
US-08-318-856A-15
US-08-318-856A-15
US-08-318-856A-15
US-08-318-856A-15
US-08-136-605-5
US-09-136-605-5
US-09-136-605-6
US-09-136-605-6
US-09-0912-3
US-08-54-06088-2
US-09-0912-3
US-08-99-299-12
US-08-99-298-29-12
US-08-99-298-29-12
US-08-99-29-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                212252 seqs, 22503292 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUMMARIES
                                                                                                                                                                          January 29, 2002, 10:24:02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                            OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                     US-09-763-397A-5
75
1 KHKKLKQPGDGNP 13
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                           Title:
Perfect score:
Sequence:
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; Patent No. 5171843

; APPLICANT: NUSSENZWEIG, VICTOR

; TITLE OF INVENTION: IMMUNOGENIC POLYPEPTIDE AND METHOD FOR

; PURIFYING IT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 135;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4; Indels
: SEED and BERRY
6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                               Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 6;
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Pred. No. 9.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 41.5; D
Pred. No. 28;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: ROSenman, Stephen J.
REGISTRATION NUMBER: 43,058
REFERENCE/DOCKET NUMBER: 401112.405C1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/175,112
FILING DATE: 30-MAR-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 754,645
FILING DATE: 9-JUL-1985
APPLICATION NUMBER: 115,634
FILING DATE: 26-OGT-1987
APPLICATION NUMBER: 649,903
FILING DATE: 12-SEP-1984
                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/937,271 FILING DATE: 15-SEP-1997 CLASSIFICATION: 424
                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 22:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               57.3%;
61.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 135 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 55.3
Best Local Similarity 56.2
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 57.3
Best Local Similarity 61.5
Matches 8; Conservative
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7 RENKLKQPGDRADGQP 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               , MOLECULE TYPE: protein US-08-937-271-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 13
                                                                                                 ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 KHKKLKQPGDGNP 13
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                                        Seattle
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  ADDRESSEE:
                                                                                COUNTRY:
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5171843-9
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PAPELICANT: VERGARA, ULISES; RUIZ, ANDRES; FERREIRA, ARTURO;
NUSSENZWEIG, RUTH S.; NUSSENZWEIG, VICTOR N. PROTECTIVE EPITOPES
TITLE OF INVENTION: CROSS REACTIVE AND PROTECTIVE EPITOPES;
OF CIRCUMPOROZOITE PROTEINS;
NUMBER OF SEQUENCES: 18
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/370,241
FILING DATE: 22-JUN-1989
PRIOR APPLICATION NUMBER: 115,534
FILING DATE: 26-OCT-1987
FILING DATE: 12-SEP-1984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.0%; Score 75; DB 1; Length 412;
Best Local Similarity 100.0%; Pred. No. 0.0004;
Matches 13; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     74.7%; Score 56; DB 6; Length 13; 100.0%; Pred. No. 0.011; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Dale, James B.
APPLICANT: Dale, James W.
TITLE OF INVENTION: RECOMBINANT MULTIVALENT M PROTEIN
TITLE OF INVENTION: VACCINE
CORRESPONDENCES: 40
CORRESPONDENCE ADDRESS:
      PatentIn Release #1.0, Version #1.30
                   CURSENT APPLICATION DATA:
APPLICATION NUMBER: US/08/313,288B
FILING DATE: January 5, 1995
CLASSIFICATION: 435
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REDESTRATION NUMBER: 28,678
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEPAX: (212) 391-0526
TELESX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 22, Application US/08937271; Patent No. 6063386; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                       INFORMATION FOR SEC ID NO: 18:
                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 412 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 74.7
Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear; MOLECULE TYPE: peptide US-08-313-288B-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              109 KHKKLKQPGDGNP 121
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US-08-937-271-22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 3
5178861-17
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ENZYME PARTICIPATING IN C-TERMINAL AMIDATION, AND METHOD OF PREPARING SAME AND USE THEREOF 21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                         TITLE OF INVENTION: AMIDATION, AND METHOD OF PREPAR
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wegner, Cantor, Mueller & Player, P.C.
STREET: 1233 Cht Street, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P-450-22830
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Patent No. 5871995
GENERAL INFORMATION:
APPLICANT: ILDA, TOSHIO
APPLICANT: FUSE, YUKA
APPLICANT: TAJIMA, MASAHIO
APPLICANT: YANAGI, MITSUO
APPLICANT: YANAGI, MITSUO
APPLICANT: YANAGI, MITSUO
APPLICANT: KISHIMOTO, JICO
APPLICANT: IFUKU, OH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Player, William E.
REGISTRATION NUMBER: 31,409
REFERENCE/DOCKET NUMBER: P-45
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-040
TELEFAX: (202) 835-0605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEX: 440706
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1020 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 53.3
Best Local Similarity 53.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | | :|:|| | |
| 899 KQKLIKEPGSGVP 911
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 TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 7
5178861-4
; Patent No. 5178861
; Patent No. 5178861
; PAPLICANT: VERGARA, ULISES; RUIZ, ANDRES; FERREIRA, ARTURO;
; NUSSENZWEIG, RUTH S.; NUSSENZWEIG, VICTOR N.
; TILLE OF INVENTION: CROSS-REACTIVE AND PROTECTIVE EPITOPES
; OF CIRCUMPOROZOITE PROTEINS
; OF CIRCUMPOROZOITE PROTEINS
; NUMBER OF SEQUENCES: 18
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/O8/370,241
; FILING DATE: 22-JUN-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 115,634
; FILING DATE: 12-OCT-1984
; FILING DATE: 12-SEP-1984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                         DB 6; Length 378;
   APPLICANT: NUSSENZWEIG, VICTOR
TITLE OF INVENTION: IMMUNOGENIC POLYPEPTIDE AND METHOD FOR
PURIFYING IT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  54.7%; Score 41; DB 6; Length 27; 70.0%; Pred. No. 4.2; 1.4ve 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                          3; Indels
                                                                                                                                                                                                                                                                                                                                       Score 41.5; DB
Pred. No. 45;
1; Mismatches
                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/175,112
FILING DATE: 30-MAR-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 754,645
FILING DATE: 9-JUL-1985
APPLICATION NUMBER: 115,634
FILING DATE: 26-07-1987
APPLICATION NUMBER: 649,903
FILING DATE: 12-SEP-1984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: IIDA, TOSHIO
APPLICANT: KAMINUMA, TOSHIHIKO
APPLICANT: FUSE, YUKE
APPLICANT: TAJIMA, MASSHITO
APPLICANT: YANGI, MILSUO
APPLICANT: OKAMOTO, HIROSHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-070-301-3
Sequence 3, Application US/08070301
Patent No. 5871995
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TAJIMA, Masahiro
YANAGI, Mitsuo
OKAMOTO, Hiroshi
KISHIMOTO, Jiro
IFUKU, Ohji
KATO, Ichiro
                                                                                                                                                                                                                                                                                                                                       55.3%;
                                                                                                                                                                                                                                                                                                                                       Query Match 55.3
Best Local Similarity 56.2
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                             : |||||| || || 89 RENKLKQPGDRADGQP 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match
Best Local Similarity 70.0
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                          1 KHKKLKQPG---DGNP 13
                                                                 NUMBER OF SEQUENCES: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 KLKQPGDGNP 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Patent No. 5171843
                                                                                                                                                                                                                                                                      LENGTH: 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
APPLICANT:
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Sequence 14, Application US/08318856A
Sequence 14, Application US/08318856A
Patent No. 5972351
GENERAL INFORMATION:
APPLICANT: Adriam V.S. Hill, et al.
APPLICANT: Adriam V.S. Hill, et al.
TITLE OF INVENTION: PLASMODIUM FALCIPARUM MHC CLASS I-
TITLE OF INVENTION: ANTIGENS (AS AMENDED)
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.
STREET: 2033 K Street, N.W., Suite 800
CITY: Washington
STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk, 3.5 inch, 1.44 mb
COMPUTER: IBM PC COMPATIBLE
                                                                                                                                                                                                                                                           PE: Floppy disk, 3.5 inch, 1.44 mb
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.
STREET: 2033 K Street, N.W., Suite 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 38; DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/318,856A FILING DATE: October 3, 1994
PRIOR APPLICATION NUMBER: GB 92 08 068.8
FILING DATE: April 3, 1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 92 17 704.7
FILING DATE: August 20, 1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/GB93/00711
FILING DATE: April 5, 1993
ATTORNEY/AGENT INFORMATION:
NAMM: CC APPLICATION NUMBER: 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. 4.7
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      40,949
ER: 263-PPIR1577US
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WordPerfect 5.1+
                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPorfect 5.1+
CURRENT APPLICATION DATA:
PPLICATION NUMBER: US/08/318,85
FILING DATE: October 3, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10 amino acid residues
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100.08; Pro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REGIETRATION NUMBER: 40,949
REFERENCE/DOCKET NUMBER: 26
TELECOMMUNICATION INFORMATION: TELEPHONE: (202) 721-820
TELEFAX: (202) 721-8250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (202) 721-8250
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHRACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       50.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.0
                                                                                                                                                  ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Flore
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear;
MOLECULE TYPE: peptide
US-08-318-856A-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC
OPERATING SYSTEM:
SOFTWARE: WordPer
                                                                                                                            Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lee Cheng
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8 PGDGNP 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 PGDGNP 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 11
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Patent No. 5972351
GENERAL INFORMATION:
APPLICANT: Adrian V.S. Hill, et al.
TITLE OF INVENTION: PLASMODIUM FALCIPARUM MHC CLASS I-
TITLE OF INVENTION: RESTRICTED CTL EPITOPES DERIVED FROM PRE-ERYTHROCYTIC STAGE
TITLE OF INVENTION: ANTIGENS (AS AMENDED)
                                         TITLE OF INVENTION: BN2YME PARTICIPATING IN C-TERMINAL TITLE OF INVENTION: AMIDATION, AND METHOD OF PREPARING SAME AND USE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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                                                                                                                                                            ADDRESSEE: Wegner, Cantor, Mueller & Player, P.C. STREET: 1233 20th Street, N.W.
                                                                                                                                                                                                                                                                                                                 ZIP: 20036-8218
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: DatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/070,301
FILING DATE: 24 -MAY-1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Player, William E..
REGISTRATION NUMBER: 31,409
REFERENCE/DOCKET NUMBER: P-450-22830
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 1-209687
FILING DATE: 15-AUG-1989
PRIOR APPLICATION NUMBER: JP 1-181933
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 1-181933
FILING DATE: 31-OCT-1989
PRIOR APPLICATION NUMBER: JP 2-76331
FILING DATE: 26-MAR-1990
PRIOR APPLICATION NUMBER: JP 2-106412
FILING DATE: 24-APR-1990
PRIOR APPLICATION NUMBER: JP 2-106412
FILING DATE: 24-APR-1990
PRIOR APPLICATION NUMBER: JP 2-205475
FILING DATE: MAR-1990
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-040
TELEFAX: (202) 835-0605
TELEX: 440706
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         52.0%;
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Best Local Similarity 53.8
Matches 7; Conservative
               KATO, Ichiro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
                                                                                                     NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | | :|:|| | :
867 KQKLVKEPGSGVP 879
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                                                                                                                                                                                                                               CITY: Washington
                                                                                                                                                                                                                                                                                     COUNTRY: U.S.A.
ZIP: 20036-8218
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US-08-318-856A-15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-070-301-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Korinek, Vladimir
APPLICANT: Morin, Patrice
APPLICANT: Morin, Patrice
APPLICANT: Winzler, Kenneth
APPLICANT: Sparks, Andrew
TITLE OF INVENTION: Beta Catenin, TCF-4, and APC
TITLE OF INVENTION: Interact to Prevent Cancer
NUMBER OF SEQUENCES: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: DOS
SOFTWARE: FSSLESD for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/003,687A
                                                     1107.05064
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1107.05064
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Banner & Witcoff, Ltd. STREET: 1001 G Street, N.W. CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/821,355
FILING DATE: 20-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Kagan, Sarah A
REGISTRATION NUMBER: 32,145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 5, Application US/09003687A
; Patent No. 5998600
NAME: Kagan, Sarah A
REGISTRATION NUMBER: 32,145
REFERENCE/DOCKET NUMBER: 1107
TELECOMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
TELEPRX: 202-508-9299
TELERX: 97430 BMB UT
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 442 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
TELEX: 97430 BMB UT
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 442 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Clevers, Hans
Korinek, Vladimir
                                                                                                                                                                                                                                                                        ; TOPOLOGY: linear
; MOLECULE TYPE: No. 5851775e
US-08-821-355A-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 58.3 Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Barker, Nick APPLICANT: Clevers, Hans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | |: ||||: |
| 405 KRKRDKQPGETN 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 KHKKLKQPGDGN 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        USA
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COUNTRY: US
ZIP: 20001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-003-687A-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Morin, Patrice
APPLICANT: Kinzler, Kenneth
APPLICANT: Kinzler, Kenneth
APPLICANT: Vogelstein, Bert
APPLICANT: Sparks, Andrew
TITLE OF INVENTION: Beta Catenin, TCF-4, and APC
TITLE OF INVENTION: Interact to Prevent Cancer
NUMBER OF SEQUENCES: 11
COMMESSOBE Banner & Witcoff, Ltd.
STREET: 1001 G Street, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: DISKetter
COMPUTER: IBM Compatible
COPERATING SYSTEM: DOS
SOFTWARE: Fast-SEG for Windows Version 2.0
CURRNY APPLICATION DATA:
APPLICATION NUMBER: US/08/821,355A
FILING DATE: 20-MAR-1997
CLASSIFCATION 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                     PRILING DATE: October 3, 1994
PRIOR PAPELICATION NUMBER: 05, 1994
PRIOR PAPELICATION DATA: 1994
PRIOR PAPELICATION DATA: 1992
PRIOR PAPELICATION DATA: 1992
PRIOR PAPELICATION DATA: 3, 1992
PRIOR PAPELICATION NUMBER: GB 92 17 704.7
PRILING DATE: August 20, 1992
PRIOR PAPELICATION NUMBER: WO PCT/GB93/00711
PRILING DATE: April 5, 1993
ATTORNEY/AGENT INFORMATION: AMAE: Lee Cheng
REGISTRATION NUMBER: 40, 949
REFERENCE/DOCKET NUMBER: 263-PPIRI577US
TELEPONMUNICATION INFORMATION: TELEPHONE: (202) 721-8200
INFORMATION FOR SEQ 1D NO: 14: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 5, Application US/08821355A Patent No. 5851775 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 9 amino acid residues
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Barker, Nick
APPLICANT: Clevers, Hans
APPLICANT: Korinek, Vladimir
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Best Local Similarity 100.
Matches 7; Conservative
         CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: peptide
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STATE: DC
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APPLICANT: He, Tong-Chuan
APPLICANT: He, Tong-Chuan
APPLICANT: Ho, Tong-Chuan
TITLE OF INVENTION: Beta Catenin, TCF-4, and APC Interact to
TITLE OF INVENTION: Prevent Cancer
FILE REFERENCE: 1107.75741
CURRENT APPLICATION NUMBER: US/09/136,605A
CURRENT APPLICATION NUMBER: 08/09/135
EARLIER APPLICATION NUMBER: 08/09/135
EARLIER PILING DATE: 1999-08-20
EARLIER PILING DATE: 1999-08-20
EARLIER PILING DATE: 1999-08-20
EARLIER PILING DATE: 1998-01-06
MUMBER OF SEQ ID NOS: 28
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                                                                                                    Score 37; DB 2; Length 442;
Pred. No. 2.5e+02;
2; Mismatches 3; Indels
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Best Local Similarity 58.3%; Pred. No. 2.5e+02;
Matches 7; Conservative 2; Mismatches 3; Indels
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APPLICANT: MILLER, WALTER L.

APPLICANT: MILLER, WALTER L.

APPLICANT: BLACK, STEPHEN M.

APPLICANT: BLACK, STEPHEN M.

TITLE OF INVENTION: CHOLESTEROL DISPOSAL FUSION ENZYMES

NUMBER OF SEQUENCES: 24

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: COOLEY GODWARD CASTRO HUDDLESON & TATUM STREET: FIVE PALO ALTO SQUARE CITY: PALO ALTO STATE: CALIFORNIA COUNTRY: USA
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 5
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                                                                                                                                                                                                                                                                                                                                  Sequence 5, Application US/09136605A Patent No. 6140052
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-075-193-2
; Sequence 2, Application US/08075193
; Patent No. 5547868
; TOPOLOGY: linear ;
; MOLECULE TYPE: No. 5998600e
US-09-003-687A-5
                                                                                                         49.3%;
                                                                                     Query Match
Best Local Similarity 58...
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COMPUTER READABLE FORM:
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ORGANISM: Homo sapiens
US-09-136-605-5
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Maximum Match 100%
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Gapop 10.0 , Gapext 0.5
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SwissProt_39:*
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Query Match 100.0%; Score 75; DB 1; 1 Best Local Similarity 100.0%; Pred. No. 1.3e-05; Matches 13; Conservative 0; Mismatches 0;

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EMBL; K02194; AAA29524.1; PIF; A03388; OZZQAF. InterPro; IPR003067; Crcmsprzolte. InterPro; IPR003084; TSP1. InterPro; PR01303; CRCMSPRZOITE. SMART; SM00209; TSP1; 1. SMART; SM00209; TSP1; 1. Malaria; Sporozoite; Repeat; Signal. SIGNAL 1 1 1 PROBABLE. CHAIN 17 412 CIRCUMSPOROZOIT DOMAIN 123 290 41 X 4 AA TANDE SEQUENCE 412 AA; 44420 MW; IEEEED3DE9090	This SWISS-PROT entry is copyright. It is probetween the Swiss Institute of Bioinformatic the European Bioinformatics Institute. There use by non-profit institutions as long as modified and this statement is not removed. entitles requires a license agreement (See ht or send an email to license@isb-sib.ch).	SCIENCE 223:993-399(1964).  - FUNCTION: THE CITCUMSPOROZOITE PROTEIN SURFACE ANTIGEN ON THE SPOROZOITE (THE MALARIA PARASTIE THAT IS TRANSMITTED FIVERTEBRATE HOST).  - MISCELLANEOUS: THE C-TERMINAL REGION IS ANCHORING THE PROTEIN TO THE CELL MEMBI MOULD BE THE SURFACE ANTIGEN OF THE ORC.  - SIMILARITY: CONTAINS 1 TSP TYPE-1 DOMA.	[1] SEQUENCE FROM N.A. MEDLINE=84250215; PubMed=6204383; MEDLINE=84250215; PubMed=6204383; Dame J.B., Williams J.L., McCutchan T.F., Hochmeyer W.T., Maloy W.L., Haynes J.D., 'S sanders G.S., Reddy E.P., Diggs C.L., Mil' "Structure of the gene encoding the immune the sporozoite of the human malaria paras: Science 255:502-5004/08/		SUL P_P
ROTEIN. EPEATS OF P- CRC64;	roduced through a collaboration ics and the EMBL outstation - sere are no restrictions on its as its content is in no way Usage by and for commercial http://www.isb-sib.ch/announce/	IS THE IMMUNODOMINANT INFECTIVE STAGE OF THE ROM THE MOSQUITO TO THE S PROBABLY USED FOR RANE. THE REPEAT SEQUENCES RANISM.	Weber J.L., Wirtz R.A., Schneider I., Roberts D., ler L.H.; Dodominant surface antigen on the Plasmodium falciparum.";	da; Plasmodium.	

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Best Local S
Matches 13
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01-AUG-1988 (Rel. (
01-AUG-1988 (Rel. (
20-AUG-2001 (Rel. 4
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SEQUENCE
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01-JAN-1990 (Rel. 13, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
CIRCUMSPOROZOITE PROTEIN PRECURSOR (CS).
Plasmodium falciparum (isolate t4 / Thailand).
Eukaryota; Alveolata; Apicomplexa; Haemosporida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the
Plasmodium falciparum Eukaryota; Alveolata; NCBI_TaxID=5848;
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                                                                      CIRCUMSPOROZOITE PROTEIN PRECURSOR (CS)
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del Portillo H.A., Nussenzweig R.S.,
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InterPro; IPR000884; TSP1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VERTEBRATE HOST)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Biochem. Parasitol. 24:289-294(1987)
                                                                                                                                                                                                                                                                                                                    KHKKLKQPGDGNP
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
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Sporozoite; Repeat; Signal.

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PROBABLE.
17 424
CIRCUMSPOROZOITE PROTEIN.
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non-profit institutions as long as its content
and this statement is not removed. Usage by ar
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                      Apicomplexa;
                                             (isolate Wellcome)
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                                                                                                update)
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RESULT 4
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Best Local :
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P05691;
01-NOV-1988
                                                                                                                                                                      SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDIINE-87308186; PubMed-2442154;
la Cruz V.F., Lal A.A., McCutchan T.F.;
Sequence variation in putative functional
Sequence variation of Plasmodium falc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
SEQUENCE
                                                                                                                          J. Biol.
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SEQUENCE FROM N.A.
MEDLINE=87115616; PubMed=3543671;
                                                                                                                                                                                                                                                                                                                                                               CIRCUMSPOROZOITE PROTEIN (CS) (FRAGMENT).

Plasmodium falcinarum (:-----
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PIR; A54529; A54529.
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01-NOV-1988 (Rel.
01-FEB-1994 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Strain variation in the circumsporozoite protein falciparum.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lockyer M.J., Schwarz
                                         <del>:</del>
                                                                                                                                                                circumsporozoite protein vaccine development.";
                                                                                                                                                                                                                                                                                                                                         Eukaryota;
                                                                                                                                                                                                                                                                                                                                                        Plasmodium falciparum
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InterPro; IPR000884; TSP1.
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SIMILARITY: CONTAINS 1 TSP TYPE-1 DOMAIN.
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                                       VERTEBRATE HOST)
MISCELLANEOUS: T
                                                                            FUNCTION: THE CIRCUMSPOROZOITE PROTEIN IS
SURFACE ANTIGEN ON THE SPOROZOITE (THE IN
MALARIA PARASITE THAT IS TRANSMITTED FROM
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                     ANCHORING THE PROTEIN TO THE CELL MEMBRANE.
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SM00209; TSP1;
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13; Conserv
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SURFACE
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09, Last sequence up
28, Last annotation
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                                         THE C-TERMINAL REGION IS PROBABLY USED FOR
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Apicomplexa;
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47 X 4 AA TANDEM REPEATS;
BD57A9A152B85E03 CRC64;
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Pred. No. 1.4
D; Mismatches
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ROM THE MOS
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                     THE REPEAT SEQUENCES
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P19597; Q25798;
01-FEB-1991 (Rel. 17, Created)
30-MAY-2000 (Rel. 39, Last sequence updat
20-AUG-2001 (Rel. 40, Last annotation upd
CIRCUMSPOROZOITE PROTEIN PRECURSOR (CS).
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SEQUENCE
                                                                                                                MEDLINE-89364998; PubMed-2671723;
Caspers P., Gentz R., Mattle H., Pink J.R.
"The Circumsporozoite protein gene from NF
isolate used in malaria vaccine trials.";
Mol. Biochem. Parasitol. 35:185-190(1989).
                                                                                                                                                                                                                                                                                                                                                                            "DNA sequence of the gene encoding a Plasmodium candidate vaccine antigen.";
Nucleic Acids Res. 17:5854-5854(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. MEDLINE=92155298; PubMed=1346766;
                                                                                                                                                                                                                                                                                                                                      Campbell
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Eukaryota; Alveolata;
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                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                Thomas A.W., Bagar Hackett C.S.;
                                                                                                                                                                                                                                                                       Davis J.R., Cortese
                                                                                                                                                                                                                                                                                                                          Submitted (JUL-1997)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=5843;
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infectivity of a cloned
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                                                                   . Biochem. Parasitol. 35:185-190(1707).
FUNCTION: THE CIRCUMSPOROZOITE PROTEIN IS THE IMMUNODOMINANT SURFACE ANTIGEN ON THE SPOROZOITE (THE INFECTIVE STAGE OF THE MALARIA PARASITE THAT IS TRANSMITTED FROM THE MOSQUITO TO TH
            MISCELLANEOUS: THE C-TERMINAL REGION IS PROBABLY USED ANCHORING THE PROTEIN TO THE CELL MEMBRANE. THE REPEAU WOULD BE THE SURFACE ANTIGEN OF THE ORGANISM.

SIMILARITY: CONTAINS 1 TSP TYPE-1 DOMAIN.
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                                                              MALARIA PARASITE THAT IS VERTEBRATE HOST).
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315
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NF54, a Plasmodium
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CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                  J. Biol. Chem. 266:6686-6689(1991).

-I- FUNCTION: THE CIRCUMSPOROZOITE PROTEIN IS THE IMMUNODOMINANT SURFACE ANTICEN ON THE SPOROZOITE (THE INFECTIVE STAGE OF THE MALARIA PARASITE THAT IS TRANSMITTED FROM THE MOSQUITO TO THE VERTEBRATE HOST).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P26694;
01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation updat
CIRCUMSPOROZOITE PROTEIN PRECURSOR (CS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL;
EMBL;
                                                                                         the European Bioinformatics Institute. There are no rest
use by non-profit institutions as for content
modified and this statement is not removed. Usage by an
entities requires a license agreement (See http://www.isb-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Circumsporozoite protein gene from Plasmodium reichenowi, a chimpanzee malaria parasite evolutionarily related to the human malaria parasite Plasmodium falciparum.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for commodified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=91201303; PubMed=2016283;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Plasmodium reichenowi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CSP_PLARE
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SMART; SM00209; TSP1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR000884; 1
Pfam; PF00090; tsp_1;
                      EMBL; M60972; AAA29561.1;
                                                                                                                                                                                             between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lal A.A., Goldman I.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=5854;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Malaria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR003067; Crcmsprzoite.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 KHKKLKQPGDGNP
                                                                                                                                                                                                                                                              MISCELLANBOUS: THE C-TERMINAL REGION IS PROBABLY USED ANCHORING THE PROTEIN TO THE CELL MEMBRANE. THE REPEAT WOULD BE THE SURFACE ANTICEN OF THE ORGANISM.
SIMILARITY: CONTAINS 1 TSP TYPE-1 DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6
                                                                                                                                                                                        SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EN
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A45527; A45527.
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                                                                        an
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               194
397
                                                                        email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Alveolata;
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397
272
194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Apicomplexa;
                                                                                         is not removed. Usage by and for agreement (See http://www.isb-sib.
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PROBABLE.
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Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CIRCUMSPOROZOITE PROTEIN.
43 X 4 AA TANDEM REPEATS
A -> ANPNANPNA (IN REF. 4
; 9EB1146F59EBCEA3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
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                                                                                                                                                                                                  a collaboration -
MBL outstation -
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                                                                                              .ch/announce/
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GGC1_HUMAN
Query Match
Best Local S
Matches 8
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Best Local
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20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
G ANTIGEN FAMILY C 1 PROTEIN (PROSTATE-ASSOCIATED GENE PROTEIN
(PAGE-4) (PAGE-1) (JM27) (GAGE-9).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
SEQUENCE
                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a clother the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mamumalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR000884; Pfam; PF00090; tsp_1;
                                                                                                                                                         EMBL;
                                                                                                                                                                                           entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. MEDLINE=98393718; PubMed=9724777;
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060829;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Strom T.M.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (APR-1998) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "PAGE-1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Brinkmann U., Vasmatzis G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                  UTERUS, AND PLACENTA, AS WELL AS IN PROSTATE CANCER, AND UTERINE CANCER.
SIMILARITY: BELONGS TO THE GAGE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                 FUNCTION: UNKNOWN.

FUNCTION: UNKNOWN.

FUNCTION: UNKNOWN.

FUNCTION: DREFERENTIALLY EXPRESSED IN NORMAL MALE AND TISSUE SPECIFICITY: PREFERENTIALLY EXPRESSED IN NORMAL MALE AND TISSUE SPECIFICITY: PREFERENTIALLY EXPRESSED IN NORMAL MALE AND TISSUE SPECIFIC TISSUES, PROSTATE CANCER, TESTICULAR

FEMALE REPRODUCTIVE TISSUES, PROSTATE CANCER, TESTICULAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KHNKLKQPGNDN 120
                                                                                                         300287;
                                                                                                                    AF275258; AAF88037.1; -. AJ005894; CAA06751.1; -. AF238380; AAF62541.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; PR01303; CRCMS
SM00209; TSP1;
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9; Conserv
 Similarity
8; Conser
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1 16 PROBABLE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        an X chromosome-linked GAGE-like gene that
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120
388 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    neoplastic prostate, testis, and uterus . Acad. Sci. U.S.A. 95:10757-10762(1998)
                                                                                       102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nyakatura G., Hellebrand H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
   Conservative
                                                                                     AA:
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267 6
42245 MW;
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75.0%;
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61.5%;
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Pred. No. 0.22
1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CIRCUMSPOROZOITE PROTEIN.
62 X 4 AA TANDEM REPEATS OF N-A-N-P.
; C031EEFBB2E35604 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 51; DB 1
Pred. No. 0.18;
L; Mismatches
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Catarrhini; Hominidae
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                                                                                                                                                                                                           (See
                                   DВ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drescher B., Rosenthal
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MBL outstation -
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Query Match
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P05957;
01-NOV-1988
01-NOV-1988
01-OCT-1989
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P05958;
01-NOV-1988
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01-OCT-1989
VPR PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Franchini G., Gallo R.C., Guo H.-G., Fargnoli K., Hall L., Wong-Staal F., "Sequence of simian immunodeficiency the human immunodeficiency viruses.";
Nature 328:559-543[1987].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no was use by non-profit institutions as long as its content is in no was
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                                                                                               NCBI_TaxID=11733; [1]
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            Chakrabarti L., Guyader M., Alizon M.
Tiollais P., Sonigo P.;
"Sequence of simian immunodeficiency
                                                             SEQUENCE FROM N.A. MEDLINE=87287230; PubMed=3649576;
                                                                                                                               Simian immunodeficiency virus (Mm142-83 isolate) (SIV-MAC) Viruses; Retroid viruses; Retroviridae; Lentivirus.
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HIV; M15897; VPR$K6W78.
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relationship
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Pfam; PF00522; VPR;
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(R ORF PROTEIN)
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(R ORF PROTEIN).
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 retroviruses
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Lentivirus.
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RESULT 10
GAT1_CHICK
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01-AUG-1990 (Rel. 15, Las
20-AUG-2001 (Rel. 40, Las
ERYTHROID TRANSCRIPTION F
PROTEIN) (NF-ElA).
                                                                   umichinski J.G., Clore G.M., Schaad O., Appella E., Stahl S.J., Gronenborn A.M.; "NNR structure of a specific DNA complete domain of GATA-1."; Science 261.47°
   Tjandra
"Use of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GAT1_CH
P17678;
                           STRUCTURE BY NMR OF 158-223. MEDLINE=97448676; PubMed=9303001;
                                                                                                                                                                                                        "Activity and tissue-specific NF-El multigene family.";
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Eukaryota: Metazoa: Chor
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                                                                                                                                                                                               Genes Dev.
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Pfam; PF00522; VPR; 1.
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Dev. 4:1650-1662(1990).
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an email to license@isb-sib.ch):
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InterPro; IPR00679; ZnF_GATA.
InterPro; IPR001164; Znf_GCS.
Pfam; PF00320; GATA; 2.
Pf1NTS; PR00619; GATAZNFINGER.
SMARF; SM00401; ZnF_GATA_ZN_FINGER_1; 2.
PROSITE; PS00344; GATA_ZN_FINGER_1; 2.
Plasmodium vivax
Eukaryota; Alveol
NCBI_TaxID=5856;
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PIR; A32993; A32993.
PDB; IGAT; 31-OCT-93.
PDB; 2CAT; 28-JAN-98.
PDB; 3CAT; 28-JAN-98.
PDB; 1GAU; 31-OCT-93.
                                                                                              CSP_PLAVS
P13826;
01-JAN-1990
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                                                01-JAN-1990 (Rel. 13, Last sequence updat. 20-AUG-2001 (Rel. 40, Last annotation upd. CIRCUMSPOROZOITE PROTEIN (CS) (FRAGMENT). Plasmodium vivax (strain Salvador I).
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-i- FUNCTION: TRANSCRIPTIONAL ACTIVATOR WHICH PROBABLY SERVES GENERAL SWITCH FACTOR FOR ERVTHROID DEVELOPMENT. IT BINDS SITES WITH THE CONSENSUS SEQUENCE (A/T)GATA(A/G) WITHIN RESIDENCE (A/T)GATA(A/G)
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DOMAIN: THE TWO FINGERS ARE FUNCTIONALLY DISTINCT AND COOPERATE
ACHIEVE SPECIFIC, STABLE DAN BUNDING. THE FIRST FINGER IS
NECESSARY ONLY FOR FULL SPECIFICITY AND STABILITY OF BINDING,
WHEREAS THE SECOND ONE IS REQUIRED FOR BINDING (BY SIMILARITY).

SIMILARITY: CONTAINS 2 GATA-TYPE ZINC FINGERS.
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SUBCELLULAR LOCATION: NUCLEAR
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PS00344; GATA_ZN_FINGER_1; 2.
PS50114; GATA_ZN_FINGER_2; 2.
ption regulation; Accitvator; DNA-binding; Erythrocyte;
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110 134 GATA-TYPE 1.
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61.5%;
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Best Local S
Matches S
ARROL D. E., Barnwell J.W., Stewart M.J.;

ARROL D. E., Barnwell J.W., Stewart M.J.;

"Does biased gene conversion influence polymorphism in the circumsporozoite protein-encoding gene of Plasmodium vivax?";

Proc. Natl. Acad. Sci. U.S.A. 85:8102-8106(1988).

-i- FUNCTION: THE CIRCUMSPOROZOITE PROTEIN IS THE IMMUNODOMINANT SURPACE ANTIGEN ON THE SPOROZOITE (THE INFECTIVE STAGE OF THE MALARIA PARASITE THAT IS TRANSMITTED FROM THE MOSQUITO TO THE
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P08677;
01-JAN-1988
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SEQUENCE FROM N.A.
MEDLINE=86044510; PubMed=2414847;
MEDLINE=86044510; PubMed=2414847;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CIRCUMSPOROZOITE PROTEIN PRECURSOR Plasmodium vivax (strain Belem). Eukaryota; Alveolata; Apicomplexa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-87194878; PubMed-2437120;
de la Cruz V.F., Lal A.A., Welsh J.A., McCutchan T.F.;
de la Cruz V.F., Lal A.A., Welsh J.A., McCutchan T.F.;
"Evolution of the immunodominant domain of the circumsporozoite
protein gene from plasmodium vivax. Implications for vaccines.";
J. Biol. Chem. 262:6464-6467(1987).
-1- FUNCTION: THE CIRCUMSPOROZOITE PROTEIN IS THE IMMUNODOMINANT
SURFACE ANTIGEN ON THE SPOROZOITE (THE INFECTIVE STAGE OF THI
MALARIA PARASITE THAT IS TRANSMITTED FROM THE MOSQUITO TO THI
VERTEBRATE HOST).
                                                                                                                                                    MEDLINE=89042133; PubMed=3054880; Arnot D.E., Barnwell J.W., Stewar
                                                                                                                                                                                                                                                    Science
                                                                                                                                                                                                                                                                        "Circumsporozoite protein of Plasmodium characterization of the immunodominant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-FEB-1996
20-AUG-2001
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SEQUENCE FROM N.A.
MEDLINE=86070222; PubMed=2416057;
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33, Last sequence update)
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; 308EFD5BBC15DFC3 CRC64;
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Q03110;
Q1-JUN-1994
Q1-JUN-1994
Q1-AUG-2001
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                                                                                                                                                                                                                                      Goldman I.F., Qari S.H., Millet P.G., Collins "Circumsporozoite protein gene of Plasmodium vivax-like monkey malaria parasite.";
                                                                                                                                                                                                                                                                                                                                                                                            Plasmodium simium.
Eukaryota; Alveolata;
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CIRCUMSPOROZOITE
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CHAIN
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InterPro; IPR000884; TSP1.
Pfam; PF00090; tsp_1; 1.
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MEDLINE=93149205; PubMed=8426613;
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modified and this statement is not removed.
entitles requires a license agreement (See )
or send an email to license@isb-sib.ch).
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                                      MISCELLANEOUS: THE C-TERMINAL REGION IS PROBABLY ANCHORING THE PROTEIN TO THE CELL MEMBRANE. THE R WOULD BE THE SURFACE ANTIGEN OF THE ORGANISM.
SIMILARITY: CONTAINS 1 TSP TYPE-1 DOMAIN.
                                                                                                                                          ax-like monkey malaria parasite.";
. Biochem. Parasitol. 57:177-180(1993).

FUNCTION: THE CIRCUMSPOROZOITE PROTEIN IS THE IMMUNODOMINANT SURFACE ANTIGEN ON THE SPOROZOITE (THE INFECTIVE STAGE OF THE MALARIA PARASITE THAT IS TRANSMITTED FROM THE MOSQUITO TO THE UPERFEDARME MALARIA PARASITE THAT IS TRANSMITTED FROM THE MOSQUITO TO THE UPERFEDARME MALARIA PARASITE.
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MISCELLANBOUS: THE C-TERMINAL REGION IS PROBA ANCHORING THE PROTEIN TO THE CELL MEMBRANE. T WOULD BE THE SURFACE ANTICEN OF THE ORGANISM. SIMILARITY: CONTAINS 1 TSP TYPE-1 DOMAIN.
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SWISS-PROT
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20ITE PROTEIN PRECURSOR (CS).
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is copyright.
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G-Q-P.
G -> E (IN REF. 1)
G -> R (IN REF. 1)
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Pred. No. 8;
1; Mismatches
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                                                                                                                                                                                                                                                                            use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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the Euro
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Morris B.A.M., Richardson K.A., Haley A., Zhan X., Thomas J.E., "The nucleotide sequence of the infectious cloned DNA component tobacco yellow dwarf virus reveals features of geminiviruses
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InterPro; IPR003067; Crcmsprzoite.
InterPro; IPR000884; TSP1.
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InterPro; IPR002621; Gemini_mov.
Pfam; PF01708; Gemini_mov; 1.
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NCBI_TaxID=31599;
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Viruses; ssDNA
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SMART; SM00209; TSP1; 1.
PROSITE; PS50092; TSP1; 1.
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6; Conserv
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Bioinformatics Institute. The
Profit institutions as long
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"Paralogous origin of the rhodopsinlike opsin genes in lizards.";

J. Mol. Evol. 40:594-600(1995).

-i- FUNCTION: VISUAL PIGMENTS ARE THE LIGHT-ABSORBING MOLECULES THAT-
-I- FUNCTION: TISION. THEY CONSIST OF AN APOPROTEIN, OPSIN, COVALENTLY
LINKED TO CIS-RETINAL. THIS OPSIN USES A VITAMIN-A2 CHROMOPHORE.
-i- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
-i- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
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P51471;
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01-OCT-1996
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01-OCT-1996 (Rel. 34, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
20-AUG-SENSITIVE OPSIN (BLUE PHOTORECEPTOR PICKENT) (RH2 OPSIN).
Anolis carolinensis (Green anole) (American chameleon).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                            DOMAIN
TRANSMEM
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DOMAIN
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PRINTS; PR00237; GPCRHODOPSN.
PRINTS; PR00238; OPSIN.
PRINTS; PR00579; RHODOPSIN.
PROSTTE; PS00737; G_PROTEIN_RECEP_F1_1;
PROSTTE; PS00238; G_PROTEIN_RECEP_F1_2;
PROSTTE; PS00238; OPSIN; 1.
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NCBI_TaxID-28377;
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Phosphorylation;
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MEDLINE=95371134; PubMed=7643409;
   TRANSMEM
                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR000276; GPCR_Rhodpsn
InterPro; IPR001760; Opsin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the El
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LRRPGEGNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                $79167; AAB35062.1; JOINED
$79124; AAB35062.1; JOINED
$79134; AAB35062.1; JOINED
$79165; AAB35062.1; JOINED
$79166; AAB35062.1; JOINED
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X
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    email to license@isb-sib.ch).
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114
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153
177
203
273
285
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Retinal protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                 G-protein
                                                                                                                                                                                                                                                                                                                                                                                                                                 coupled receptor;
4 (POTENTIAL).
EXTRACELLULAR.
5 (POTENTIAL).
CYTOPLASMIC.
6 (POTENTIAL).
EXTRACELLULAR.
7 (POTENTIAL).
                                                                                                                                                                                                                                                2 (POTENTIAL).
EXTRACELLULAR.
3 (POTENTIAL).
                                                                                                                                                                                       CYTOPLASMIC.
                                                                                                                                                                                                                                                                                                            CYTOPLASMIC 2 (POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                    EXTRACELLULAR.
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                                                                                                                                                                                                                                            (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                     (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Transmembrane;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             G-PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            There are no rest
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                                                                                                                                                                                                                                                                                                                                                                                                                             e; Glycoprotein; Vision;
Lipoprotein; Palmitate.
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FT DOMAIN

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355

CYTOPLASMIC. ..) (POTENTIAL).

FT CARBOHYD

15

15

N-LINKED (GLCNAC. ..) (POTENTIAL).

FT CARBOHYD

200

N-LINKED (GLCNAC. ..) (POTENTIAL).

FT CARBOHYD

200

N-LINKED (GLCNAC. ..) (POTENTIAL).

FT CARBOHYD

300

N-LINKED (GLCNAC. ..) (POTENTIAL).

FT BINDING

296

FT LIPID

322

322

PALMITATE (BY SIMILARITY).

FT LIPID

323

323

PALMITATE (BY SIMILARITY).

FT LIPID

325

FT LIPID

327

SEQUENCE

355

AA;

39983

MW;

555B671A4DE96EA6 CRC64;

Ouery Match

Best Local Similarity

87.5%;

Pred. No. 9.1;

Matches

7;

Conservative

1;

Mismatches

0;

Indels

0;

Gaps

0;

Od

1 KHKKLKOP

1 KHKKLKOP

1 KHKKLROP

1 KHKKLROP

1 STORMAN

Search completed: January

29, 2002, 11:13:38

Job time: 814 sec
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088021 chimpanzee Q88041 chimpanzee Q88045 chimpanzee Q88047 chimpanzee Q88048 chimpanzee Q88051 chimpanzee Q88052 chimpanzee Q88060 chimpanzee Q85050 human t-cel Q1785 chimpanzee Q85017 chimpanzee Q95017 chimp
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Zheng C., Xie P., Chen Y.;
Zheng C., Xie P., Chen Y.;
Zheng C., Xie P., Chen Y.;
Molecular closhing and expression of circumsporozoite protein gene "Molecular closhing and expression of circumsporozoite protein gene from Plasmodium falciparum FCC-1/HN strain in mycobacterium.";
Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF315469; AAG37074.1;
InterPro; IPR000884; TSP.
InterPro; IPR000884; TSP.
Pfam; PF00090; tsp_1; 1
PRINTS; PR01303; CRCMSPRZOITE.
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
CIRCUMSPOROZOITE PROTEIN (FRAGMENT).
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Q8
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01-NOV-1996 (TrEMBLrel. 01, Created)
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Q9BPK7
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Q25212
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         Query Match 100.
Best Local Similarity 100.
Matches 13; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=5833;
      SEQUENCE
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Q25829
ID Q2
AC Q2
DT 01
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                                    version 4.5
- 2000 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                   - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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sp_bacteria:*
sp_fung1:*
sp_human:*
sp_invertebrate:*
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                                    GenCore
Copyright (c) 1993
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sp_vertebrate:*
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sp_phage:*
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Match Length
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01-NOV-1996 (TrEMBLrel. 01,
01-NOV-1996 (TrEMBLrel. 01,
01-JUN-2001 (TrEMBLrel. 17,
                                                                                                                                                                                Query Match 100.
Best Local Similarity 100.
Matches 13; Conservative
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Best Local Similarity 100.
Matches 13; Conservative
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                                                                                                                                                                                                                                                 109 KHKKLKQPGDGNP 121
                                                                                           Pfam; PF00090; tsp_1;
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      SEQUENCE FROM N.A.
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                   STRAIN=K1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=K1;
MEDLINE=84250215; PubMed=6204383;
Dame J.B., Williams J.L., McCutchan T.F., Weber J.L., Wirtz R.A.,
Dame J.B., Williams J.L., McCutchan T.F., Weber J.L., Wirtz R.A.,
Hockmeyer W.T., Maloy W.L., Haynes J.D., Schneider I., Roberts D.,
Sanders G.S., Reddy P.E., Diggs C.L., Miller L.H.;
"Structure of the gene encoding the immunodominant surface antigen on
the sporozolic of the human malaria parasite Plasmodium falciparum.";
Science 225:593-599(1984).
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                                                              Alveolata; Apicomplexa; Haemosporida; Plasmodium.
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 75; DB 5; Length 416; 100.0%; Pred. No. 4.8e-05; live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                  Submitted (MAR-1992) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      la Cruz V.F.;
Submitted (MAR-1992) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                     D3EF560B2D368DE9 CRC64;
01-NOV-1996 (TrEMBLrel. 01, Last sequence update) 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                420 AA.
                                                                                                                                                                                                                                                                                                                 Jongwutiwes S., Tanabe K., Kanbara H.;
Mol. Biochem. Parasitol. 0:0-0(0).
EMBL; M83172; AAA29550.1;
                                                                                                                                                                                                                                                                                                                                                    Interpro; IPR000884; TSP1.
InterPro; IPR03067; Crcmsprzoite.
Pfam; PF00090; tsp_1; 1.
PRINTS; PR01303; CRCMSPRZOITE.
SMART; SM00209; TSP1; 1.
                                                                                                              STRAIN=MAD20;
MEDLINE=84250215; PubMed=6204383;
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           01-JUN-2001 (TrEMBLrel. 1 CIRCUMSPOROZOITE PROTEIN.
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Best Local Similarity 100.
Matches 13; Conservative
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                                                  Plasmodium falciparum.
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                                                              Eukaryota; Alveo
NCBI_TaxID=5833;
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                                                                                                                                                                                                                                            STRAIN=MAD20;
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                                                                                                                                                                                                                                                                                                                         Length 420;
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                                                                                                                                                         PRINTS; PR01303; ČRCMSPRZOITE.
PR0SITE; PS500924; TSP1; 1.
SMART; SM00209; TSP1; 1.
SEQUENCE 420 AA; 45318 MW; F7F70F1C4939DEA7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     45155 MW; 3A85B92432C2893C CRC64;
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Last annotation update)
                                                                                                                                                                                                                                                                                           100.0%; Score 75; DB 5; I
100.0%; Pred. No. 4.8e-05;
Micmatches 0;
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MOI Biochem. Parasitol. 0:0-0(0).
EMBL; M83161; AAA29574.1; -
InterPro: IPR000884; TSP1.
InterPro: IPR003067; Crcmsprzoite.
PRIMTS; PR01303; CRCMSPRZOITE.
SMART; SM00209; TSP1: 1.
Jongwutiwes S., Tanabe K., Kanbara H., Mol. Biochem. Parasitol. 0:0-0(0). EMBL; M83174; AaA29552.1; InterPro; IPR000884; TSPl. InterPro; IPR003067; Cromsprzoite.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
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MEDLINE=84250215; PubMed=6204383;
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MEDLINE-84250215; PubMed-6204383;
Dame J.B., Williams J.L., McCutchan T.F., Weber J.L., Wirtz R.A.,
Hockmeyer W.T., Maloy W.L., Haynes J.D., Schneider I., Roberts D.,
Sanders G.S., Reddy P.E., Diggs C.L., Miller L.H.;
"Structure of the gene encoding the immunodominant surface antigen on
the sporozoite of the human malaria parasite Plasmodium falciparum.";
-I- MISCELLANEOUS: THE C-TERMINAL REGION IS PROBABLY USED FOR ANCHORING THE PROTEIN TO THE CELL MEMBRANE. THE REPEAT SEQUENCES WOULD BE THE SURFACE ANTIGEN OF THE ORGANISM.

EMBL. M57499; AAA63422.1;

InterPro: IPR000884; TSP1.

InterPro: IPR000884; TSP1.

PFRM: PFR00090; tsp_1: 1.

PRINTS, PR01303; CRCMSPRZOITE.

SMART; SM0209; TSP1: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Plasmodium falciparum.
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5833;
                                                                                                                                                                                                                                                                                                    Length 424;
                                                                                                                                                                                                                                                                                                                                    Indels
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Submitted (MAR-1992) to the EMBL/GenBank/DDBJ databases.
EMBL; M83155; AAA295681; -
EMBL; M83152; AAA295481; -
EMBL; M83152; AAA2956511; -.
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                                                                                                                                                                           BY SIMILARITY.
CIRCUMSPOROZOITE PROTEIN.
4-RESIDUE TANDEM REPEATS.
                                                                                                                                                                                                                                               BF6D0F906C664B8F CRC64;
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Last annotation update)
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Pred. No. 4.9e-05;
; Mismatches 0;
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                                                                                                                                                           Malaria; Repeat; Sporozoite; Signal
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Interpro; IPR003067; Crcmsprzoite.
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SMART; SM00209; TSP1; 1.
SEQUENCE 432 ***
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Best Local Similarity 100.0%;
Matches 13; Conservative 0
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424 AA;
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SEQUENCE
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01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1990 (TrEMBLrel. 17, Last annotation update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
CIRCUMSPOROZOITE PROTEIN (CS) PRECURSOR, VARIANT 2 (FRAGMENT).
                                                                                                                                                         Plasmodium falciparum.
Eukaryota: Alveolata; Apicomplexa; Haemosporida; Plasmodium.
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 75; DB 5; Length 424; 100.0%; Pred. No. 4.9e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Jongwitiwes S., Tanabe K., Kanbara H.;
Submitted (MAR-1992) to the EMBL/GenBank/DDBJ databases.
EMBL: M83169; AAA29547.1; -.
EMBL: M83149; AAA29562.1; -.
InterPro: IPR00884; TSP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (MAR-1992) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     45592 MW; F20CEB60636DB98E CRC64;
                                  Q27425 PRELIMINARY; PRT; 424 AA. Q27425; 01-NOY-1996 (TrEMBLrel. 01, Created) 1.NOY-1996 (TrEMBLrel. 01, Last sequence update) 01-JUN-2001 (TrEMBLrel. 17, Last annotation update) CIRCUMSPOROZOITE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
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MEDLINE~91270295; PubMed~2052038;
                                                                                                                                                                                                                                              STRAIN-844;
MEDLINE-84250215; PubMed-6204383;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00090; tsp_1; 1.
PRINTS; PR01303; CRCMSPRZOITE.
SMART; SM00209; TSP1; 1.
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Matches 13; Conserv
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SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
                                                                                                                                                                                           NCBI_TaxID=5833;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-844;
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Length 432; DB 5;

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MEDLINE=84250215; PubMed=6204383;
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5833;
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NCBI_TaxID=5833;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
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100.0%; Pred. No. 4.9e-05;
Live 0; Mismatches 0;
 Pred. No. 4.9e-05;
Mismatches 0;
                                                                                                                                                                                       432 AA.
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                     Mismatches
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Mol. Blochem. Parasitol. 0:0-0(0).
EMBL, M83165, AAA29543.1, -
Interpro; IPR000884; TSP1.
Interpro; IPR000884; TSP1.
Interpro; IPR000804; TSP1.
Pfam; PF001909; tsp.1; 1.
PRINTS; PR01303; CRCMSPRZOITE.
SEQUENCE 432 AA; 46385 WW; 2CE8D9.
                                                                                                                                                                                                                            Created)
                                                                                                                                                                                       PRT;
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MEDLINE-84250215; PubMed-6204383;
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 100.0%;
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   Best Local Similarity 100 Matches 13; Conservative
                                                                                                                                                                                       PRELIMINARY;
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                                                                              Plasmodium falciparum.
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Best Local Similarity
Matches 13; Conserv
                                                          1 KHKKLKQPGDGNP
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SEQUENCE FROM N.A.
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01-JUN-2001
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01-NOV-1996
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MEDLINE=84200215; PubMed=6204383;

MEDLINE=84200215; PubMed=6204383;

Dame J.B., Williams J.L., McCutchan T.F., Weber J.L., Wirtz R.A.,

Hockmeyer W.T., Maloy W.L., Haynes J.D., Schneider I., Roberts D.,

Sanders G.S., Reddy P.E., Diggs C.L., Miller L.H.;

"Structure of the gene encoding the immunodominant surface antigen on
the sporozoite of the human malaria parasite Plasmodium falciparum.";

Science 225:593-599(1984).
Dame J.B., Williams J.L., McCutchen T.F., Weber J.L., Wirtz R.A., Hockmeyer W.T., Maloy W.L., Haynes J.D., Schneider I., Roberts D., Sanders G.S., Reddy P.E., Diggs C.L., Miller L.H.; "Structure of the gene encoding the immunodominant surface antigen on the sporozoite of the human malaria parasite Plasmodium falciparum."; Science 225:593-599(1984).
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NCBL_TaxID=5833;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 436;
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Submitted (MAR-1992) to the EMBL/GenBank/DDBJ databases.
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Submitted (MAR-1992) to the EMBL/GenBank/DDBJ databases.
EMBL; M83164; AAA295421; ...
EMBL; M83163; AAA295531; ...
EMBL; M83163; AAA29576.1; ...
                                                                                                                                                                                                                                                                   la Cruz V.F.; Submitted (MAR-1992) to the EMBL/GenBank/DDBJ databases
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Last annotation update)
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100.0%; Pred. No. 5e-05;
iive 0; Mismatches 0;
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Jongwutiwes S., Tanabe K., Kanbara H.;
Mol. Blochem, Parasitol. 0:0-0(0).
EMBL, M83167; AAA29545.1; -
InterPro; IPR000884; TSPI.
InterPro; IPR003067; Cromsprzoite.
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InterPro; IPR000884; TSP1.
InterPro; IPR003067; Crcmsprzoite.
PRMTS; PR01303; CRCMSPRZOITE.
SMART; SM00209; TSP1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      46688 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 13; Conserv
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Dame J.B., Williams J.L., McCutchan T.F., Weber J.L., Wirtz R.A., Hockmeyer W.T., Maloy W.L., Haynes J.D., Schneider I., Roberts D., Sanders G.S., Reddy P.E., Diggs C.L., Miller L.H.; "Structure of the gene encoding the immunodominant surface antigen on the sporozoite of the human malaria parasite Plasmodium falciparum."; Science 225:593-599(1984).
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-1- MISCELLANEOUS: THE C-TERMINAL REGION IS PROBABLY USED FOR ANCHORING THE PROTEIN TO THE CELL MEMBRANE. THE REPEAT SEQUENCES WOULD BE THE SURFACE ANTIGEN OF THE ORGANISM.

EMBL, M57489, AAA63421.1;

Interpro, IPR000884; TSP1.

Interpro, IPR0003067; Cromsprzoite.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein gene.";
Mol. Biochem. Parasitol. 45:179-182(1991).
-!- FUNCTION: THE CIRCUMSPOROZOITE PROTEIN IS THE IMMUNODOMINANT
SURFACE ANTIGEN ON THE SPOROZOITE (THE INFECTIVE STAGE OF THE
MALARIA PARASITE THAT IS TRANSMITTED FROM THE MOSQUITO TO THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Clonal variation in the Plasmodium falciparum circumsporozoite
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-2001 (TrEMBLrel. 17, Last annotation update)
CIRCUMSPOROZOITE PROTEIN (CS) PRECURSOR, VARIANT 1 (FRAGMENT).
                                  Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBL_TaxID=5833;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 452;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                   Submitted (MAR-1992) to the EMBL/GenBank/DDBJ databases
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100.0%; Pred. No. 5.2e-05;
tive 0; Mismatches 0;
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Mol. Biochem. Parasitol. 0:0-0(0).
EMBL; M83156; AAA29569.1;
InterPro; IPR000884; TSP1.
InterPro; IPR03067; Crcmsprzoite.
PRAM: PR00090; ESP1: 1.
PRINTS; PR01303; CRCMSPRZOITE.
PROSITE; PS50092; TSP1: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. MEDLINE-91270295; PubMed-2052038;
                                                                                                                                 MEDLINE-84250215; PubMed-6204383;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SMART; SM00209; TSP1; 1.
SEQUENCE 452 AA; 48431 MW;
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PRINTS; PR01303; CRCMSPRZOITE.
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Best Local Similarity 100.
Matches 13; Conservative
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                      Plasmodium falciparum.
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                                                                                                                                                                                                                                                                                                                           la Cruz V.F.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Plasmodium falciparum.
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5833;
                                                                                                             100.0%; Score 75; DB 5; Length 436; 100.0%; Pred. No. 5e-05; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 75; DB 5; Length 442; 100.0%; Pred. No. 5.1e-05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BFAF9D939D7862FF CRC64;
                                                    46875 MW; F102683C5C1DC85A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            025834 PRELIMINARY; PRT; 452 AA. 025834; ILNOV-1996 (TrEMBLrel. 01, Created) 01-NOV-1996 (TrEMBLrel. 01, Last sequence update) 01-JUN-2001 (TrEMBLrel. 17, Last annotation update) CIRCUMSPOROZOITE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                             01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                               442 AA
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Jongwithwes S., Tanabe K., Kanbara H.;
Mol. Biochem. Parasitol. 0.0-0(0).
EMBL; M83173; AAA29551.1; -.
                                                                                                                                                                                                                                                                                                                               PRT;
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InterPro; IPR003067; Crcmsprzoite.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00090; tsp.1; 1. PRINTS; PR01303; CRCMSPRZOITE, SMART; SM00209; TSP1; 1. SEQUENCE 447 A.
PRINTS; PR01303; CRCMSPRZOITE
                  PROSITE; PS50092; TSP1; 1.
                                                                                                      Ouery Match
Best Local Similarity 100.
Matches 13, Conservative
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Best Local Similarity 100.
Matches 13; Conservative
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                                  SMART; SM00209; TSP1;
SEQUENCE 436 AA; 46
                                                                                                                                                                                         1 KHKKLKQPGDGNP 13
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Novembre F.J., Hirsch V.M., McClure H.M., Fultz P.N., Johnson P.R.;
"SIV from stump-tailed macaques: molecular characterization of a
highly transmissible primate lentivirus.";
Virology 186:783-787(1992).
EMBL; M83293; AAA91943.1; -.
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5833;
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STRAIN-SANTA LUCIA, SAL1;

AQATI S.H., Lal A.A.;

Usubmitted (FEB-1955) to the EMBL/GenBank/DDBJ databases.

REMBL; U20969; AAA63153.1;

InterPro; IPR00084; TSP1.

R InterPro; IPR000867; Cremsprzoite.

R PRINTS; PR01303; CRCMSPRZOITE.

R PRINTS; SM00209; TSP1.1.

SEQUENCE 408 AA; 43871 MW; A545BE517822515C CRC64;
                                                                                                                                                  92.0%; Score 69; DB 5; Length 393; 92.3%; Pred. No. 0.0005; Live 0; Mismatches 1; Indels
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Pred. No. 0.00052;
0; Mismatches 1; Indels
SMART; SM00209; TSP1; 1.
Malaria; Repeat: Sporozoite; Signal.

1 16 POTENTIAL.

1 7 > 393 CIRCUMSPOROZOITE PROTEIN.
4-RESIDUE TANDEM REPEATS.
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
CIRCUMSPOROZOITE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
VPR PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chimpanzee immunodeficiency virus (SIV(cpz)) (CIV). Viruses: Retroid viruses; Retroviridae; Lentivirus.
                                                                                                                                                                                                                                                                                                        408 AA.
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Best Local Similarity 92.3%;
Matches 12; Conservative
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                                                                                             Score 48; DB 12; Length 101;
Pred. No. 0.62;
3; Mismatches 3; Indels
InterPro; IPR000012; HIV_ORFXR.
Pfam; PF00522; VPR; 1.
PRUMTS; PR044; HIVVPRVPX.
PRQUENCE 101 AA; 11448 MW; 2E48F2E2AA187911 CRC64;
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                                                                                                64.0%;
53.8%;
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Best Local Similarity 53.8
Matches 7; Conservative
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January 29, 2002, 11:06:40 ; Search time 353.23 Seconds (without alignments) 17.293 Million cell updates/sec
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Sequence 2, Al
Sequence 34, Al
Sequence 34, Sequence 513, Sequence 613, Sequence 613,
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| cgn2_6/ptodata/2/paa/USO6_COMB.pep:*
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Copyright (c) 1993 - 2000 Compugen Ltd.
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US-00-292-638-6
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US-08-911-312A-34
US-08-974-549-613
US-09-432-503-613
US-09-376-330-4
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Maximum Match 100%
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## ALIGNMENTS

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Sequence 25, Application US/09763397A

Sequence 25, Application US/09763397A

GENERAL INFORMATION:

APPLICANT: The Government of the United States of America, as represented by the APPLICANT: Secretary of the Department of Health and Human Services, Centers for APPLICANT: Lal, Altaf A.

APPLICANT: Dail, Altaf A.

APPLICANT: Plug Shi, Ya

APPLICANT: Hasnain, Seyed E.

TITLE OF INVENTION: Recombinant Multivalent Malarial Vaccine Against Plasmodium Fa
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100.0%; Pred. No. 4.8e-07;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/763,397A CURRENT FILING DATE: 2001-02-16 PRIOR APPLICATION NUMBER: US 60/097,703 PRIOR FILING DATE: 1998-08-21 PRIOR APPLICATION NUMBER: PCT / US99/18869 PRIOR FILING DATE: 1999-08-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 26
SOFTWARE: PatentIn version 3.1
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Best Local Similarity 100.C
Matches 22; Conservative
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US-09-763-397A-25
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                                                                                APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin B.
APPLICANT: Harley, Calvin B.
TITLE OF INVENTION: Telomerase Reverse Transcriptase NUMBER OF SEQUENCES: 170
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
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100.0%; Pred. No. 1.1e-05;
Live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/911,312 FILING DATE: 14 AUG 1997 CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Binhorn, Gregory P.
REGISTRATION NUMBER: 38,440
REPERENCE/DOOKET NUMBER: 015389-002500US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEPHONE: (415) 576-0300
INFORMATION FOR SEQ ID NO: 34:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CCASSITECATION 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-0CT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/866,017
FILING DATE: 25-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
PRIOR APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible OPERATING SYSTEM: 'PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MKFLVNVALVEMVVISYIYAD 22
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           Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 1189 amino acids
                                                                                                                                                                                                                                                                                                                                                                        Floppy disk
Cech, Thomas R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 100.9
Best Local Similarity 100.9
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 , MOLECULE TYPE: protein US-08-911-312-34
                                                                                                                                                                                                                                                                                                                          ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                              CITY: San Francisco
STATE: California
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                                                                                                                                                                                                                                                                                                            USA
                                                                                                                                                                                                                                                                                                            COUNTRY:
                                         APPLICANT:
APPLICANT:
  APPLICANT:
                       APPLICANT
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; Sequence 2, Application US/09763397A
; GENERAL INFORMATION:
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America, as represented by the
; APPLICANT: Control and Prevention
; APPLICANT: Lal, Altaf A.
APPLICANT: Hasnahi, Seyed E.
; APPLICANT: Hasnahi, Seyed E.
; APPLICANT: Hasnahi, Seyed E.
; APPLICANT: Ping Shi, Ya
APPLICANT: Pring Shi, Ya
APPLICANT: Pang Shi, Ya
APPLICANT: NUMBER: US/09/763,397A
CURRENT FILING DATE: 1999-08-21
; PRIOR APPLICATION NUMBER: DCT / US99/18869
; RRIOR FILING DATE: 1999-08-19
; RRIOR FILING DATE: 1999-08-19
; NUMBER OF SEQ ID NOS: 26
; SEQ ID NO 2
; LENGTH: 350
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 129;
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                                                                                                                            Sequence 6, Application US/60292638

GENERAL INFORMATION:

APPLICARMY: MOSSEY, Mohamad A.

TITLE OF INVENTION: Non-anaphylactogenic IgE vaccines

FILE REFERENCE: PC11011A

CURRENT APPLICATION NUMBER: US/60/292,638

CURRENT FILIKO DATE: 2001-05-22

NUMBER OF SEQ ID NOS: 28

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 6

LENGTH: 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 10%; DB 21;
100.0%; Pred. No. 4.1e-06;
Live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 108; DB 24;
100.0%; Pred. No. 1.9e-06;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: PRT;
; ORGANISM: Baculovirus expressed human CH3 domain
US-60-292-638-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; CTHER INFORMATION: Recombinant DNA/Protein US-09-763-397A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         %208-911.312-34
; Sequence 34, Application US/08911312
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MKFLVNVALVEMVVYISYIYAD 22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MKFLVNVALVEMVVXISYIYAD 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MKFLVNVALVFMVVYISYIYAD 22
         1 MKFLVNVALVFMVVYISYIYAD 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 100.
Best Local Similarity 100.
Matches 22; Conservative
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                                                                                                                        US-60-292-638-6
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US-08-911-312A-34

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APPLICANT: Harley, Calvin
APPLICANT: Harley, Calvin
APPLICANT: Andrews, William H.
TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND TITLE OF INVENTION: THERAPEUTIC METHODS
NUMBER OF SEQUENCES: 335
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/912,951
FILING DATE: 14-AUG-1997
CLASSIFICATION ADATA:
APPLICATION NUMBER: US/08/912,951
FILING DATE: 09-MAY-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/846,419
FILING DATE: 18-APR-1997
CLASSIFICATION ADATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 18-APR-1997
CLASSIFICATION ADATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
CLASSIFICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
CLASSIFICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
CLASSIFICATION NUMBER: US 08/724,643
FELING DATE: US 08/724,643
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: United States of America ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPAtible
                                                                                         Sequence 325, Application US/08912951
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Greeg B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 325:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1189 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid STRANDEDNESS:
                                 RESULT 6
US-08-912-951-325
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                                                                                         APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Nakamura, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin B.
APPLICANT: Andrews, William
TITLE OF INVENTION: Telomerase Reverse Transcriptase
NUMBER OF SEQUENCES: 171
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: TBM PC compatible
CUERATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, version #1.30
CUEASIFICATION NUMBER: US/08/911,312A
FILING DATE: 14-AuG-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 10-CT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
FILING DATE: 25-APR-1997
FILING DATE: 25-APR-1997
FILING DATE: 25-APR-1997
FILING DATE: 05-APR-1997
FILING APPLICATION NUMBER: US 08/851,843
FILING RAPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor CITY: San Francisco STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Einhorn, Gregory P.
REGISTRATION NUMBER: 38,440
REFERENCE/DOCKET NUMBER: 015389-002500US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
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FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 08/854,050 FILING DATE: 09-MAY-1997 PRIOR APPLICATION DATA:
Sequence 34, Application US/08911312A
GENERAL INFORMATION.
APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
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TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 34:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH:
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Length 1189; Indels

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOUTHWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: 05/08/974,549 FILING DATE: 19-NOV-1997 CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E: Townsend and Townsend and Crew LLP Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE DOCKET NUMBER: 015389-002610US TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PALLOCATION UNBER: US 08/912,951
PRIOR APPLICATION UNBER: US 08/912,951
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION SASO
PRIOR APPLICATION DATA
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-007-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/811,312
FILING DATE: 14-AUG-1997
PRIOR APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
                                                                                                                                                                 Sequence 613, Application US/08974549
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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REGISTRATION NUMBER: 36,429
                     1 MKFLVNVALVFMVVXISYIYAD 22
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INFORMATION FOR SEQ ID NO: 6
SEQUENCE CHARACTERISTICS:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
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STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  USA
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                                                                                                                                                 US-08-974-549-613
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melittin signal sequence and full length
hTRT protein"
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                                                                                                                                                                                                                                                                                            Length 1189;
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TITLE OF INVENTION: Human Telomerase Catalytic Subunit NUMBER OF SEQUENCES: 727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: FLOPDY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/432,503
FILING DATE: 02-Nov-1999
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Townsend and Townsend and Crew LLP
                                                                                                                                                                                                                                                                                            100.0%; Score 108; DB 13;
illarity 100.0%; Pred. No. 1.1e-05;
Conservative 0; Mismatches 0;
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APPLICATION NUMBER: 08/974,549
FILING DATE: CUNKNOWN>
PELLING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/865,1843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
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FILING DATE: 14-AUG-1997
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FILING DATE: 14-AUG-1997
PEPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 613, Application US/09432503
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
                                                                                                                                                                                                                                                                                                                                                                                  1 MKFLVNVALVFMVVYISYIYAD 22
                                                                                                                                                                                                                                                                                                                                                                                                      1 MKFLVNVALVFMVVXISYIYAD 22
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Harley, Calvin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
LENGTH: 1189 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
ZIP: 94111-3834
                                                                                  MOLECULE TYPE: protein
                                                                                                      FEATURE:
NAME/KEY: Protein
LOCATION: 1.1189
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
US-08-974-549-613
                   amino acid
                                                                  linear
                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 22; Conserv
                        TYPE: amino STRANDEDNESS
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TITLE OF INVENTION: SOLUBLE MHC METHODS OF (
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APPLICANT: Rhode, Peter R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Acevedo, Jorge
Burkhardt, Martin
Jiao, Jin-an
Wong, Hing C.
                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/960,190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: CORIESS, PETER F
REGISTRATION NUMBER: 33,860
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 48
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MKFLVNVALVEMVVYISYIYA 21
                                                                                                                                                                                                                       MEDIUM TYPE: Diskette COMPUTER: IBM COMPatible OPERATING SYSTEM: DOS
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COMPUTER READABLE FORM:
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LENGTH: 21 amino acids
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Best Local Similarity 100.
Matches 21; Conservative
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STRANDEDNESS: single
TOPOLOGY: linear
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; MOLECULE TYPE: protein
US-09-766-378-36
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MEDIUM TYPE: Diskett
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                                                                                                                                                                   COUNTRY:
                                                                                                                                            STATE:
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GENERAL INFORMATION:
APPLICANT: Tessier, Daniel C.
APPLICANT: Dignard, Daniel C.
APPLICANT: Bergeron, John J.M.
APPLICANT: Bergeron, John J.M.
APPLICANT: Thomas, David Y.
TITLE OF INVENTION: Wethod for screening for
TITLE OF INVENTION: und nucleic acid encoding for UGGT activity
FILE REFERENCE: 2139-9 "UG"
CURRENT APPLICATION NUMBER: US/09/376,330
CURRENT FILING DATE: 1999-08-18
NUMBER OF SEQ ID NOS: 35
SURPARE: FastSEQ for Windows Version 3.0
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                                                                                                                                                                                                                                                                                                    ; melittin signal sequence and full length; hTRT protein" sequence and full length; hTRT protein"; SEQUENCE DESCRIPTION: SEQ ID NO: 613:
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NAME: APPLE, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFRAT (415) 576-0300
INFORMATION FOR SEQ ID NO: 613:
SEQUENCE CHARACTERISTICS:
LENGTH: 1189 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 108; DB 18;
100.0%; Pred. No. 1.1e-05;
iive 0; Mismatches 0;
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100.0%; Pred. No. 2.8e-06;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT (CREANISM: Melittin Signal Peptide sequence US-09-376-330-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 36, Application US/09766378
GENERAL INFORMATION:
APPLICANT: Rhode, Peter R.
APPLICANT: Acevedo, Jorge
APPLICANT: Burkhardt, Martin
APPLICANT: Jiao, Jin-an
                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MKFLVNVALVFMVVXISXIYAD 22
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                                                                                                                                                                                                                                                                                     Protein
                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
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Best Local Similarity 100.
Matches 22; Conservative
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Best Local Similarity 100.
Matches 21; Conservative
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US-09-766-378-36
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LENGTH: 21
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Gaps
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ADDRESSEE: Dike, Bronstein, Roberts & Cushman, LLP
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APPLICANT: Wong, Hing C.
TITLE OF INVENTION: SOLUBLE MHC COMPLEXES AND
TITLE OF INVENTION: METHODS OF USE THEREOF
CORRESPONDENCE: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dike, Bronstein, Roberts & Cushman, LLP
STREET: 130 Water Street
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        94.4%; Score 102; DB 21; 100.0%; Pred. No. 2.8e-06;
                                                                                                                                                                                                                                                                             SOFTWARE: FSSISED FOR WINDOWS VERSION 2.0 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/766,378
FILING DATE:
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Washington
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US-08-782-481-43
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STATE:
                                                                                                                                 SEQ ID NO 5
LENGTH: 177
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                                                                                                                                                                        TYPE: PRT
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GENERAL INFORMATION:

APPLICANT: JOHNSON et al.

ITLE OF INVENTION: INHIBITION OF THE MHC CLASS II ANTIGEN PRESENTATION

TITLE OF INVENTION: PATHWAY AND PRESENTATION TO CD4+ CELLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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US-09-847-208-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 70;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Zhang, Ke
APPLICANT: Zhu, Daoccheng
TITLE OF INVENTION: EVSION MOLECULES AND TREATMENT OF
TITLE OF INVENTION: IGE-MEDIATED ALLERGIC DISEASES
FILE REPERENCE: UG67.002A
CURRENT APPLICATION NUMBER: US/09/847,208
CURRENT FILING DATE: 2001-05-01
FastSEQ for Windows Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match

94.4%; Score 102; DB 22;
Best Local Similarity 100.0%; Pred. No. 7.2e-06;
Matches 21; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94.4%; Score 102; DB 21;
100.0%; Pred. No. 2.8e-06;
live 0; Mismatches 0;
            CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/766,378A
FILING DATE: 19-Jan-2001
CLASSIFICATION NUMBER: US/09/766,378A
PRIOR APPLICATION NUMBER: 08/960,190
FILING DATE: 29-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: COTIESS, PETER F
REGISTRATION NUMBER: 33,860
FEFERENCE/DOCKET NUMBER: 34,860
TELEPHONE: 617-523-3400
TELEPHONE: 617-523-3400
                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 36:
US-09-766-378A-36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT FILING DATE: 2001-05-01
NUMBER OF SEQ ID NOS: 177
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 26, Application US/09847208
GENERAL INFORMATION:
APPLICANT: Saxon, Andrew
                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
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Best Local Similarity
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US-09-847-208-26
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LENGTH: 70
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APPLICANT: Johnson et al.

TITLE OF INVENTION: INHIBITION OF THE MHC CLASS II ANTIGEN PRESENTATION
TITLE OF INVENTION: PATHWAY AND PRESENTATION TO CD4+ CELLS
FILE REPERBACE: 0899-59399
CURRENT FILING DATE: 2000-68-01
PRIOR APPLICATION NUMBER: US/09/890, 806
CURRENT FILING DATE: 2000-00-01
PRIOR PELLING DATE: 2000-00-02
PRIOR PELLING DATE: 1999-02-02
NUMBER OF SEQ ID NOS: 7
SOFTWARE PALENTIN VET: 2.1
SEQ ID NO 5
LENGTH: 177
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GENERAL INFORMATION:
APPLICANT: Hean, Mich B.
APPLICANT: Hiatt, Andrew C.
APPLICANT: Fitchen, John H.
TITLE OF INFORTION: NOVEL EPITHELIAL TISSUE TARGETING AGENT NUMBER OF SEQUENCES: 108
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: Description of Artificial Sequence: chimera US-09-890-806-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 177;
                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: Description of Artificial Sequence: chimera
                                                                                                                                                                                                                                                                                                                                                                                                    Score 102; DB 1; Length 177;
Pred. No. 1.5e-05;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              score 102; DB 22;
Pred. No. 1.5e-05;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 102;
FILE REFERENCE: 0899-54203 Johnson
CURRENT APPLICATION NUMBER: PCT/US00/02740
CURRENT FILING DATE: 2000-02-02
EARLIER APPLICATION NUMBER: 60/118,287
EARLIER FILING DATE: 1999-02-02
SALLIER FILING DATE: 1999-02-02
NUMBER OF SEO ID NOS: 7
SOFTWARE: PATENTIN Ver. 2.1
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100.0%; Pre
0; )
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                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 94.4%; Sc
Best Local Similarity 100.0%; P
Matches 21; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MKFLVNVALVFMVVYISYIYA 21
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                                                                                                                                                                                                                                                         ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 21; Conservative
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COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Decompatible
COMPUTER: Decompat
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Search completed: January 29, 2002, 11:06:41 Job time: 623 sec

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us-09-763-397a-25.rapn

e 2, Appli 24, A

Sequence Sequence S

Sequence Sequence

ALIGNMENTS

2, Appli 73229, A 108, App

Sequence

Sequence Sequence Sequence

1, Appli 1, Appli 5313, Ap 18, Appl 84, Appl

Sequence Sequence Sequence Sequence Sequence

Sequence

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Sequence 613, Application US/09402181A
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin B.
Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTY: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIDLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor
              US-09-966-262-328

US-09-886-055-349

US-09-804-291-349

US-09-991-212-1

US-09-965-521-1

US-09-966-521-18

US-09-966-521-18

US-09-966-521-18

US-09-966-521-13

US-09-966-521-13

US-09-830-123-15

US-09-830-123-15

US-09-889-442-108

US-09-989-442-108

US-09-989-442-108

US-09-986-443-34

US-09-968-443-34
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FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-CCT-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRICE DATE: 29-Sep-197
CLASSIFICATION NUMBER: US/09/402,181A
FILING DATE: 29-Sep-1997
CLASSIFICATION: CUNKNOWN>
PRIOR APPLICATION NUMBER: US 08/724,643
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: US 08-851,843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 633
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: San Francisco
STATE: California
                  0000000000000
 US-09-402-181A-613
 Sequence 128, App
Sequence 367, App
Sequence 367, App
Sequence 12, App11
Sequence 147, App
Sequence 186, App
Sequence 19299, A
Sequence 3624, Ap
Sequence 3624, Ap
Sequence 3624, Ap
Sequence 17561, A
Sequence 27, App1
Sequence 27, App1
Sequence 227, App1
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Sequence 10432, A
Sequence 211, App
Sequence 2, Appli
                                                                                                                                       (without alignments)
26.919 Million cell updates/sec
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Sequence 12942, A
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Sequence 12940,
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                                                                                                                   January 29, 2002, 11:07:15; Search time 29.91 Seconds
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pending_Patents_AA_New:*

'cgn2_6/ptodata/2/paa_YCT_NEW_COMB.pep:*

'cgn2_6/ptodata/2/paa_VUS06_NEW_COMB.pep:*

'cgn2_6/ptodata/2/paa_VUS08_NEW_COMB.pep:*

'cgn2_6/ptodata/2/paa_VUS08_NEW_COMB.pep:*

'cgn2_6/ptodata/2/paa_VUS09_NEW_COMB.pep:*

'cgn2_6/ptodata/2/paa_VUS09_NEW_COMB.pep:*

'cgn2_6/ptodata/2/paa_VUS08_NEW_COMB.pep:*

'cgn2_6/ptodata/2/paa_VUS08_NEW_COMB.pep:*
                GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                           173191 seqs, 36597120 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUMMARIES
                                                                                                                                                                                                        108
1 MKFLVNVALVFMVVXISYIYAD 22
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Maximum Match 100%
Listing first 45 summaries
                                                                                    protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB s
                                                                                  OM protein
                                                                                                                                                                                                                            Sequence:
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                                                                                                                   Run on:
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Gaps
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TITLE OF INVENTION: Joentification of Essential Genes in TITLE OF INVENTION: Deckaryotes
FILE REFERENCE: ELITRA, 0.114
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/291,078
PRIOR PELING DATE: 2000-03-21
PRIOR PELING DATE: 2000-03-23
PRIOR PLILING DATE: 2000-05-23
PRIOR PLILING DATE: 2000-05-33
PRIOR FILING DATE: 2000-10-33
PRIOR PLILING DATE: 2000-10-33
PRIOR PLILING DATE: 2000-10-33
PRIOR PLILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
     APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-C0T-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-C0T-1997
ATTORNEY/AGENT INFORMATION:
NAME: APPLe, Randolph Ted
REGISTRATION NUMBER: 36,429
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 108; DB 5; 100.0%; Pred. No. 5.3e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE DESCRIPTION: SEQ ID NO: 613: US-09-721-477-613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 10432, Application US/09815242 GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 60/269,308 FILING DATE: 2001-02-16
                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 613:
SEQUENCE CHARACTERISTICS:
LENGTH: 1189 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MKFLVNVALVFMVVYISYIYAD 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ohlsen, Kari L.
Zyskind, Judith W.
Wall, Daniel
Trawick, John D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Carr, Grant J.
Yamamoto, Robert T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protein
1..1189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY:
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US-09-815-242-10432
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APPLICANT:
APPLICANT:
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PRIOR
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                                                                                                                                                                                                                                                                                                                                            NAME/KEY: Protein
LOCATION: 1..1189
OTHER INFORMATION: /note= "fusion protein composed of malittin signal sequence and full length hTRT protein" SEQUENCE DESCRIPTION: SEQ ID NO: 613:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.0%; Pred. No. 5.3e-08;
Matches 22; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 22-Nov-2000
CLASSIFICATION: -UNknown>
PRIOR APPLICATION DATE: -(08/974,549
FILING DATE: -UNknown>
FILING DATE: -UNKnown>
APPLICATION NUMBER: 08/974,419
FILING DATE: -US 08/844,419
APPLICATION NUMBER: US 08/844,419
APPLICATION NUMBER: US 08/846,017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Harley, Calvin B.
Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
CORRESPONDENCE TOwnsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
NAME: Ausenhus, Scott L.
REGISTRATION NUMBER: 42,271
REFERENCE/DOCKET NUMBER: 015389-002620US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFRAT: (415) 576-0300
INFORMATION FOR SEQ ID NO: 613:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/851,843
ELING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 08/911,312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 613, Application US/09721477
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Raren B.
Morlin, Gregg B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
                                                                                                                                                                                                    LENGTH: 1189 amino acids
                                                                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS: <Unknown>
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                                                                                                                                                                                                                                                                            TOPOLOGY: linear MOLECULE TYPE: protein
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APPLICANT: Scadden, David T.
APPLICANT: Poznansky, Mark C.
APPLICANT: Diszak, Ivona T.
APPLICANT: Brown, Edward M.
TITLE OF INVENTION: THE CAR RECEPTOR AS A MEDIATOR OF
TITLE OF INVENTION: THE CAR RECEPTOR AS A MEDIATOR OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 6; Length 1078;
60;
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2;
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Pred. No. 2;
4; Mismatches
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CURRENT FILING DATE: 2001-11-01
PRIOR APPLICATION NUMBER: PCT/US00/15440
PRIOR FILING DATE: 2000-06-02
PRIOR FILING DATE: 2000-06-02
SOFTWARE: FASTEED for Windows Version 3.0
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; OTHER INFORMATION: Ca-sensing Receptor US-10-002-854-2
                                                                        PRIOR FILING DATE: 1997-08 18
PRIOR APPLICATION NUMBER: 60/055,947
PRIOR FILING DATE: 1997-08-18
PRIOR APPLICATION NUMBER: 60/055,964
PRIOR APPLICATION NUMBER: 60/056,360
PRIOR APPLICATION NUMBER: 60/056,360
PRIOR FILING DATE: 1997-08-18
                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: 60/055, 684
PRIOR PELLING DATE: 1997-08-18
PRIOR PELLING DATE: 1997-08-18
PRIOR PELLING DATE: 1997-08-18
PRIOR PELLING DATE: 1997-08-18
PRIOR APPLICATION NUMBER: 60/055, 954
PRIOR FILING DATE: 1997-09-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR FILING DATE: 1997-09-12
PRIOR APPLICATION NUMBER: 60/058,661
PRIOR FILING DATE: 1997-09-12
NUMBER OF SEQ ID NOS: 947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NESCH. 10-002-854-2; Sequence 2, Application US/10002854; GENERAL INFORMATION:
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50.0%;
                                                        APPLICATION NUMBER: 60/1 FILING DATE: 1997-08-18
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Best Local Similarity 50.0
Matches 9; Conservative
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Best Local Similarity 45.0
Matches 9; Conservative
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LENGTH: 1078
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                                                                                                                                                                                                                          Length 127;
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TITLE OF INVENTION: 123 Human Secreted Proteins
FILE REFERENCE: PO1002
CURRENT APPLICATION NUMBER: 05/09/973,278
CURRENT APPLICATION NUMBER: 00/239,899
PRIOR PILING DATE: 2000-10-13
PRIOR PAPLICATION NUMBER: 00/227,357
PRIOR PLING DATE: 1999-01-08
PRIOR FILING DATE: 1999-01-08
PRIOR PLING DATE: 1999-07-07
PRIOR PLING DATE: 1997-07-08
PRIOR PLING DATE: 1997-08-18
                                                                                                                                                                                                                          Score 47; DB 5;
Pred. No. 3.5;
                                                                                                                                                                                                                                                                           7; Mismatches
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 10432
LENGTH: 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 211, Application US/09973278 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                       1 MKFLVNVALVFMVVYISYIYAD 22
                                                                                                                                                                                                                                                                                                                                                        43.5%;
                                                                                                                                                                                                   Query Match
Best Local Similarity 40.9%
                                                                                                    ; TYPE: PRT
; ORGANISM: Escherichia coli
US-09-815-242-10432
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US-09-973-278-211
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Gaps

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Gaps

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NAME/KEY: peptide;
; LOCATION: (1)..(542)
; OTHER INFORMATION: Amino acid sequence of protein regulating the pH of vacuoles
US-09-830-123-2
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; Sequence 2, Application US/09830123
; Sequence 2, Application US/09830123
; GENERAL INFORMATION:
APPLICANT: Inda, Shigeru
APPLICANT: Inda, Shishide
TITLE OF INVENTION: Genes Encoding Proteins Regulating the pH of Vacuoles
FILE REFERENCE: 101500-137
; FILE REFERENCE: 101500-137
; CURRENT APPLICATION NUMBER: PCT/JP00/05722
; PRIOR APPLICATION NUMBER: PCT/JP00/05722
; PRIOR APPLICATION NUMBER: PT 1/236800
; PRIOR FILING DATE: 1999-08-24
; PRIOR FILING DATE: 1999-08-24
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Version 3.1
; SEQ ID NO 2
: LENTAL PARTICAL PARTIC
Sequence 367, Application US/09804291

Sequence 367, Application US/09804291

Sequence 367, Application US/09804291

Sequence 367, Application SERGEY

TITLE OF INFORMATION: HUMAN OLFACTORY RECEPTORS AND GENES ENCODING SAME

FILE REFERENCE: P 0278005

CURRENT FILING DATE: 2000-03-13

PRIOR PELLOR INORMERE: 60/188,914

PRIOR PELLOR DATE: 2000-03-23

PRIOR FILING DATE: 2000-03-24

PRIOR PELLOR DATE: 2000-04-14

PRIOR FILING DATE: 2000-04-14

PRIOR FILING DATE: 2000-04-24

PRIOR FILING DATE: 2000-06-23

PRIOR PELLOR TOWN NUMBER: 60/29,335

PRIOR FILING DATE: 2000-06-23

PRIOR PELLOR DATE: 2000-06-23

PRIOR PELLOR DATE: 2000-09-26

PRIOR FILING DATE: 2000-09-07

PRIOR PELLOR DATE: 2000-09-07
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Best Local Similarity 40.0°
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| 204 NIFFVLLVIFISYLF 218
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   US-09-804-291-367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-830-123-2
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APPLICANT: Recipon, Herve
APPLICANT: Cafferkey, Robert
APPLICANT: Cafferkey, Robert
APPLICANT: All, Shujath
APPLICANT: Liu, Chenghua
TITLE OF INVENTION: Compositions and Methods Relating to Prostate Specific Genes and FILE REFERENCE: DEX-0281
CURRENT APPLICATION NUMBER: US/10/001,879
CURRENT FILING DATE: 2001-11-20
PRIOR PAPLICATION NUMBER: 60/252,188
PRIOR FILING DATE: 2000-11-21
NUMBER OF SEQ ID NOS: 201
SOFTWARE: Patentin version 3.1
SEQ ID NO 128
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Sequence 367, Application US/09886055
GENERAL INFORMATION:
APPLICANT: STRYER, LUBERT
APPLICANT: SOZULYA, SERGET
TITLE OF INVENTION: RECEPTOR FINGERPRINTING, SENSORY PERCEPTION, AND
TITLE OF INVENTION: BIOSENSORS OF CHEMICAL SENSANTS
FILE REFERENCE: 078003-0277150
CURRENT APPLICATION NUMBER: US/09/886,055
CURRENT FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 522
NUMBER OF SEQ ID NOS: 522
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Mismatches
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Pred. No.
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                                                                                                                                                                                                                                                       Sequence 128, Application US/10001879 GENERAL INFORMATION:
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                                                                           805 KEITESMLIFFIVWISFIPA 824
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44.48;
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                                       2 KFLVNVALVFMVVXISYIYA 21
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                                                                                                                                                                                                                                                                                                                         APPLICANT: Salceda, Susana
APPLICANT: Macina, Roberto
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Best Local Similarity 44.4
Matches 8; Conservative
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204 NIFFVLLVIFISYLF 218
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US-09-886-055-367
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US-10-001-879-128
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Best Local Similarity
Matches 6; Conserv
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LENGTH: 309
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APPLICANT: Ruben et al.
TITLE OF INVENTION: 90 Human Secreted Proteins
FILE REFERENCE: P2013P2
                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/969,730
CURRENT FILING DATE: 2001-10-04
PRIOR APPLICATION NUMBER: 09/774,639
PRIOR FILING DATE: 2001-02-01
PRIOR FILING DATE: 2000-10-06
PRIOR FILING DATE: 2000-10-06
PRIOR FILING DATE: 15009-02-04
PRIOR PLILNG DATE: 1999-02-04
PRIOR APPLICATION NUMBER: 09/244,112
PRIOR APPLICATION NUMBER: 09/244,112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR FILING DATE: 1998-08-04
PRIOR PELICATION NUMBER: 60/056,371
PRIOR PELING DATE: 1997-08-19
PRIOR PELING DATE: 1997-08-19
PRIOR PELING DATE: 1997-08-19
PRIOR FILING DATE: 1997-08-19
PRIOR PELING DATE: 1997-08-19
PRIOR FILING DATE: 1997-08-19
PRIOR FILING DATE: 1997-08-19
PRIOR PELING DATE: 1997-08-18
PRIOR PELING DATE: 1997-08-18
PRIOR PELING DATE: 1997-08-18
PRIOR PELING DATE: 1997-08-18
PRIOR PELING DATE: 1997-08-05
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PRIOR APPLICATION NUMBER: 60/054,798
PRIOR FILING DATE: 1997-08-05
PRIOR APPLICATION NUMBER: 60/055,309
PRIOR FILING DATE: 1997-08-05
PRIOR FILING DATE: 1997-08-05
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293 RFTQNISAIEPLIVFMFSYLSYLAAE 318
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                                                                                                                                                                                             Sequence 147, Application US/09969730 GENERAL INFORMATION:
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SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 147
LENGTH: 61
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APPLICANY: Ballerman, Karen
APPLICANY: Bacoougall, John
APPLICANY: Stone, David
TITLE OF INVENTION: Novel Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-074 US
CURRENT PLILIG DATE: 2001-07-30
FRIOR APPLICATION NUMBER: 60/221,409
FRIOR APPLICATION NUMBER: 60/223,752
FRIOR APPLICATION NUMBER: 60/223,752
FRIOR APPLICATION NUMBER: 60/223,769
FRIOR APPLICATION NUMBER: 60/223,769
FRIOR FILING DATE: 2000-08-08
FRIOR PELING DATE: 2000-08-08
FRIOR APPLICATION NUMBER: 60/225,146
FRIOR PELING DATE: 2000-08-14
FRIOR APPLICATION NUMBER: 60/225,46
FRIOR FILING DATE: 2000-08-16
FRIOR PELING DATE: 2000-08-16
FRIOR FILING DATE: 2000-08-16
FRIOR PELING DATE: 2000-08-16
FRIOR FILING DATE: 2001-02-01
FRIOR FILING DATE: 2001-03-05
FRIOR FILING DATE: 2001-03-05
FRIOR FILING DATE: 2001-03-07
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                                     Indels
                                     3;
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34.6%; Pred. No. 91;
tive 7; Mismatches
                                     5; Mismatches
      Pred. No.
                                                                                                                                                                                                                                                                                                                      Sequence 12, Application US/09918779
GENERAL INFORMATION:
APPLICANT: Taupier, Raymond
                                                                                                                                                                                                                                                                                                                                                                                                                 Padigaru, Muralidhara
Rastelli, Luca
Spaderna, Steven
Shimkets, Richard
Zerhusen, Bryan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gusev, vladimir
Grosse, William
Alsobrook, John
Lepley, Denise
Burgess, Catherine
Gerlach, Valerie
Best Local Similarity 50.0%;
Matches 8; Conservative
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Shenoy, Suresh
Li, Li
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MacDougall, John
                                                                                                                                       253 VALMMLMSYLSYIMAE 268
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Best Local Similarity 34.6
Matches 9; Conservative
                                                                                              7 VALVFMVVYISYIYAD 22
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SOFTWARE: PatentIn Ver.
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US-09-918-779-12
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APPLICANT:
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APPLICANT:
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Sequence 3623, Application US/09708427

GENERAL INFORMATION:
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID
TITLE OF INVENTION: THEREBY
TITLE REFERENCE: 2750-1243P
CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SEQ ID NO 3623
SEQ ID NO 3623
                                                                                                                                                                                                   Sequence 3624, Application US/09708427

GENERAL INFORMATION:
APPLICANT: N. ALEXANDROV et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID
TITLE OF INVENTION: THEREBY
FILLE REPERBENCE: 2750-1243P
CURRENT APPLICATION NUMBER: US/09/708,427

CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SSEQ ID NO 3624
LENGTH: 347
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 Length 217;
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                                       Indels
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Score 42; DB 5;
Pred. No. 32;
9; Mismatches
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Pred. No. 61;
6; Mismatches
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Pred. No. 51;
6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: 1..347
OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc_feature
LOCATION: 1..347
OTHER INFORMATION: Ceres Seq. ID 1810723
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; OTHER INFORMATION: Ceres Seq. ID 1810722
US-09-708-427-3623
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43.8%;
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OTHER INFORMATION: Xaa is any
NAME/KEY: misc_feature
   38.9%;
29.4%;
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Best Local Similarity 43.8.
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161 VALMMLMAYLSYMLAE 176
                                                                                                     34 VSFSIIIIIVFVYYLYA 50
                                                                             5 VNVALVEMVVXISYIYA 21
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                                         Conservative
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Best Local Similarity
Matches 7; Conserv
                   Best Local Similarity
Matches 5; Conserv
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US-09-708-427-3623
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US-09-708-427-3624
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       Query Match
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GENERAL INFORMATION:
APPLICANT: N. ALEXANDROV et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: THEREBY
FILE REFERENCE: 2750-1243P
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TILLE OF INVENTION: 90 Human Secreted Proteins
FILLE REFERENCE: P2013P1
CURRENT APPLICATION NUMBER: US/09/774,639
CURRENT FILING DATE: 2001-07-09
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/244,112
PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-04
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                                                                                                   Length 61;
                                                                                                                                       Indels
                                                                                                 Score 42; DB 5;
Pred. No. 8.7;
'; Mismatches 4
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Pred. No. 8.9;
; Mismatches
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; OTHER INFORMATION: Xaa equals stop translation

US-09-774-639-186
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                                                                                                                                                                                                                                                                                                             Sequence 186, Application US/09774639 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Arabidopsis thaliana
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LOCATION: 1..217
OTHER INFORMATION: Xaa is any
                                                                                                 Query Match 38.9%;
Best Local Similarity 35.3%;
Matches 6; Conservative
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35.3%;
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 186
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8 FILNIIVIFCIVIDSYL 24
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Best Local Similarity 35.3
Matches 6; Conservative
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LOCATION: 1..217
         ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-969-730-147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Homo sapiens
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LENGTH: 217
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US-09-774-639-186
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Search completed: January 29, 2002, 11:07:16 Job time: 534 sec

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Section 1

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Perfect score:

Sequence:

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Sequence 34, Appli
Sequence 1, Appli
Sequence 6, Appli
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Sequence 25, Appli
Sequence 55, Appli
Sequence 1, Appli
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Sequence 32, Appl
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Sequence 7, Appli
Sequence 7, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 7, Application PC/TUS0025239
GENERAL INFORMATION:
APPLICANT: Schenk, Dale B.
APPLICANT: Schenk, Dale B.
APPLICANT: Elan Pharmaceuticals
TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
FILE REFERENCE: 152701-005900PC
CURRENT FPLICATION NUMBER: PCT/US00/25239
CURRENT FILING DATE: 1090-06-01
PRIOR APPLICATION NUMBER: US 60/137,010
PRIOR FILING DATE: 1999-06-01
NUMBER OF SEQ ID NOS: 34
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: Description of Artificial Sequence: tetanus toxoid COTHER INFORMATION: TT 830-844 universal T-cell epitope PCT-US00-25239-7
                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                             Sequence 4
                                               Sequence
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Pred. No. 1.2e-06;
Mismatches 0;
US-09-148-711-7

US-09-148-711-7

US-09-362-731-13

US-09-362-731-13

US-09-36-731-13

US-09-36-731-13

US-09-405-986-12

US-09-56-818-23

US-09-56-818-23

US-09-56-015-49

US-09-56-015-49

US-09-56-016-49

US-09-56-016-49

US-09-78-21-2

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US-09-78-21-2

US-09-78-21-2

US-09-13-23-3

US-09-13-23-3

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US-09-13-23-3

US-09-16-878-18

US-08-05-16-878-18

US-08-05-16-878-18

US-08-05-16-878-18

US-08-05-16-878-18
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US-08-926-296-7
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ilarity 100.0%;
Conservative 0;
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   Local Similarity
les 15; Conserv
   PCT-US00-25239-7
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Best Local Si
Matches 15;
  SEQ ID NO 7
LENGTH: 15
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Sequence 2, Appli
Sequence 69, Appl
Sequence 2, Appli
Sequence 4, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 1, Appli
                                                                              Search time 353.23 Seconds (without alignments) 11.791 Million cell updates/sec
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                                                                                                                                                                                                                                      3148936
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1: /cgn2_6/ptodateJ2/paa/WS06_COMB.pep:*

3: /cgn2_6/ptodateJ2/paa/WS06_COMB.pep:*

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16: /cgn2_6/ptodataJ2/paa/WS096_COMB.pep:*

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19: /cgn2_6/ptodataJ2/paa/WS096_COMB.pep:*

20: /cgn2_6/ptodataJ2/paa/WS096_COMB.pep:*

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Compugen Ltd
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PCT-US99-06325-2
US-08-161-889-69
US-08-161-889A-69
US-08-406-916B-2
1 US-08-716-249-4
US-09-049-847A-1
4 US-09-049-847A-1
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Copyright (c) 1993 - 2000
                                                                               2002, 11:06:40
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Maximum Match 100%
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74
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VACCINES AND ANTIGENIC CONJUGATES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 74; DB 5; 100.0%; Pred. No. 1.2e-06;
                                                                                                                                                                                                                                                                                  RESULT 4
US-08-161-889A-69
US-08-161-889A-69
Sequence 69, Application US/08161889A
GENERAL INFORMATION:
APPLICANT: Geysen, H. Mario
APPLICANT: Redda, Stuart J.
TITLE OF INVENTION: T-Cell Epitopes
NUMBER OF SEQUENCES: 74
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/08406916B
GENERAL INFORMATION:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 510-601-2706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Grant D. Green
STREET: 4560 Horton St.
CITY: Emeryville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 510-655-3542
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
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Best Local Similarity 100.
Matches 15; Conservative
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            ; MOLECULE TYPE: peptide US-08-161-889-69
                                                                                                                                                                             1 QYIKANSKFIGITEL 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
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Best Local Similarity
Matches 15; Conserv
TOPOLOGY: linear
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US-08-406-916B-2
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                                                   Sequence 2, Application PC/TUS9906325
GENERAL INFORMATION:
APPLICANT: Sudhir Paul
APPLICANT: Larry J. Smith
APPLICANT: Gennady Golobbov
TITLE OF INVENTION: Methods for Identifying Inducers and
TITLE OF INVENTION: Inhibitors of Catalytic Antibodies, Compositions and Their
TITLE OF INVENTION: Use
TITLE OF INVENTION: UNMER: PCT/US99/06325
CURRENT APPLICATION NUMBER: PCT/US99/06325
CURRENT FILING DATE: 1999-03-23
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FastSEQ for Windows Version 3.0
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COUNTRY: USA

ZIP: 94608

COMPUTER READABLE FORM:

MEDIUW TYPE: Floppy disk

COMPUTER: IBM PC COMPATIBLE

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30B

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/161,889

FILING DATE: 02-DEC-1993

CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 100.0%; Score 74; DB 1; 1
Best Local Similarity 100.0%; Pred. No. 1.2e-06;
Matches 15; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 69, Application US/08161889
GENERAL INFORMATION:
APPLICANT: Geysen, H. Mario
APPLICANT: Rodda, Stuart J.
TITLE OF INVENTION: T-Cell Epitopes
NUMBER OF SEQUENCES: 75
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Green, Grant D.
REGISTRATION NUMBER: 31,259
REFERENCE/DOCKET NUMBER: 0222.002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/984,852
FILING DATE: 02-DEC-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
TELEPHONE: 510-601-2706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Grant D. Green
STREET: 4560 Horton St.
CITY: Emeryville
                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: PRT
; ORGANISM: Clostridium tetani
PCT-US99-06325-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 510-655-3542 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 QYIKANSKFIGITEL 15
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                                             PCT-US99-06325-2
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LENGTH: 15
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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Bay, Sylvie
APPLICANT: Leclerc, Claude
APPLICANT: Lorden, Richard
TITLE OF INVENTION: Mutiple antigen alycopeptide carbohydrate, vaccine
TITLE OF INVENTION: Mutiple antigen alycopeptide
TITLE OF INVENTION: Comprising the same and use thereof
FILE REFERENCE: 102.166A
CURRENT FILING DATE: 1998-03-27
EARLIER APPLICATION NUMBER: 60/041,726
EARLIER FILING DATE: 1997-03-27
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Pred. No. 1.2e-06;
                 CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/FR95/00292
FILING DATE: 13-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Calvetti, Frederick F.
REGISTRATION NUMBER: 28.557
REFERENCE/DOCKET NUMBER: GROFO 7001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (2021414-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
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GENERAL INFORMATION:
APPLICANT: Bay, Sylvie
APPLICANT: Cantacuzene, Daniele
APPLICANT: Leclerc, Claude
APPLICANT: Leclerc, Claude
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100.0%;
                                                                                                                                                                                                                TELEPHONE: (202)414-4000
TELEFAX: (202)414-4040
INPORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENOTH: 15 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: PRT
; ORGANISM: Clostridium tetani
US-09-049-847-1
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1
LENGTH: 15
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Best Local Similarity 100.
Matches 15; Conservative
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Best Local Similarity
Matches 15; Conserv
  FILING DATE:
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US-08-716-249-4
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GENERAL INFORMATION:
APPLICANT: Gulchard, Gilles
APPLICANT: Muller, Sylviane
APPLICANT: Briand, Jean-Paul
APPLICANT: Regenmortel, Marc
TITLE OF INVENTION: Retropeptides, Antibodies Thereto, and
TITLE OF INVENTION: Uses Thereof for Vaccination and In Vitro Diagnosis
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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100.0%; Pred. No. 1.2e-06;
Live 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/716,249
                                                                                                                                    COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB
COMPUTER: IBM PS/2 COMPATIBLE 486 DX 33
OPERATING SYGTEM: MS DOS 6.2

SOFTWARE: WORDPERFECT FOR MS DOS 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/406,916B
FILING DATE: 27 MAR 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/08370
FILING DATE: 30 SEP 1992
ATTORNEY/AGENT INFORMATION:
NAME: KREMBLAS, FRANCIS T., JR.
REGISTRATION NUMBER: 22,773
REFERENCE/DOCKET NUMBER: 22,773
REFERENCE/DOCKET NUMBER: URF 2 056 3 3 3
TELECOMMUNICATION NUMBER: URF 2 056 3 3 3
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STREET: 1100 New York Avenue, Suite 300E
CITY: Washington, D.C.
                                      ADDRESSEE: MILLARD, SIDNEY W.
STREET: 7612 SLATE RIDGE BOULEVARD
CITY: REYNOLDSBURG
STATE: OHIO
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: T cell epitope
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (614) 575 2100
TELEFAX: (614) 575 2149
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 100.
Matches 15; Conservative
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                      CORRESPONDENCE ADDRESS:
NUMBER OF SEQUENCES:
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XX: linear
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Pred. No. 1.2e-06;
Mismatches 0;
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/460,502
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/148,711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: PC-DOS/MS-DOS
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NAME: GOLICK, MATY E.
REGISTRATION NUMBER: 34,829
REFERENCE/DOCKET NUMBER: 2272:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (216) 241-0816
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                               Sequence 7, Application US/09148711
  ilarity 100.0%; P
Conservative 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Floppy disk
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Best Local Similarity 100.
Matches 15; Conservative
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STRANDEDNESS: single
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Best Local Similarity
Matches 15; Conserv
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44114-2688
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TITLE OF INVENTION: Mutiple antigen glycopeptide carbohydrate, vaccine FITLE OF INVENTION: comprising the same and use thereof FILE REFERENCE: 102.166 CURRENT APPLICATION NUMBER: US/09/049,847A CURRENT APPLICATION NUMBER: US/09/041,726 PRIOR APPLICATION NUMBER: 60/041,726 PRIOR PAPLICATION NUMBER: 60/041,726 PRIOR FILING DATE: 1999-03-27 NUMBER OF SEQ ID NOS: 6 SEQ ID NOS: 6 SEQ ID NOS: 6 LENGTH: 15
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/102,716
FILING DATE: 22-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/661,052
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chezian Somasundaram
TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRISED
OF ANTI-FC RECEPTOR ANTIBODIES
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STREET: 60 State Street, Suite 510
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Arnold, Beth E.
REGISTRATION NUMBER: 35,430
REFERENCE/DOCKET NUMBER: MXI-043CP
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (617)227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 6, Application US/09102716 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: <Unknown>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Yashwant M. Deo
Joel Goldstein
Robert Graziano
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COUNTRY: USA
ZIP: 02109-1875
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: peptide FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                        ; ORGANISM: Clostridium tetani
US-09-049-847A-1
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Best Local Similarity
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Length 15;

Query Match

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                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Bakaletz, Lauren O.
APPLICANT: Kaumaya, Parvin T.
TITLE OF INVENTION: Synthetic Chimeric Fimbrin Peptides
NUMBER OF SEGUENCES: 11
CORRESPONDENCE ADDRESS:
Indels
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GENERAL INFORMATION:
APPLICAM: The Ohlo State University
TITLE OF INVENTION: Synthetic Chimeric Fimbrin Peptides
FLLE REFERENCE: 18525-04010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Version #1.25
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100.0%; Pred. No. 1.2e-06;
Live 0; Mismatches 0;
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CURRENT APPLICATION NUMBER: US/09/148,711A
CURRENT FILING DATE: 1998-09-04
PRIOR APPLICATION NUMBER: 08/460,502
NUMBER FILING DATE: 1955-06-02
NUMBER OF SEQ ID NOS: 12
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Gaps
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GENERAL INFORMATION:
APPLICANT: M&E Biotech A/S
APPLICANT: HAKIER, Torben
APPLICANT: HAANING, Jesper
TITLE OF INVENTION: Method for Down-Regulating Osteoprotegerin Ligand
TITLE OF INVENTION: Activity
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    Length 15;
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GENERAL INFORMATION:
APPLICANT: Yashwant M. Deo, et al.
TITLE OF INVENTION: THERREUTIC COMPOUNDS COMPRISED
TITLE OF INVENTION: OF ANTI-FC RECEPTOR ANTIBODIES
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street, 24th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM: PC_DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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100.0%; Pred. No. 1.2e-06;
iive 0; Mismatches 0;
  100.0%; Score 74; DB 17; 100.0%; Pred. No. 1.2e-06;
                                             Mismatches
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APPLICATION NUMBER: US 09/188,082
FILING DATE: 07-JUNE-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/484,172
FILING DATE: 07-JUNE-1995
ATTORNEY AGENT INFORMATION:
REGISTRATION NUMBER: 38,872
REFERENCE/DOCKET NUMBER: MXI-043CP2
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/09/364,088 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (617)227-7400
TELERAX: (617)742-7414
INFORMATION FON EGG ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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Best Local Similarity 100.
Matches 15; Conservative
                                             Conservative
                                                                                                              1 QYIKANSKFIGITEL 15
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                      Best Local Similarity
Matches 15; Conserv
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FRAGMENT TYPE:
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US-09-364-088-6
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    Query Match
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GENERAL INFORMATION:
APPLICANTY U.C.B. S.A.
TITLE CANTY U.C.B. CANDOUND AND METHOD FOR THE PREVENTION AND/OR THE
TITLE OF INVENTION: TREATMENT OF ALLERGY
FILE REPERENCE: P.UCB.09/WO
CURRENT APPLICATION NUMBER: US/09/362,731
CURRENT FILING DATE: 1999-07-29
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 13
LENGTH: 15
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US-09-362-731-13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Heegaard, Peter Mikael Helweg
APPLICANT: Heegaard, Peter Mikael Helweg
TITLE OF INVENTION: Non-Dendritic Backbone Peptide Carrier
FILE REFERENCE: 2316.1009-000
CURRENT FILING DATE: 1998-10-02
CURRENT FILING DATE: 1997-004-03
EARLIER APPLICATION NUMBER: PCT/DK97/00146
FARLIER PILING DATE: 1997-04-03
EARLIER PILING DATE: 1996-04-03
SARLIER FILING DATE: 1996-04-03
SARLIER FILING DATE: 1996-04-03
SARLIER FILING DATE: 1996-04-03
SOFTWARE: FASTSEQ for Windows Version 3.0
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                                                                                                                                                                      Query Match 100.0%; Score 74; DB 15; Best Local Similarity 100.0%; Pred. No. 1.2e-06; Matches 15; Conservative 0; Mismatches 0;
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US-09-165-878-71
Sequence 71, Application US/09165878B
GENERAL INFORMATION:
  PatentIn version 3.0
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ORGANISM: Artificial Sequence
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                                                                                   ; ORGANISM: clostridium tetani
US-09-148-711A-7
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Matches 15; Conserva
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LENGTH: 15
SOFTWARE:
SEQ ID NO 7
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; FILE REFERENCE: 22021 PC 1
; CURRENT APPLICATION NUMBER: US/09/396,937
; CURRENT FILLICATION NUMBER: US/09/396,937
; CURRENT FILLICATION NUMBER: US/09-15
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 34
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Clostridium tetani
US-09-396-937-34

Query Match

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US-09-677-374-19
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SEQ ID NO 34
LENGTH: 15
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18.354 Million cell updates/sec
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(g012_6/ptodata/2/paa/USO6_NEW_COMB.pep:*
(g012_6/ptodata/2/paa/USO7_NEW_COMB.pep:*
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               GenCore version 4.5
(c) 1993 - 2000 Compugen Ltd.
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US-09-677-374-19
US-09-980-916-23
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US-09-806-703A-16
US-09-980-916-14
US-09-980-916-32
US-09-980-916-32
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                                                                                                             January 29, 2002, 11:07:15
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Maximum Match 100%
Listing first 45 summaries
                                                                               protein search, using sw model
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1 QYIKANSKFIGITEL 15
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Sequence 42, Appl
Sequence 4901, Ap
Sequence 10491, A
Sequence 5048, Ap
Sequence 5943, Ap
Sequence 503, Ap
Sequence 2, Appli
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                               US-09-980-916-44
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US-09-806-703A-39
US-09-806-703A-37
US-09-909-46-01
US-09-909-460-42
US-09-815-242-4901
US-09-815-242-10491
US-09-897-516-6808
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Gaps
Sequence 34, Application US/09787126
GENERAL INFORMATION:
Sequence 34.
Sequence 34.
Application US/09787126
GENERAL INFORMATION:
BAPLICANT:
HALKIER, Torben
APPLICANT:
HAANING, Jesper
TITLE OF INVENTION: Method for Down-Regulating Osteoprotegerin Ligand
TITLE OF INVENTION: Activity
File Reference: 3631-0108P
CURRENT APPLICATION NUMBER: US/09/787,126
CURRENT APPLICATION NUMBER: 2001-10-09
NUMBER OF SEQ ID NOS: 36
SOFTWARE: PatentIn Ver. 2.1
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Pred. No. 1e-07;
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100.0%;
Best Local Similarity 100.0%;
Matches 15; Conservative 0.
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US-09-787-126-34
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Sequence 19, Application US/09677374
GENERAL INFORMATION:
APPLICANT: Burian, Julian
APPLICANT: Thornton, Julian
APPLICANT: Ray, William
TITLE OF INVENTION: VACCINES AND AGENTS FOR INDUCING IMMUNITY AGAINST
TITLE OF INVENTION: RICKETYSIAL DISEASES, AND ASSOCIATED PREVENTATIVE THERAPY
FILLE REFERENCE: IDCOJ/60485/US
CURRENT APPLICATION NUMBER: US 60/154,437
PRIOR APPLICATION NUMBER: US 60/154,437
PRIOR PLIING DATE: 2000-09-15
PRIOR FILING DATE: 2000-09-15
PRIOR FILING DATE: 2000-09-18

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Nielsen, Klaus
APPLICANT: Ralsson, Guillla
APPLICANT: Ralsson, Guillla
APPLICANT: Rasmussen, Peter
TITLE OF INVENTION: Novel Methods for Therapeutic Vaccination
FILE REFERENCE: 3631-01099
CURRENT APPLICATION UNBER: US/09/806,703A
CURRENT FILING DATE: 2001-04-04
PRIOR FILING DATE: 1999-10-05
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: US 60/105,011
PRIOR APPLICATION NUMBER: US 60/105,011
PRIOR FILING DATE: 1998-10-05
PRIOR FILING DATE: 1998-10-05
PRIOR FILING DATE: 1998-10-05
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US-09-806-703A-15
Sequence 15, Application US/09806703A
SERERAL INFORMATION:
APPLICANT: Steinaa, Lucilla
APPLICANT: Gautam, Soren
APPLICANT: Gautam, Ahand
APPLICANT: Dalum, Iben
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ORGANISM: Artificial Sequence
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Gautam, Anand
Dalum, Iben
                                                                                        TYPE: PRT; Clostridium tetani
US-09-980-916-23
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APPLICANT: Mouritsen, Sorer
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Leach, Dana
Nielsen, Klaus
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Leach, Dana
Nielsen, Klaus
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SOFTWARE: Patentin Ver. 3.0
SEQ ID NO 15
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NUMBER OF SEQ ID NOS: 65
SOFTWARE: PatentIn Ver. 3
SEQ ID NO 23
LENGTH: 15
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US-09-806-703A-16
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APPLICANT:
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APPLICANT: Leach, Dana
APPLICANT: Leach, Dana
APPLICANT: Railson, Klaus
APPLICANT: Railson, Gunilla
APPLICANT: Rasmussen, Peter
ITLE OF INVENTION: NOVel Methods for Therapeutic Vaccination
FILE REFERENCE: 3631-0109P
CURRENT PAPPLICATION NUMBER: US/09/806,703A
CURRENT FILING DATE: 2001-04-04
PRIOR APPLICATION NUMBER: PCT/DK99/00525
PRIOR PILING DATE: 1999-10-05
PRIOR PLING DATE: 1999-10-05
PRIOR FILING DATE: 1998-10-05
PRIOR FILING DATE: 1998-10-05
NUMBER OF SED 10 NOS-14
SOFTWARE: PATENTIN OF 1998-10-20
NUMBER OF SED 10 NOS: 41
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Sequence 13, Application US/09980916
GENERAL INFORMATION:
APPLICANT: M.E Biotech A/S
APPLICANT: Klysner, Steen
TITLE OF INVENTION: Method For Down-Regulating IL5 Activity
FILE REPERENCE: 3631-0112P
CURRENT APPLICATION NUMBER: US/09/980,916
CURRENT FILING DATE: 2001-10-23
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                                                                                                                                                                                                                                                                                        100.0%; Score 74; DB 5; Length 15; ilarity 100.0%; Pred. No. 1e-07; Conservative 0; Mismatches 0; Indels
      PRIOR APPLICATION NUMBER: GB 0022825.4
PRIOR FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: CL 2544-2000
PRIOR FILING DATE: 2000-09-15
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin version 3.0
SEQ ID NO 19
LENGTH: 15
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US-09-806-703A-12
                                                                                                                                                                                           ; TYPE: PRT
; ORGANISM: Clostridium tetani
US-09-677-374-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Steinaa, Lucilla
APPLICANT: Mouritsen, Soren
APPLICANT: Gautam, Anand
APPLICANT: Dalum, Iben
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Best Local Similarity 100.
Matches 15; Conservative
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Best Local Similarity
Matches 15; Conserv
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US-09-980-916-23
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OTHER INFORMATION: Description of Artificial Sequence:Murine IL5 OTHER INFORMATION: modified by substitution with tetanus toxoid P2
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OTHER INFORMATION: epitope
NAME/KEY: mUTAGEN
LOCATION: (30). (44)
OTHER INFORMATION: Tetanus toxoid P2 epitope (SEQ ID NO: 23)
NAME/KEY: SIMILAR
LOCATION: (1). (29)
OTHER INFORMATION: Identical to residues 1-29 in SEQ ID NO: 12
NAME/KEY: SIMILAR
LOCATION: (45)..(116)
OTHER INFORMATION: Identical to residues 42-113 in SEQ ID NO: 12
US-09-980-916-14
                                                                                                                                                                                                                                                                                                                    APPLICANT: Klysner, Steen
TITLE OF INVENTION: Method For Down-Regulating IL5 Activity
FILE REFERENCE: 3631-0112P
CURRENT APPLICATION NUMBER: US/09/980,916
CURRENT FILING DATE: 2001-10-23
NUMBER OF SEQ ID NOS: 65
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 14
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CURRENT FILING DATE: 2001-10-23
NUMBER OF SEQ ID NOS: 65
SOFTWARE: PATENTIN VET: 2.1
                                                                                                                                                                                            US-09-980-916-14; Sequence 14, Application US/09980916; GENERAL INFORMATION:
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Matches 15; Conservative
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                      6 QYIKANSKFIGITEL 20
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US-09-980-916-52
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APPLICANT: Gautem, Aband
APPLICANT: Dalum, Iben
APPLICANT: Dalum, Iben
APPLICANT: Haaning, Jesper
APPLICANT: Haaning, Jesper
APPLICANT: Haaning, Jesper
APPLICANT: Ranssen, Gunilla
APPLICANT: Railsson, Gunilla
APPLICANT: Railsson, Gunilla
APPLICANT: Railsson, Gunilla
APPLICANT: Railsson, Gunilla
APPLICANT: Novel Methods for Therapeutic Vaccination
FILE REFERENCE: 3631-01099
FILE REFERENCE: 3631-01099
FILE REFERENCE: 2001-04-04
FILING DATE: 2001-04-04
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: US 60/105,011
PRIOR APPLICATION NUMBER: US 60/105,011
PRIOR APPLICATION NUMBER: US 60/105,011
PRIOR FILING DATE: 1998-10-05
SOFTWARE: Patentin Ver: 3.0
SOFTWARE: Patentin Ver: 3.0
APPLICANT: Karlsson, Gunilla
APPLICANT: Rasmussen, Peter
TITLE OF INVENTION: Novel Methods for Therapeutic Vaccination
FILE REFERENCE: 3631-0109P
CURRENT APPLICATION NUMBER: US/09/806,703A
CURRENT FILING DATE: 2001-04-04
PRIOR APPLICATION NUMBER: ET/DNS9/00525
PRIOR FLILING DATE: 1999-10-05
PRIOR FLILING DATE: 1998-10-05
PRIOR FLILING DATE: 1998-10-05
PRIOR FLILING DATE: 1998-10-20
NUMBER OF SEQ ID NOS: 41
SEQ ID NO 16
FEACH OF THE PARTIE OF THE 
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FEATURE:
CHER INFORMATION: Description of Artificial Sequence: Fusion of
CHER INFORMATION: tetanus toxold epitope and PSM
US-09-806-703A-16
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Gautam, Anand
Dalum, Iben
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Matches 15; Conservative
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Best Local Similarity
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Length 116;
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GENERAL INFORMATION:
APPLICANT: M&E Biotech A/S
APPLICANT: Klysner, Steen
TITLE OF INVENTION: Method For Down-Regulating IL5 Activity
FILE REFERENCE: 3631-0112P
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Best Local Similarity 100.0%; Pred. No. 1.2e-06;
Matches 15; Conservative 0; Mismatches 0;
                                              0; Mismatches
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SEO ID NO 3 TYPE: PRT

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OTHER INFORMATION: Description of Artificial Sequence:Murine IL5 OTHER INFORMATION: modified by substitution with tetanus toxoid P2 OTHER INFORMATION: epitope
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LOCATION: (72)..(122)
COTHER INFORMATION: Identical to residues 63-113 in SEQ ID NO: 12
US-09-980-916-15
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OTHER INFORMATION: Identical to residues 1-83 in SEQ ID NO: 12
NOMECKEY: SHMLAR
LOCATION: (99)..(122)
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OTHER INFORMATION: Tetanus toxoid P2 epitope (SEQ ID NO: 23)
NAMES/EEY: SIMILAR
LOCATION: (1)..(56)
OTHER INFORMATION: Identical to residues 1-56 in SEQ ID NO:
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GENERAL INFORMATION:
APPLICANT: ME Biotech A/S
APPLICANT: MISSINGE, Steen
TITLE OF INVENTION: Method For Down-Regulating IL5 Activity
FILIE REFERENCE: 3631-0112P
CURRENT APPLICATION NUMBER: US/09/980,916
CURRENT FILING DATE: 2001-10-23
NUMBER OF SEQ ID NOS: 65
SOFTWARE: PATENTIN Ver: 2.1
SEQ ID NO 15
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TITLE OF INVENTION: Method For Down-Regulating IL5 Activity
FILE REFERENCE: 3631-0112P
CURRENT APPLICATION NUMBER: US/09/980,916
CURRENT FILING DATE: 2001-10-23
NUMBER OF SEQ ID NOS: 65
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 16
LENGTH: 122
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OTHER INFORMATION: Tetanus toxoid P2 epitope (SEQ ID NAME/KEY: SIMILAR
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Best Local Similarity 100.0%; Pred. No. 1.3e-06;
Matches 15; Conservative 0; Mismatches 0;
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APPLICANT: MEE Biotech A/S
APPLICANT: Klysner, Steen
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ORGANISM: Artificial Sequence
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32 QYIKANSKFIGITEL 46
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US-09-980-916-15
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CTHER INFORMATION: Identical to residues 44-115 in SEQ ID NO: US-09-980-916-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: SIMILAR
LOCATION: (1)..(31)
OTHER INFORMATION: Identical to residues 1-31 in SEQ ID NO: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 118;
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LOCATION: (32)...(46)
OTHER INFORMATION: Tetanus toxoid P2 epitope (SEQ ID NO: 23)
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TITLE OF INVENTION: Method For Down-Regulating IL5 Activity
FILE REFERENCE: 3631-0112P
CURRENT APPLICATION NUMBER: US/09/980,916
CURRENT FILING DATE: 2001-10-23
NUMBER OF SEQ ID NOS: 65
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                    APPLICANT: Klysner, Steen
TITLE OF INVENTION: Method For Down-Regulating IL5 Activity
FILE REFERENCE: 3631-0112P
CURRENT FILING DATE: 2001-10-23
NUMBER OF SEO ID NOS: 65
SOFTWARE: Patentin Ver. 2.1
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100.0%; Pred. No. 1.2e-06;
Vernatches 0;
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ilarity 100.0%; Pred. No. 1.2e-06;
Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                        Sequence 3, Application US/09980916 GENERAL INFORMATION:
APPLICANT: M&E Blotech A/S
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                      30 QYIKANSKFIGITEL 44
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Best Local Similarity
Matches 15; Conserv
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Best Local Similarity
Matches 15; Conserv
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US-09-980-916-3
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SEQ ID NO 36 TYPE: PRT

FEATURE:

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OTHER INFORMATION: modified by substitution with tetanus toxoid P2
OTHER INFORMATION: epitope
OTHER INFORMATION: epitope
LOCATION: (59)..(73)
OTHER INFORMATION: Tetanus toxoid P2 epitope (SEQ ID NO:23)
ANMEKEY: SIMILAR
LOCATION: (1)..(58)
OTHER INFORMATION: Identical to residues 1-58 in SEQ ID NO: 1
LOCATION: (71)..(124)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Description of Artificial Sequence: Murine Il-5; OTHER INFORMATION: modified by substitution with tetanus toxoid; OTHER INFORMATION: epitope US-09-980-916-54
. OTHER INFORMATION: Identical to residues 90-113 in SEQ ID NO: 12 US-09-980-916-16
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                                                                                                  Length 122
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APPLICANT: MAE Blotech A/S
APPLICANT: Klysner, Steen
TITLE OF INVENTION: Method For Down-Regulating IL5 Activity
FILE REFERENCE: 3631-0112P
CURRENT APPLICATION NUMBER: US/09/980,916
CURRENT FILING DATE: 2001-10-23
NUMBER OF SEQ ID NOS: 65
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 4, Application US/09980916
GENERAL INFORMATION:
APPLICANT: M&E Biotech A/S
APPLICANT: Klysner, Steen
TITLE OF INVENTION: Method For Down-Regulating IL5 Activity
FILE REFERENCE: 3631-0112P
                                                                                                Query Match 100.0%; Score 74; DB 5; Length 12
Best Local Similarity 100.0%; Pred. No. 1.3e-06;
Matches 15; Conservative 0; Mismatches 0; Indels
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CURRENT FILING DATE: 2001-10-23
NUMBER OF SEQ ID NOS: 65
SOFWARE: Patentin Ver. 2.1
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                RESULT 14
US-09-980-916-54
Sequence 54, Application US/09980916
GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 15; Conservative
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TYPE: PRT
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i, OTHER INFORMATION: Identical to residues 65-115 in SEQ ID NO: 1
US-09-980-916-4
Query Match
Best Local Similarity 100.0%; Score 74; DB 5; Length 124;
Best Local Similarity 100.0%; Pred. No. 1.3e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps
Qy 1 QYIKANSKFIGITEL 15
IIIIIIIIIIIIIII
Db 59 QYIKANSKFIGITEL 73
Search Completed: January 29, 2002, 11:07:15
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(without alignments)
13.363 Million cell updates/sec
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2: /cgn2_6/ptodata/2/paa/JUSO_COMB.pep:*
3: /cgn2_6/ptodata/2/paa/JUSO_COMB.pep:*
4: /cgn2_6/ptodata/2/paa/JUSOB_COMB.pep:*
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9: /cgn2_6/ptodata/2/paa/JUSOB_COMB.pep:*
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/cgn2_6/ptodata/2/paa/US60_COMB.pep:*
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3148936 segs, 277657034 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                 OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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84
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Maximum DB seq length: 200000000
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Sequence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Sequence 23, Appl	Sequence 2, Appli	Sequence 17817, A	Sequence 4656, Ap	Sequence 3442, Ap	Sequence 4746, Ap	Sequence 25566, A	Sequence 121, App	Sequence 122, App
SUMMARIES	ΩI	US-09-763-397A-23	US-09-763-397A-2	US-09-248-796-17817	US-09-583-110-4656	US-09-107-433-3442	US-60-269-308-4746	US-09-417-507-25566	PCT-US00-07726-121	PCT-US00-07726-122
	DB	21	21	16	19	15	24	18	7	Н
	Length	17	350	743	169	174	225	62	86	86
æ	Query e Match Length DB	100.0	100.0	53.6	52.4	52.4	52.4	51.2	51.2	51.2
	Score	84	84	45	44	44	44	43	43	43
	Result No.	-	7	9	4	S	9	7	80	σ

1711, 4	1643	1703	Sequence 1/93, Ap	221.	27800				66	3853	3852,		882, 1	10, A	10,	⋖	Sequence 6, Appli		Seguence 14, Appl	Sequence 36938, A	Sequence 36939, A	Seguence 17910, A	Sequence 1564, Ap	Sequence 2, Appli	Sequence 17012, A		Sequence 15, Appl	Sequence 16, Appl	Sequence 5	Seguence 1829	Sequence 10, Appl	Sequence 16, Appl		Sequence 11, Appl
ď	11-00-323-300-T	15-00-140-394-10 115-00-760-476-1	US-09-160-4/3-1/9	115-60-245-201-2	US-60-173-464	US-60-191-637-3	US-60-191-681-2825	-09-SD	US-60-216-770-	US-09-391-631-	US-09-391-631	US-09-391-631-38	ns	ns	US-08-697-826A					PCT-US01-08631-	PCT-US01-08631-3	US-60-324-109-179	US-09-573-655A-	ď	US-60-324-109-1	ns-0		US-08-1	US-09-270-767-577	US-09-27(	US-09-147-729-1	US-09-284-327	us-09-632-426	US-09-632-570-11
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51.2	-	-	51.2	-		51.2		50.0				50.0			48.8		•	•				47.6					٠		46.4		46.4			46.4
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10	11	77	71	1,1	16	17	18	19	20	21	22	23	24	25	56	27	28	29	30	31	32	33	34	35	36	37	38	39	40		42	43	44	45

## ALIGNMENTS

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APPLICANT: The Government of the United States of America, as represented by the APPLICANT: The Government of the Department of Health and Human Services, Centers for APPLICANT: Control and Prevention
APPLICANT: Lal, Altaf A.
APPLICANT: Ping Shi, Ya
APPLICANT: Ping Shi, Ya
APPLICANT: Ping Shi, Xe
TITLE OF INVENTION: Recombinant Multivalent Malarial Vaccine Against Plasmodium Fa
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                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/763,397A CURRENT FILING DATE: 2001-02-16
                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: US 60/097,703
PRIOR FILING DATE: 1998-08-21
PRIOR APPLICATION NUMBER: PCT / US99/18869
PRIOR FILING DATE: 1999-08-19
Sequence 23, Application US/09763397A GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Plasmodium falciparum
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SOFTWARE: Patentin version 3.1
SEQ ID NO 23
LENGTH: 17
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; ORGANISM: Pla
US-09-763-397A-23
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APPLICANT: Lynn Doucette-Stamm et al.
APPLICANT: Lynn Doucette-Stamm et al.
APPLICANT: Lynn Doucette-Stamm et al.
TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococc TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics
TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics
FILE REFERENCE: PATHOD-07A
CURRENT APPLICATION NUMBER: US/09/583,110
CURRENT FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 60/085,131
PRIOR APPLICATION NUMBER: US 60/085,131
PRIOR FILING DATE: 1998-05-12
PRIOR FILING DATE: 1997-07-02
NUMBER OF SEQ ID NOS: 5322
SEQ ID NO 4656
LEMOTH: 169
LEMOTH: 169
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 19;
50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:

MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: CUNKNOWN>
COMPUTER: CUNKNOWN>
CORPATING SYSTEM: CUNKNOWN>
SOFTWARE: CUNKNOWN>
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,433
FILING DATE: 30-Un-1998
PRIOR APPLICATION NUMBER: 60,085131
FILING DATE: May 12, 1998
APPLICATION NUMBER: 60/051553
FILING DATE: JULY 2, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-011
TELECOMMUNICATION:
TELEPHONE: (781)893-5007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 44;
Pred. No.
           Sequence 4656, Application US/09583110 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 100 Beaver Street
                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Streptococcus pneumoniae US-09-583-110-4656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 3442: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 5206
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THE
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STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    52.4%;
50.0%;
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57 SRFLKKYKHELQDF 70
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                                                                                        Sequence 2, Application US/09763397A

Sequence 2, Application US/09763397A

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: The Government of the United States of America, as represented by the APPLICANT: The Government of the Department of Health and Human Services, Centers for Dis APPLICANT: Control and Prevention
APPLICANT: Lal, Altaf A.
APPLICANT: Lal, Altaf A.
APPLICANT: Hasnain, Seyed E.
TITLE OF INVENTION: Recombinant Multivalent Malarial Vaccine Against Plasmodium Falci
TITLE OF INVENTION NUMBER: US/09/763,397A
CURRENT APPLICATION NUMBER: US 60/097,703
PRIOR FILING DATE: 1998-08-11
PRIOR FILING DATE: 1998-08-21
PRIOR FILING DATE: 1998-08-19
NUMBER OF SEQ ID NOS: 26
SEPTIMARE: Patentin Version 3.1
SSETTIMA OF THE SETTIMA DATE: 1998-08-19
NUMBER OF SEQ ID NOS: 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 17817, Application US/09248796
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: WELLE ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: 107196.132
CURRENT APPLICATION UNMBER: US/09/248,796
CURRENT FILING DATE: 1999-02-12
NUMBER OF SEQ ID NOS: 28206
SEQ ID NO 17817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: Identity of amino acid sequences at the above locations are unknd US-09-248-796-17817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
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Pred. No. 2e+02;
2; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 84; DB 21;
illarity 100.0%; Pred. No. 2.5e-05;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: Recombinant DNA/Protein US-09-763-397A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 53.6%;
Best Local Similarity 64.3%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             317 LATRIMKKFKAEIRDFF 333
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 LATRLMKKFKAEIRDFF 17
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1 LATRLMKKFKAEIRDFF
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Best Local Similarity
Matches 17; Conservat
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US-09-248-796-17817
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                                                                                        RESULT 2
US-09-763-397A-2
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                                   Gaps
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Pred. No. 33;
3; Mismatches 4; Indels
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                                      Indels
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PCT-USO0-07726-121
Sequence 121, Application PC/TUSO007726
Sequence 121, Application PC/TUSO007726
GENERAL INFORMATION:
TITLE OF INVENTION: 50 Human Secreted Proteins
FILE REFERENCE: PS538PCT
CURRENT APPLICATION NUMBER: PCT/USO0/07726
CURRENT FILING DATE: 2000-03-23
EARLIER APPLICATION NUMBER: 60/126,597
EARLIER FILING DATE: 1999-03-26
EARLIER FILING DATE: 2000-01-07
NUMBER OF SEQ ID NOS: 128
SOFTWARE: PAPLICATION NUMBER: 60/174,877
FARLIER FILING DATE: 2000-01-07
NUMBER OF SEQ ID NOS: 128
SOFTWARE: PALENTIN Ver. 2.0
SEQ ID NO 121
FAMILY FILING DATE: 2.0
SEQ ID NO 121
FAMILY FILING DATE: 2.0
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Sequence 122, Application PC/TUSO007726
GENERAL INFORMATION:
TITLE OF INVENTION: 50 Human Secreted Proteins
FILE REFRENCE: PS538PCT
CURRENT FILING DATE: 2000-03-23
EARLIER PFLING DATE: 1999-03-26
EARLIER PILING DATE: 1999-03-26
EARLIER PILING DATE: 1999-03-26
EARLIER PILING DATE: 1999-03-26
EARLIER PILING DATE: 1990-03-26
EARLIER PILING DATE: 1990-03-26
SARUER PILING DATE: 1990-03-26
SARUER PILING DATE: 1990-03-26
SARUER PILING DATE: 2000-01-07
NUMBER OF SEQ ID NOS: 128
SOFTWARE: PALENTING PATE: 2000-01-07
SEQ ID NO 122
LENGTH: 86
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33;
        Pred. No. 22;
2; Mismatches
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Pred. No.
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53.3%;
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        72.78;
        Best Local Similarity 72.7
Matches 8; Conservative
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Best Local Similarity 53.3
Matches 8; Conservative
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Best Local Similarity 53.3
Matches 8; Conservative
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PCT-US00-07726-122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: Homo sapiens
PCT-US00-07726-121
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34 TRMMKEFKGEI 44
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PCT-US00-05988-1711
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ORGANISM:
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Sequence 4746, Application US/60269308

Sequence 4746, Application US/60269308

SEQUENCE 4746, Application Sequence 4746, Application Sequence 4746, Application September 4746

APPLICANT: Haselbeck, RW

APPLICANT: Syskind, JW

APPLICANT: Trawick, JD

TITLE OF INVENTION: Identification of Essential Genes in Staphylococcus aureus, Pseuch TITLE OF INVENTION: Application of Essential Genes in Staphylococcus aureus, Pseuch TITLE OF INVENTION: Application of Essential Genes in Staphylococcus aureus, Pseuch TITLE OF INVENTION: Application of Essential Genes in Staphylococcus aureus, Pseuch TITLE OF INVENTION: Application of Essential Genes in Staphylococcus aureus, Pseuch TITLE OF INVENTION: Application of Essential Genes in Staphylococcus aureus, Pseuch TITLE OF INVENTION: Application of Essential Genes in Staphylococcus aureus, Pseuch TITLE OF INVENTION: Application of Essential Genes in Staphylococcus aureus, Pseuch TITLE OF INVENTION: Application of Essential Genes in Staphylococcus aureus, Pseuch TITLE OF INVENTION: Application of Essential Genes in Staphylococcus aureus, Pseuch TITLE OF INVENTION: Application of Essential Genes in Staphylococcus aureus, Pseuch TITLE OF INVENTION: Application of Essential Genes in Staphylococcus aureus, Pseuch TITLE OF INVENTION: Application of Essential Genes in Staphylococcus aureus, Pseuch TITLE OF INVENTION: Application of Essential Genes in Staphylococcus aureus, Pseuch TITLE OF INVENTION: Application of Essential Genes in Staphylococcus aureus, Pseuch TITLE OF INVENTION: Application of Essential Genes in Staphylococcus aureus, Pseuch TITLE OF INVENTION: Application of Essential Genes in Staphylococcus aureus, Pseuch TITLE OF INVENTION: Application of Essential Genes in Staphylococcus aureus, Pseuch TITLE OF INVENTION: Application of Essential Genes in Staphylococcus aureus, Pseuch TITLE OF INVENTION: Application of Essential Genes in Staphylococcus aureus, Pseuch TITLE OF INVENTION: Application of Essential Genes in Staphylococcus aureus, Pseuch TITLE OF
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: KEITH G. WEINSTOCK ET AL.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ASPERGILLUS
TITLE OF INVENTION: FUNIGATUS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: PATH99-10
CURRENT APPLICATION NUMBER: US/09/417,507
CURRENT FILING DATE: 1999-10-14
NUMBER OF SEQ ID NOS: 44312
SEQ ID NO 25566
LENGTH: 62
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Pred. No. 52;
5; Mismatches 2; Indels
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                                                                                                                ORGANISM: Streptococcus pneumoniae
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LOCATION: (B) LOCATION 1...174
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SEQUENCE DESCRIPTION: SEQ ID NO: 3442:
US-09-107-433-3442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; ORGANISM: Enterococcus faecalis US-60-269-308-4746
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60.0%;
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 50.0
Matches 7; Conservative
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92 TNTMRDFEAEIRDEF 106
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62 SRFLKKYKHELQDF 75
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; ORGANISM: A.fumigatus
US-09-417-507-25566
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Best Local Similarity
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US-09-417-507-25566
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Sequence 1793, Application US/09760475

GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FITLE OF INVENTION: NUMBER: US/09/760.475
CURRENT APPLICATION NUMBER: US/09/760.475

CURRENT APPLICATION DATE: 2001-01-16
Prior application data removed - consult PALM or fille wrapper
NUMBER OF SEQ ID NOS: 4122

SEQ ID NO 1793

LIENGTH: 301
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Pred. No. 1.6e+02;
3; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PAPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies FILE REFERENCE: PT249
CURRENT APPLICATION NUMBER: US/09/760,475
CURRENT APPLICATION NUMBER: 2001-01-16
Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 4122
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 3102
LENGTH: 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 301;
                                                                  DB 24; Length 155;
67;
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Pred. No. 1.5e+02;
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                                                                                                                                   1; Mismatches
                                                                                              Score 43;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 3012, Application US/09760475 ; GENERAL INFORMATION:
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US-60-245-201-221
; Sequence 221, Application US/60245201
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53.3%;
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53.3%;
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81.8%;
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Best Local Similarity 53.3
Matches 8; Conservative
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Best Local Similarity 53.3
Matches 8; Conservative
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282 LATRFLKSFKANLEN 296
                                                                                                                                     Conservative
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CORGANISM: Homo sapiens
US-09-760-475-3012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: Homo sapiens
US-09-760-475-1793
                                                                                                                                                                                                    || |:||||||
53 LALRVMKKFKA 63
; TYPE: PRT
; ORGANISM: Drosophila
US-60-146-394-1642
                                                                                                                                                                               1 LATRLMKKFKA 11
                                                                                                Query Match
Best Local Similarity
Matches 9; Conserv
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                                                          TITLE OF INVENTION: Human Prostate Cancer Associated Gene Sequences and Polypeptides FILE REFERENCE: PA101PCT
CURRENT APPLICATION NUMBER: PCT/USO0/05988
CURRENT FILING DATE: 2000-03-08
EARLIER APPLICATION NUMBER: 60/124,270
EARLIER FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1890
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1111
LENGTH: 98
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US-60-146-394-1642
US-60-146-394-1642
Sequence 1642, Application US/60146394
GENERAL INFORMATION:
GENERAL INFORMATION:
TATLE OF INVENTION: ALOLATED DROSOPHILA PROTEINS, NUCLEIC
TITLE OF INVENTION: ALOLATED MOLECULES ENCODING DROSOPHILA PROTEINS, AND USES THERE
TITLE OF INVENTION: ACLO MOLECULES ENCODING DROSOPHILA PROTEINS, AND USES THERE
CURRENT APPLICATION NUMBER: US/60/146,394
CURRENT FILING DATE: 1999-07-29
NUMBER OF SEQ ID NOS: 1866
SOFTWARE: FastSEQ for Windows Version 3.0
SOFTWARE: FastSEQ for Windows Version 3.0
SOFTWARE: 156
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APPLICANT: Steve Ruben
TITLE CAP STEVE RUBen
TITLE CAP STEVE RUBEN
TITLE CAP STEVE RUBEN
CURRENT APPLICATION NUMBER: US/09/925,300
CURRENT APPLICATION NUMBER: PCT/US00/05988
PRIOR APPLICATION NUMBER: PCT/US00/05988
PRIOR APPLICATION NUMBER: PCT/US00/05988
PRIOR FILING DATE: 2000-03-08
PRIOR PLICATION NUMBER: 60/124,270
PRIOR PLICATION NUMBER: 1999-03-12
NUMBER OF SEQ ID NOS: 1890
SEQ ID NO 1711
LENGTH: 98
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Pred. No. 38;
3; Mismatches 4
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-925-300-1711; Sequence 1711, Application US/09925300; GENERAL INFORMATION:
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53.3%;
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Best Local Similarity 53.3
Matches 8; Conservative
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79 LATRELKSFKANLEN 93
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79 LATRFLKSFKANLEN 93
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US-09-925-300-1711
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PCT-US00-05988-1711
                                     APPLICANT: Craig Rosen, APPLICANT: Steve Ruben
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Matches 8; Conserv
                    GENERAL INFORMATION:
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LENGTH: 155

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GENERAL INFORMATION:

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TITLE OF INVENTION: DRUG-METABOLIZING PRASE II
TITLE OF INVENTION: DRUG-METABOLIZING PROFEINS, NUCLEIC ACID MOLECULES ENCODING
TITLE OF INVENTION: HUMAN DRUG-METABOLIZING PHASE II PROTEINS, AND USES THEREOF
TITLE OF INVENTION: HUMAN DRUG-METABOLIZING PHASE II PROTEINS, AND USES THEREOF
CURRENT APPLICATION NUMBER: US/60/245,201
CURRENT FILING DATE: 2000-11-03
NUMBER OF SEQ ID NOS: 381
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 221
LENGTH: 509
LENGTH: 509
LENGTH: 509
LYPE: PRT
ORGANISM: Human
US-60-245-201-221
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Pred. No. 2.8e+02;
3; Mismatches 4; Indels
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Best Local Similarity 53.3%;
Matches 8; Conservative
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490 LATRFLKSFKANLEN 504
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Query Match 52.4
Best Local Similarity 60.0
Matches 9; Conservative
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20.801 Million cell updates/sec
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/cgn2_6/ptodata/2/paa/NG6_NEW_COMB.pep:*
/cgn2_6/ptodata/2/paa/US07_NEW_COMB.pep:*
/cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep:*
/cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep:*
/cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep:*
/cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep:*
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-09-815-242-10689

US-09-708-427-10555

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US-09-708-427-30719

US-09-708-427-30719

US-09-708-427-30719

US-09-708-427-30718

US-09-708-427-29819

US-09-708-427-29818

US-09-708-427-29818

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US-09-708-427-29818

US-09-708-427-258149

US-09-708-427-58149

US-09-708-427-58148

US-09-708-427-35551

US-09-708-427-35551

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US-09-708-427-35551

US-09-708-427-35560

US-09-708-427-35560

US-09-708-427-58818

US-09-708-427-56869

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US-09-708-427-57881
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 173191 segs, 36597120 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUMMARIES
                                                                                                                                                                          January 29, 2002, 11:07:15
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                     OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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84
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Maximum DB seq length: 2000000000
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Match
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Sequence:
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Sequence 32986, A
Sequence 32981, A
Sequence 15113, A
Sequence 15113, A
Sequence 15111, A
Sequence 7669, Ap
Sequence 7669, Ap
Sequence 25460, A
Sequence 25460, A
Sequence 24589, A
Sequence 24589, A
Sequence 2459, A
Sequence 63471, A
Sequence 63469, A
Sequence 63471, A
Sequence 63471, A
Sequence 63469, A
Sequence 7373, Ap
       US-09-708-427-32985
US-09-708-427-32984
US-09-708-427-15113
US-09-708-427-15113
US-09-708-427-15111
US-09-620-394B-7669
US-09-620-394B-7667
US-09-708-427-25458
US-09-708-427-25458
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US-09-708-427-63469
US-09-760-446A-1237
US-09-897-516-7949
US-09-760-446A-1213
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1073
11122
1206
1807
191
191
207
337
483
330
330
1715
1715
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167
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APPLICANT: Obligation, Kari L.
APPLICANT: Obligation, Kari L.
APPLICANT: Wall, Daniel
APPLICANT: Wall, Daniel
APPLICANT: Traniel, John D.
APPLICANT: Traniel, John D.
APPLICANT: Traniel, John D.
APPLICANT: Traniel, John D.
APPLICANT: Vanamoto, Robert T.
APPLICANT: Vanamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: 1000-03-21
FILE REFERENCE: ELITRA, 011A
CURRENT FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-25
PRIOR FILING DATE: 2000-05-25
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/253,931
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-10-16
PRIOR PRILING DATE: 2000-10-16
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-24
PRIOR FILING DATE: 2000-10-26
Length 225 DB 5; Score 44; DB 5 Pred. No. 5.4; 2; Mismatches SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 5021 LENGTH: 225 Sequence 5021, Application US/09815242 GENERAL INFORMATION: APPLICANT: Haselbeck, Robert ; ORGANISM: Enterococcus faecalis US-09-815-242-5021 52.4%; 60.0%;

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Gaps

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Indels

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Sequence 10553 Application US/09708427
GENERAL INFORMATION:
APPLICANT: N. ALEXANDROW et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID
TITLE OF INVENTION: THEREBY
FILE REFERENCE: 2750-1243P
CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: Patentin version 3.1
SEQ ID NO 10553
LENGTH: 353
                                                                                                                                                                                                   US-09-108-427-10554
US-09-08-427-10554
US-09-08-427-10554
US-09-08-427-10554
Sequence 10554, Application US/09708427
GENERAL INFORMATION:
APPLICANT: N. ALEXANDROW et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID
TITLE OF INVENTION: THEREBY
FILE REPRESENCE: 2750-1243
CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT PILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 8354
SSEQ ID NO 10554
LENGTH: 335
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Length 297;
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Pred. No. 12;
4; Mismatches
  Score 43; DB 5;
Pred. No. 11;
1; Mismatches
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OTHER INFORMATION: Xaa is any amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc_feature
; LOCATION: 1..335
; OTHER INFORMATION: Ceres Seq. ID 1821589
08-09-708-427-10554
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LOCATION: 1.353
CTHER INFORRATION: Ceres Seq.
US-09-708-427-10553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc_feature
LOCATION: 1..335
OTHER INFORMATION: Xaa is any
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58.3%;
      51.2%;
58.3%;
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Matches 7; Conservative
                                                  Conservative
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74 LDKFKSDIQDFF 85
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36 LDKFKSDIQDFF 47
                                                                                           6 MKKFKAEIRDFF 17
      Query Match
Best Local Similarity
Matches 7; Conserv
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Sequence 10555, Application US/09708427

Sequence 10555, Application US/09708427

Sequence 10555, Application US/09708427

GENERAL INFORMATION:

APPLICANT: N. ALEXANDROV et al.

TITLE OF INVENTION: THEREBY

TITLE OF INVENTION: THEREBY

TITLE OF INVENTION: THEREBY

CURRENT APPLICATION NUMBER: US/09/708, 427

CURRENT PELING DATE: 2000-11-09

NUMBER OF SEQ ID NOS: 85364

SOFTWARE: PATENTIN VERSION 3.1

SEQ ID NO 10555
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TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 5;
                                                                                                                                                                                                                                                                                          FILE REFERENCE: ELITRA JULA
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR PELLING DATE: 2001-03-21
PRIOR FILING DATE: 2000-03-21
PRIOR PRILING DATE: 2000-03-23
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR PRILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR SPLICATION NUMBER: 60/259,308
PRIOR FILING DATE: 2001-02-05
PRIOR SEQ ID NOS: 14110
SOFTWARE: FASSERQ FOR WINDOWS VERSION 4.0
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LOCATION: 1.297
OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc_feature
LOCATION: 1.297
OTHER INFORMATION: Ceres Seq. ID 1821590
US_09-708-427-10555
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Pred. No.
             Sequence 10689, Application US/09815242 GENERAL INFORMATION:
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US-09-815-242-10689
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                                                                                                                                            Trawick, John D.
Carr, Grant J.
Yamamoto, Robert T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       52.4%;
60.0%;
                                                                                Ohlsen, Kari L.
Zyskind, Judith W.
Wall, Daniel
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Best Local Similarity 60.0
Matches 9; Conservative
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92 TNTMRDFEAEIRDEF 106
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SEQ ID NO 10689
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APPLICANT:
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THE REAL PROPERTY.

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APPLICANT: N. ALEXANDROV et al.

TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID
TITLE OF INVENTION: THEREBY
FILE REPERENCE: 2750-1243P
CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILIG DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PAPLICANT: N. ALEXANDROV et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID
TITLE OF INVENTION: THEREBY
FILE REFERENCE: 2750-1243P
CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: Patentin version 3.1
SEQ ID NO 29820
LENGTH: 593
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Pred. No. 22;
1; Mismatches
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34;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 42;
Pred. No. 3
                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; LOCATION: 11.398
; OTHER INFORMATION: Ceres Seq. ID 1830097
US-09-708-427-30717
                                                                                                                             ; Sequence 30717, Application US/09708427; GENERAL INFORMATION:
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GENERAL INFORMATION:
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61.5%;
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Best Local Similarity 60.0.
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Best Local Similarity 61.5
Matches 8; Conservative
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165 ATRLFKKLRVEIEMF 179
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   2 ATRLMKKFKAEIRDF 16
                                    85 ATRLFKKLRVEIEMF 99
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LOCATION: 1..398
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                                                                                         RESULT 8
US-09-708-427-30717
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                                                                                                                                                                                                                                                                                                            SEQ ID NO 30717
LENGTH: 398
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Sequence 30718, Application US/09708427
Sequence 30718, Application US/09708427
GENERAL INFORMATION:
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: THEREBY
TITLE OF INVENTION: THEREBY
TITLE OF INVENTION: THEREBY
CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: PATENTIN version 3.1
SEQ ID NO 30718
LENGTH: 318
                                                                                                                                                                                                                 APPLICANT: N. ALEXANDROV et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: THERBY
TITLE OF INVENTION: THERBY
FILE REFERENCE: 2750-1243P
CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: Patentin version 3.1
SEQ ID NO 30719
LENGTH: 313
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                    Gaps
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                    Indels
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17;
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Pred. No. 17;
1; Mismatches
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Pred. No. 13;
4; Mismatches
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LOCATION: 1..313
OTHER INFORMATION: Xaa is any amino acid
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; LCCATION: 1.313
. CTHER INFORMATION: Ceres Seq. ID 1830099
US-09-708-427-30719
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NAME/KEY: misc_feature
LOCATION: 1..318
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                                                                                                                                            RESULT 6
8-09-708-427-30719
Sequence 30719, Application US/09708427
GENERAL INFORMATION:
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60.0%;
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 58.3%;
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Best Local Similarity 60.0
Matches 9; Conservative
 Best Local Similarity 58.3
Matches 7; Conservative
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Matches 9; Conservative
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92 LDKFKSDIQDFF 103
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LOCATION: 1..318
                                                     6 MKKFKAEIRDFF 17
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US-09-708-427-19349

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Sequence 16 Application US/09708427

Sequence 17 ALEXANDROV et al.

APPLICANT: N. ALEXANDROV et al.

TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID

TITLE OF INVENTION: THEREBY

FILE REFERENCE: 2750-1143P

CURRENT APPLICATION NUMBER: US/09/708,427

CURRENT APPLICATION NUMBER: 2000-11-09

NUMBER OF SEQ ID NOS: 85364

SOCTHARRE: Patentin version 3.1

SEQ ID NO 19349
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TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID
TITLE OF INVENTION: THEREBY
TITLE OF INVENTION: THEREBY
FILE REFERENCE: 2750-1243P
CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 19348
LENGTH: 314
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24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 5;
23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 41; DB 5
Pred. No. 23;
3; Mismatches
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NAME/KEY: misc_feature
CACATION: 1.314
US-09-708-427-19348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 41;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: Ceres Seq. ID 1835886 US-09-708-427-19349
                                                                                                                                                                                                                                                                                                                                                    amino acid
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US-09-708427-19347
; Sequence 19347, Application US/09708427
; GENERAL INFORMATION:
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; Sequence 19348, Application US/09708427
; GENERAL INFORMATION:
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ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                          ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                             NAME/KEY: misc_feature
LOCATION: 1..303
OTHER INFORMATION: Xaa is any
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Best Local Similarity 66.7
Matches 8; Conservative
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LOCATION: 1..314
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| 139 RVMKKVQAEIRE 150
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128 RVMKKVQAEIRE 139
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Matches 8; Conserv
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GENERAL INFORMATION:
APPLICANT: N. ALEXANDROV et al.
APPLICANT: N. ALEXANDROV et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: THEREBY
FILE REFERENCE: 2750-1243P
FURBER APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: Patentin version 3.1
SEQ ID NO 29818
LENGTH: 743
                                                                   Sequence 29819, Application US/09708427
GENERAL INFORMATION:
APPLICANT: N. ALEXANDROV et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: THEREBY
FILE REFERENCE: 2750-1243P
CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 1000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: PATENTIN VERSION 3.1
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40;
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Pred. No. 44;
1; Mismatches
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Pred. No. 40;
1; Mismatches
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LOCATION: 1..743
OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc_feature
LOCATION: 1..743
OTHER INFORMATION: Ceres Seq. ID 1827156
                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc_feature
CCATION: 1..686
CTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc_feature
CCATION: 1..686
CTHER INFORMATION: Ceres Seq. ID 1827157
US-09-708-427-29819
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61.5%;
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61.5%;
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Best Local Similarity 61.5
Matches 8; Conservative
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285 LMKKFQTSTRDLF 297
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Best Local Similarity
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US-09-708-427-29818
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LENGTH: 686
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us-09-763-397a-23.rapn

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US-09-708-427-58150
Sequence 58150, Application US/09708427
GENERAL INFORMATION:
TERRETAIN OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: THEREBY
TITLE OF INVENTION: THEREBY
FILE REFERENCE: 2750-1243P
CURRENT PPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOGTWARE: PATENTIN VEXSION 3.1
SEQ ID NO 58150
LENGTH: 302
APPLICANT: N. ALEXANDROV et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: THEREBY
FILE REFERENCE: 2750-1243P
FILE REFERENCE: 2750-1243P
CURRENT PILLOGATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: PATENTIN VERSION 3.1
LENGTH: 503
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Pred. No. 41;
3; Mismatches 1; Indels
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NAME/KEY: misc_feature
LOCATION: 1..302
OTHER INPORMATION: Xaa is any amino acid
NAME/KEY: misc_feature
LOCATION: 1..302
COCATION: 1..302
COTHER INFORMATION: Ceres Seq. ID 1941286
US-09-708-427-58150
                                                                                                                                                                                                                                                                                                               NAME/KEY: misc_feature
LOCATION: 1..503
COTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc_feature
LOCATION: 1..503
COTHER INFORMATION: Ceres Seq. ID 1835884
US-09-708-427-19347
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ORGANISM: Zea mays subsp. mays
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Best Local Similarity 66.7%;
Matches 8; Conservative
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119 RVMKKLQAEVRAY 131
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328 RVMKKVQAEIRE 339
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Search completed: January 29, 2002, 11:07:15 Job time: 533 sec

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Best Local Similarity 100.
Matches 17; Conservative
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Sequence 15071, A
Sequence 15071, A
Sequence 408, App
Sequence 26094, A
Sequence 26094, A
Sequence 26094, A
Sequence 26094, A
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13.363 Million cell updates/sec
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1: /cgn12_6/ptodata/2/paa/US06_COMB.pep:*
2: /cgn2_6/ptodata/2/paa/US06_COMB.pep:*
3: /cgn2_6/ptodata/2/paa/US080_COMB.pep:*
4: /cgn2_6/ptodata/2/paa/US081_COMB.pep:*
5: /cgn2_6/ptodata/2/paa/US081_COMB.pep:*
6: /cgn2_6/ptodata/2/paa/US081_COMB.pep:*
7: /cgn2_6/ptodata/2/paa/US081_COMB.pep:*
8: /cgn2_6/ptodata/2/paa/US082_COMB.pep:*
9: /cgn2_6/ptodata/2/paa/US086_COMB.pep:*
10: /cgn2_6/ptodata/2/paa/US086_COMB.pep:*
11: /cgn2_6/ptodata/2/paa/US086_COMB.pep:*
12: /cgn2_6/ptodata/2/paa/US080_COMB.pep:*
13: /cgn2_6/ptodata/2/paa/US091_COMB.pep:*
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16: /cgn2_6/ptodata/2/paa/US091_COMB.pep:*
17: /cgn2_6/ptodata/2/paa/US092_COMB.pep:*
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13: /cgn2_6/ptodata/2/paa/US092_COMB.pep:*
14: /cgn2_6/ptodata/2/paa/US092_COMB.pep:*
15: /cgn2_6/ptodata/2/paa/US092_COMB.pep:*
16: /cgn2_6/ptodata/2/paa/US092_COMB.pep:*
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18: /cgn2_6/ptodata/2/paa/US092_COMB.pep:*
19: /cgn2_6/ptodata/2/paa/US092_COMB.pep:*
10: /cgn2_6/ptodata/2/paa/US092_COMB.pep:*
11: /cgn2_6/ptodata/2/paa/US092_COMB.pep:*
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/cgn2_6/ptodata/2/paa/US098_COMB.pep:*
/cgn2_6/ptodata/2/paa/US099_COMB.pep:*
/cgn2_6/ptodata/2/paa/US60_COMB.pep:*
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-09-763-397A-2
US-60-191-637-15071
US-60-191-681-11903
US-60-324-109-26094
US-60-324-109-26094
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US-09-715-774-10
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Maximum Match 100%
Listing first 45 summaries
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    protein search, using sw model

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Gapop 10.0 , Gapext 0.5
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Match 1
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Maximum DB
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No.
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Gaps

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Length 17; Indels

Score 79; DB 21; Pred. No. 0.00015; Mismatches 0;

g

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GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: LI, Peter, W.D.

TITLE OF INVENTION: ISOLATED DROSOPHILA PROTEINS, NUCLEIC

TITLE OF INVENTION: ACID MOLECULES ENCODING ISOLATED DROSOPHILA PROTEINS AND

TITLE OF INVENTION: USES THERDER.

FILE REFERENCE: C1000390

CURRENT PILING DATE: 2000-03-23

NUMBER OF SEQ ID NOS: 30973

SOFTWARE: Faster for Windows Version 4.0

SEQ ID NO 11903

LENGTH: 2559
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: (51)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Xea equals any of the naturally occurring L-amino acids US-09-758-443-408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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US-09-758-443-408
US-09-758-443-408
Sequence 408, Application US/09758443
GENERAL INFORMATION:
APPLICANT: ROSEN et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REPERENCE: PM039
CURRENT FILING DATE: 2001-01-11
PRIOR PPLICATION NUMBER: 60/179,065
PRIOR FILING DATE: 2000-01-31
PRIOR FILING DATE: 2000-01-31
PRIOR FILING DATE: 2000-01-31
PRIOR FILING DATE: 2000-01-34
NUMBER OF SEQ ID NOS: 432
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 408
LENGTH: 81
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Pred. No. 7.98+02;
1; Mismatches 2; Indels
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Sequence 11903, Application US/60191681
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58.8%;
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Best Local Similarity 58.8
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 63.3
Best Local Similarity 76.9
Matches 10; Conservative
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645 PSSTDNSPSNAKS 657
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                                                                                                                                                                                                                                                                                                                                 ; ORGANISM: DROSOPHILA
US-60-191-681-11903
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US-60-324-109-26094
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US-09-763-397A-2

US-09-763-397A-2

Sequence 2, Application US/09763397A

Sequence 2, Application US/09763397A

Sequence 2, Application US/09763397A

Sequence 2, Application US/09763397A

Sequence 2, Applicant: Content of the United States of America, as represented by the APPLICANT: Secretary of the Department of Health and Human Services, Centers for Dis APPLICANT: Control and Prevention

APPLICANT: Lal, Altaf A.

APPLICANT: Lal, Altaf A.

APPLICANT: Seved E.
                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Recombinant Multivalent Malarial Vaccine Against Plasmodium Falci
TITLE OF INVENTION: Recombinant Multivalent Malarial Vaccine Against Plasmodium Falci
FILE REFERRNCE: 6395-57049
FILE REFERRNCE: 6395-57049
CURRENT PAPLICATION NUMBER: US/09/763,397A
CURRENT FILING DATE: 2001-02-16
PRIOR APPLICATION NUMBER: US 60/097,703
PRIOR PAPLICATION NUMBER: PCT / US99/18869
PRIOR PAPLICATION NUMBER: PCT / US99/18869
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patentin version 3.1
SSQ ID NO SEQ ID NOS: 26
LENGTH: 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: UNCLEIC ACID DETECTION KITS COMPRISING
TITLE OF INVENTION: UNCLEIC ACID DETECTION KITS COMPRISING
TITLE OF INVENTION: GENE SEQUENCES EXPRESSED FROM THE DROSOPHILA GENOME, AND
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: CLOO0392
CURRENT APPLICATION UNMBER: US/60/191,637
CURRENT FILING DATE: 2000-03-23
NUMBER OF SEQ ID NOS: 42660
SOFTMARRE: FastSEQ for Windows Version 4.0
SEQ ID NO 15071
LENGTH: 2559
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Pred. No. 0.16;
0; Mismatches 0; Indels 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: Recombinant DNA/Protein US-09-763-397A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 15071, Application US/60191637 GENERAL INFORMATION:
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94.4%;
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Matches 10; Conservative
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Best Local Similarity 94.4
Matches 17; Conservative
                 1 SSPSSTKSSPSNVKSAS 17
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645 PSSTDNSPSNAKS 657
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US-60-191-637-15071
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US-60-191-681-11903

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; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-09-715-774-10
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    SOFTWARE: Patentin Ver. 2.0
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Matches 11; Conservative
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Best Local Similarity 64.7
Matches 11; Conservative
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ORGANISM: Homo sapiens
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LOCATION: (1)...(106)
                                                             TYPE: PRT CORGANISM: Arabidopsis PCT-US99-08954-2
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                     SEQ ID NO 2
LENGTH: 328
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Sequence 2 Application PC/TUS9908954
Sequence 2 Application PC/TUS9908954
Sequence 2 Application PC/TUS9908954
Sequence 2 Application PC/TUS9908954
Sequence 2 Application Fair Edit Policy Proceedings  
APPLICANT: Secondary, Howard M.
APPLICANT: Goodman, Howard M.
APPLICANT: Goodman, Howard M.
TITLE OF INVENTION: QUALITY AND COLD-TOLERANCE
FILE REFERENCE: 480.89(HV)
CURRENT APPLICATION NUMBER: PCT/US99/08954
CURRENT PILING DATE: 1999-04-27
NUMBER OF SEQ ID NOS: 16
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                               APPLICANT: Cao, Yongwei
APPLICANT: Edgerton, Michael D
APPLICANT: Edgerton, Michael D
APPLICANT: Hinkle, Gregory J.
APPLICANT: Liu, Jingdong
APPLICANT: Liu, Jingdong
APPLICANT: Stein, Joshua
TITLE OF INVENTION: CDNA SEQUENCES AND USES FOR PLANT IMPROVEMENT
FILE REFERENCE: 38-10(52726)8
CURRENT APPLICATION NUMBER: US/60/324,109
CURRENT FILING DATE: 2001-09-21
NUMBER OF SEQ ID NOS: 33196
SEQ ID NO 26094
LENGTH: 179
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Pred. No. 74;
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Pred. No. 1.5e+02;
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GENERAL INFORMATION:
SAPPLICANT: Helentjaris, Tim
TITLE OF INVENTION: Modulation of Abscisic Acid
FILE REFERENCE: 35718/205302
CURRENT ELLING DATE: 2000-11-27
PRIOR PILING DATE: 1999111-17
PRIOR FILING DATE: 199911-17
NUMBER OF SEQ ID NOS: 12
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2; Mismatches
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Sequence 26094, Application US/60324109 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                             60.8%;
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64.7%;
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Matches 11; Conservative
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Matches 11; Conservative
                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                  US-60-324-109-26094
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Sequence 1145. Application US/60173469
GENERAL INFORMATION:
APPLICANT: BONAZZI, VIVIEN
TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
TITLE OF INVENTION: USES THEREOF
TITLE OF INVENTION: USES THEREOF
                                                                                                                                  Sequence 18722, Application US/6017571

SEQUENCE INFORMATION:
APPLICANT: BONAZZI, VIVIEN
APPLICANT: BONAZZI, VIVIEN
TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS,
TITLE OF INVENTION: AND USES THEREOF
FILE REPERENT ELING DATE: 2000-01-27
UURRENT FILING DATE: 2000-01-27
NUMBER OF SEQ ID NOS: 5082
SOFTWARE: FRALESE for Windows Version 4.0
SEQ ID NO 3322
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CURRENT FILING DATE: 2001-01-11

PRIOR FILING DATE: 2000-01-31

PRIOR FILING DATE: 2000-02-04

NUMBER OF SEQ ID NOS: 406

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 176;
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Pred. No. 1.6e+02;
1; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 46; DB 24;
Pred. No. 1.4e+02;
1; Mismatches 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-758-459-219; Sequence 219, Application US/09758459; GENERAL INFORMATION:
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64.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100 SSPSSLSTSPPEVFSAS 116
                          145 SSPSSLSTSPPEVFSAS 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 SSPSSTKSSPSNVKSAS 17
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Best Local Similarity 64.7
Matches 11; Conservative
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Best Local Similarity 64.7;
Matches 11; Conservative
  1 SSPSSTKSSPSNVKSAS 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
CORGANISM: Homo sapiens
US-09-758-459-219
                                                                                                                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: HUMAN
US-60-177-571-3322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 15
US-60-173-469-1145
                                                                                                          RESULT 13
US-60-177-571-3322
                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
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TITLE OF INVENTION: USCLATED HUMAN SECRETED PROTEINS,
TITLE OF INVENTION: USES THEREOF
FILLE OF INVENTION: USES THEREOF
FILLE REFERENCE: CLOOOLS4
CURRENT APPLICATION NUMBER: US/60/169,840
SURRENT FILLNE DATE: 1999-12-09
NUMBER OF SEQ ID NOS: 9628
SOFTWARE: FASTESEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                         US-60-324-109-18117

Sequence 18117, Application US/60324109

SERNEAL INFORMATION:

APPLICANT: Cao, Yongwei

APPLICANT: Edgerton, Michael D

APPLICANT: Movalic, David K.

APPLICANT: Kovalic, David K.

APPLICANT: Liu, Jingdong

APPLICANT: Liu, Jingdong

APPLICANT: CDNA SEGUENCES AND USES FOR PLANT IMPROVEMENT

FILE REFERENCE: 38-10(52726)B

CURRENT APPLICATION UNMBER: US/60/324,109

CURRENT APPLICATION 12001-09-21

NUMBER OF SEQ 1D NOS: 33196

SEQ 1D NO 18117
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                                                                                      Length 106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4; Indels
                                                                                                                                  4; Indels
; OTHER INFORMATION: Xaa - X or * as defined in Table PCT-US01-08631-37162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 46; DB 24; L
Pred. No. 1.4e+02;
1; Mismatches 5;
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Pred. No. 1.2e+02;
                                                                                      Score 46; DB 1;
Pred. No. 79;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
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COCATION: (1)...(174)
COTHER INFORMATION: Xaa = Any Amino Acid
US-60-169-840-5493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 5493, Application US/60169840 GENERAL INFORMATION:
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ilarity 64.7%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 58.2%;
Best Local Similarity 58.8%;
Matches 10; Conservative
                                                                                           58.2%;
58.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 SSPSSTKSSPSNVKSAS 17
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                                                                                                                                                                                                     41 SSPSSSSPSPSSSSSS 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Bonazzi, Vivien
                                                                                                                                      Conservative
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Best Local Similarity
Matches 11; Conserv
                                                                                           Query Match
Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Zea mays
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ORGANISM: Human
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LENGTH: 174
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Sequence 16088, A Sequence 384, App Sequence 119, App Sequence 119, App Sequence 119, App Sequence 8245, A Sequence 118, App Sequence 3137, Ap Sequence 3137, Ap Sequence 3136, Ap Sequence 3889, Ap Sequence 3689, Ap Sequence 5596, Ap Sequence 76259, A
                                                                                                                                                                                     (without alignments)
20.801 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                            Search time 29.91 Seconds
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Compugen Ltd
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US-09-801-368-384

US-09-637-780B-120

US-09-637-780B-119

US-09-708-427-82454

US-09-708-427-82455

US-09-708-427-82453

US-09-708-427-118

US-09-708-427-1137

US-09-708-427-1137

US-09-708-427-3136

US-09-708-427-3136

US-09-708-427-33689

US-09-708-427-33008

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US-09-708-427-5596

US-09-708-427-5596

US-09-708-427-76259

US-09-708-427-76258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           173191 seqs, 36597120 residues
                                                                                                                                                      January 29, 2002, 10:58:22;
GenCore version
Copyright (c) 1993 - 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                         sw model
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                     1 SSPSSTKSSPSNVKSAS 17
                                                                                                         protein search, using
                                                                                                                                                                                                                                                     US-09-763-397A-22
79
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Match Length
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Sequence:
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Maximum DB
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                                                                                                                                                            Run on:
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No.
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Sequence 16088, Application US/09708427
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: N. ALEXANDROV et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID
TITLE OF INVENTION: THEREBY
FILE REPERENCE: 2750-1143P
CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOOTHARE: Patentin version 3.1
SEQ ID NO 16088
LENGTH: 328
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     4982, Ap
4981, Ap
3568, Ap
17129, A
17128, A
17127, A
3567, Ap
                                                                                                                                                                                                424, Appl
2, Appli
4152, Ap
47194, A
761, App
47193, A
4151, Ap
                                                                                                                                                                                                                                                                                                                                                                                           66585, A
7376, Ap
61, Appl
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                           Sequence Seq
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US-09-620-111B-4982

US-09-620-11B-4981

US-09-708-427-3568

US-09-708-427-17129

US-09-708-427-17129

US-09-708-427-17127

US-09-708-427-3567

US-09-801-388-424

US-09-964-238-2

US-09-964-238-2

US-09-964-238-2

US-09-964-238-2

US-09-9620-111B-4152

US-09-620-111B-761

US-09-620-111B-761

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US-09-620-111B-760

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Pred. No. 2.7;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc_feature
LOCATION: 1..328
COTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc_feature
LOCATION: 1..328
OTHER INFORMATION: Ceres Seq. ID 1830172
US-09-708-427-16088
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 384, Application US/09801368 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    60.8%;
64.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Busby, Robert
APPLICANT: Cali, Brian
APPLICANT: Hecht, Peter
APPLICANT: Holtzman, Doug
APPLICANT: Madden, Kevin
APPLICANT: Maxon, Mary
APPLICANT: Milne, Todd
APPLICANT: Norman, Thea
APPLICANT: Salama, Sofie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               113 SSPSSVSSSSSSVSAAS 129
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Matches 11; Conservative
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US-09-801-368-384
       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
     Dp
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TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptid;
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptid;
TITLE OF INVENTION: Thereby
FILE OF EMPRINE: 2750-1096F
CURRENT FILING DATE: 2000-08-11
NUMBER OF SEQ ID NOS: 1401
SEQ ID NO 119
LENGTH: 200
                                                                                                                             APPLICANT: BROVER, Vyacheslav
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptid
TITLE OF INVENTION: Thereby
FITE REFERENCE: 2750-1096P
CURRENT APPLICATION NUMBER: US/09/637,780B
CURRENT APPLICATION NUMBER: US/09/637,780B
SEQ ID NOS: 1401
SEQ ID NOS: 1401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 46; DB 5; Length 208; Pred. No. 3.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 200;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 46; DB 5;
Pred. No. 3.3;
3; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: Ceres Seq. ID 1481702 US-09-637-780B-119
                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc_feature
LCCATION: 1..200
CTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc_feature
LCCATION: 1..200
OTHER INFORMATION: Ceres Seq. ID 1481703
US-09-637-780B-120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: Xaa is any amino acid
                                                              Sequence 120, Application US/09637780B GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                   ORGANISM: Arabidopsis thaliana
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58.8%;
                                                                                                        APPLICANT: ALEXANDROV, Nickolai
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58.8%;
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LOCATION: 1..208
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Best Local Similarity
Matches 10; Conserv
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Best Local Similarity
Matches 10; Conserv
                                 RESULT 4
JS-09-637-780B-120
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APPLICANT: Sherman, Amir
APPLICANT: Silva, Jeff
APPLICANT: Summers, Eric
APPLICANT: Summers, Eric
APPLICANT: Summers, Eric
TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungi
FILE REFERENCE: 109272.147
CURRENT PAPLICATION NUMBER: 0S/09/801,368
CURRENT PAPLICATION NUMBER: US 09/487,558
PRIOR PILING DATE: 2000-03-07
PRIOR FILING DATE: 2000-03-07
PRIOR PILING DATE: 1999-10-20
NUMBER OF SEQ ID NOS: 440
SEQ ID NO 384
LENGTH: 515
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TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production
TITLE OF INVENTION: in Fungi
                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                    DB 5; Length 515;
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3; Mismatches
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CURRENT APPLICATION NUMBER: US/09/487,558
CURRENT FILING DATE: 2000-01-19
PRIOR APPLICATION NUMBER: US/09/801,368
PRIOR APPLICATION NUMBER: US 09/487,558
PRIOR PLING DATE: 2000-01-19
PRIOR PLING DATE: 2000-01-19
PRIOR PLING DATE: 1999-10-20
                                                                                                                                                                                                                                                                                                                                                                                                        Score 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 384, Application US/09487558
GENERAL INFORMATION:
APPLICANT: Busby, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Saccharomyces cerevisiae US-09-487-558-384
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Best Local Similarity 56.2

Best Local 9; Conservative
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Hecht, Peter
Holtzman, Doug
Madden, Kevin
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Best Local Similarity 56.2
Matches 9; Conservative
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Salama, Sofie
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Milne, Todd
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APPLICANT:
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Gaps 0 SIPTSLKSSPAPVTSGS 141 1 SSPSSTKSSPSNVKSAS 17 RESULT

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Gaps

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130 SPSSTNSTPSTIQGLS 145

2 SPSSTKSSPSNVKSAS 17

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...rllCanT: BROVER, Vyacheslav
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptid
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptid
TITLE OF INVENTION: Thereby
FILE REFERENCE: 2750-1096P
CURRENT APPLICATION NUMBER: US/09/637,780B
CURRENT FILING DATE: 2000-08-11
NUMBER OF SEQ ID NOS: 1401
LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: N. ALEXANDROW et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID
TITLE OF INVENTION: THEREBY
FILE REPERENCE: 2750-1243P
CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 89364
SEQ TWARE: Patentin version 3.1
LENGTH: 297
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; GENERAL INFORMATION:
; APPLICANT: N. ALEXANDROV et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID;
; TITLE OF INVENTION: THEREBY
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5;
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Pred. No. 5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3; Mismatches
                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc_feature
LOCATION: 1..297
UOCHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc_feature
LOCATION: 1..297
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Pred. No. 5
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CATTON: 1..297

SOTHER INFORMATION: Ceres Seq. ID 1960817

19.09-708-427-82453
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US-09-637-780B-118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 82453, Application US/09708427; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Zea mays subsp. mays
                                                                                                                                                                                                                                                                                            ORGANISM: Arabidopsis thaliana
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58.8%;
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58.8%;
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Best Local Similarity 58.8
Matches 10; Conservative
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LOCATION: 1..297
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US-09-708-427-11927
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                                                                                                                               Sequence 82454, Application US/09708427
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRACMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: THEREBY
TITLE OF INVENTION: THEREBY
TITLE OF INVENTION: THEREBY
TITLE OF INVENTION: THEREBY
CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
SOFTWARE: PALENTING DATE: 2000-11-09
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Pred. No. 4.5;
3; Mismatches
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; LOCATION: 1..273
: OTHER INFORMATION: Ceres Seq. ID 1960818
US-09-708-427-82454
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US-09-708-427-82455
                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION: Xaa is any amino acid
                                                                                               Sequence 82455, Application US/09708427 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Zea mays subsp. mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Zea mays subsp. mays
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58.8%;
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Best Local Similarity 58.8
Matches 10; Conservative
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Best Local Similarity 58.8
Matches 10; Conservative
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LOCATION: 1..272
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LOCATION: 1..272
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LOCATION: 1..273
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APPLICANT: BROVER, Vyacheslav
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptid
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptid
FILE REFERENCE: 2750-1067P
CURRENT APPLICATION NUMBER: US/09/620,394B
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 9131
SEQ ID NO 3870
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-708-427-3135
Sequence 3135, Application US/09708427
Sequence 3135, Application US/09708427
GENERAL INFORMATION:
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID
TITLE OF INVENTION: THEREBY
FILLE REFERENCE: 2750-1243P
CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT APPLICATION NUMBER: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 3135
LENGTH: 1194
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Pred. No. 45;
4; Mismatches
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46;
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LOCATION: 1..1194
OTHER INFORMATION: Xaa is any amino acid
NAME/KFF: misc_feature
LOCATION: 1..1194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; LOCATION: 1..1194
; OTHER INFORMATION: Ceres Seq. ID 1810130
US-09-708-427-3135
                                                                      TYPE: PRT
ORGANISM: Arabidopsis thaliana
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1..1170
OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc_feature
LOCATION: 1..1170
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Pred. No.
                                                                                                                                                                                                                      OTHER INFORMATION: Ceres Seq. ID 1810131
US-09-708-427-3136
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GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Arabidopsis thaliana
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            SOFTWARE: PatentIn version 3.1
SEQ ID NO 3136
LENGTH: 1170
                                                                                                                                                                                                                                                                                                     55.7%;
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838 NSPSSSSSSSTTPIPSPS 854
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                                                                                                                                                                                                                                                                                                                                                                           1 SSPSSTKSSPSNVKSAS 17
                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 52.9
Matches 9; Conservative
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NUMBER OF SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
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GENERAL INFORMATION:
APPLICANT: N. ALEXANDROV et al.
APPLICANT: N. ALEXANDROV et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: THEREBY
TITLE OF INVENTION: THEREBY
TITLE OF INVENTION: THEREBY
TITLE OF INVENTION: THEREBY
CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: N. ALEXANDROV et al.
APPLICANT: N. ALEXANDROV et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: THEREBY
FILE REPERBENCE: 2750-11243P
CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SEQ ID NO 3137
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                                                                                                                                                                                                                                                                                                                                                                                                         4; Indels
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Pred. No. 44;
                                                                                                                                                                                                                                                                                                                                                                     Score 44; DB 5;
Pred. No. 7.7;
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                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                            LOCATION: 1..239
CTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc_feature
LOCATION: 1..229
CTHER INFORMATION: Ceres Seq. ID 1824027
US-09-708-427-11927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ID 1810132
                      CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOCTWARE: PatentIn version 3.1
EEQ ID NO 11927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 3137, Application US/09708427 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc_feature
CATOTON: 1..1157
CTHER INFORMATION: Xaa is any am;
NAME/KEY: misc_feature
CATION: 1..1157
CTHER INFORMATION: Ceres Seq. IE
US-09-708-427-3137
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58.8%;
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                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 58.8
Matches 10; Conservative
          FILE REFERENCE: 2750-1243P
                                                                                                                                                                                                      NAME/KEY: misc_feature LOCATION: 1..229
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Best Local Similarity
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US-09-708-427-3136
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RESULT 15
US-09-620-394B-3869
US-09-620-394B-3869
Sequence 3869, Application US/09620394B
Sequence 3869, Application US/09620394B
GENERAL INFORMATION:
APPLICANT: ALEXANDROY, Nickolai
APPLICANT: BROVER, Vyacheslav
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
TITLE OF INVENTION: Thereby
TITLE OF INVENTION: Thereby
CURRENT APPLICATION NUMBER: US/09/620,334B
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 9131
SEQ ID NO 3869
LENGTH: 231
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 54.4%; Score 43; DB 5; Length 231; Best Local Similarity 58.8%; Pred. No. 11; Matches 10; Conservative 3; Mismatches 4; Indels
              YPPE: PRT
ORGANISM: Arabidopsis thaliana
FEATURE:
NAME/KEY: misc_feature
COTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc_feature
NAME/KEY: misc_feature
SUCCATION: 1..215
COTHER INFORMATION: Ceres Seq. ID 1387751
US-09-620-3948-3870
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : NAME/KEY: misc_feature
: LOCATION: 1.231
: UCCATION: 1.231
: NAME/KEY: misc_feature
: LOCATION: 1.231
: LOCATION: 1.231
: COCATION: Ceres Seq. ID 1387750
US-09-620-394B-3869
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ORGANISM: Arabidopsis thaliana
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LENGTH: 215
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Run on:

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Sequence 21, Application US/09763397A

Sequence 21, Application US/09763397A

GENERAL INFORMATION:
APPLICANT: The Government of the United States of America, as represented by the APPLICANT: The Government of the United States of America, as represented by the APPLICANT: Control and Prevention
APPLICANT: Lal, Altaf A.
APPLICANT: Lal, Altaf A.
TATLE OF INVENTION: Recombinant Multivalent Malarial Vaccine Against Plasmodlum Fa TITLE OF INVENTION: Recombinant Multivalent Malarial Vaccine Against Plasmodlum Fa CURRENT FILING DATE: 2001-02-16
PRIOR APPLICATION NUMBER: US 60/097,703
PRIOR APPLICATION NUMBER: PCT / US99/18869
PRIOR APPLICATION NUMBER: PCT / US99/18869
PRIOR APPLICATION NUMBER: PCT / US99/18869
Sequence 7160, Apply Sequence 775, Apply Sequence 80152, Apply Sequence 60152, Apply Sequence 7015, Apply Sequence 7017, Apply Sequence 7017, Apply Sequence 2611, Apply Sequence 2741, Apply Sequence 5749, Apply Sequence 7191, Apply Sequence 7191, Apply Sequence 22857, Apply Sequence 2011, Apply Se
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Sequence 964, App
Sequence 4681, Ap
Sequence 7145, Ap
Sequence 2730, Ap
Sequence 6302, Ap
Sequence 11, App1
Sequence 11, App1
Sequence 11, App1
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US-09-328-352-7160

US-00-146-055-775

US-00-147-055-775

US-09-270-469B-189381

US-09-270-767-4698

US-09-270-767-4698

US-00-173-464-7042

US-00-191-637-8177

US-00-191-637-8177

US-00-191-637-8177

US-09-270-767-4564

US-09-270-767-4564

US-09-270-767-4564

US-09-270-767-4564

US-09-107-532-5749

US-00-107-507-3786-1993

US-00-107-507-3785-1

US-00-107-00-2169

US-00-209-188-725A-2302

US-00-209-218-118
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Pred. No. 2.9e+06;
Mismatches 0;
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                                                                     NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patentin versions ID NO 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 LTPLEELY 8
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       ORGANISM:
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Sequence 2, Appli
Sequence 2603, Ap
Sequence 113, App
Sequence 35531, A
Sequence 440, Ap
Sequence 4656, Ap
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Sequence 60, Appl
Sequence 2, Appli
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1.262 Million cell updates/sec
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1: /cgn2_6/ptodata/2/paa/PCTUS_COMB.pep:*
2: /cgn2_6/ptodata/2/paa/PCGCOMB.pep:*
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18: /cgn2_6/ptodata/2/paa/USOB_COMB.pep:*
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                          version 4.5
- 2000 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                         3148936 segs, 277657034 residues
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                                                                                                                                                              January 29, 2002, 10:56:13
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                      protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                   BLOSUM62
Gapop 10.0 , Gapext 0.5
                          GenCore
Copyright (c) 1993
                                                                                                                                                                                                                                                        US-09-763-397A-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Match Length
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Perfect score:
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Database

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Gaps

Result ş us-09-763-397a-21.rapm

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Sequence 35531. Application US/09417507
Sequence 35531. Application US/09417507
SEQUENCE SETTH G. WEINSTOCK ET AL.
APPLICANT: KETTH G. WEINSTOCK ET AL.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ASPERGILLUS
TITLE OF INVENTION: FUMIGATUS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: PATH99-10
CURRENT APPLICATION NUMBER: US/09/417,507
CURRENT FILING DATE: 1999-10-14
NUMBER OF SEQ ID NOS: 44312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABPELICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH TYPE II DIABETES AND OBESITY, METHODS OF DETECTION AND
TITLE OF INVENTION: USES THEREOF
FILE REPERENCE: CLO00786
CURRENT APPLICATION NUMBER: US/09/948,947
PRIOR APPLICATION NUMBER: 60/231,397
PRIOR FILING DATE: 2000-09-08
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ed. No. 59;
Mismatches 0; Indels
                                                                                          Sequence 2603, Application US/09760475

GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVEWIION: Nucleic Acids, Proteins, and Antibodies
TITLE OF INVEWIION: Nucleic Acids, Proteins, and Antibodies
TITLE OF INVEWIION: NUMBER: US/09/760,475
CURRENT APPLICATION NUMBER: US/09/760,475
CURRENT FILING DATE: 2001-01-16
PRIOR APPLICATION OF 1412
NUMBER OF SEQ ID NOS: 4122
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 39; DB 21; Length 242;
Pred. No. 24;
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87.5%; Pred. No. 5
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SOFTWARE: FastSEQ for Windows Version 4.0
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Best Local Similarity 87.5.
7. Conservative
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CORGANISM: Homo sapiens
US-09-760-475-2603
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Best Local Similarity
Matches 7; Conserv
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92 ITPLEELY 99
176 LTPLEELY 183
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US-09-417-507-35531
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ORGANISM: Human
                                                                       RESULT 4
US-09-760-475-2603
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Sequence 2, Application US/09763397A

Sequence 2, Application US/09763397A

SERVICANT: The Government of the United States of America, as represented by the APPLICANT: Secretary of the Department of Health and Human Services, Centers for Dis APPLICANT: Control and Prevention

APPLICANT: Lal, Allaf A.

APPLICANT: Hasnain, Seyed E.

TITLE OF INVENTION: Recombinant Multivalent Malarial Vaccine Against Plasmodium Falci TITLE OF INVENTION NUMBER: US/09/763,397A

CURRENT FILING DATE: 1001-02-16

PRIOR FILING DATE: 1998-08-21

PRIOR FILING DATE: 1998-08-19

NUMBER OF SEQ ID NOS: 26

SSOFTWARE: PatentIn Version 3.1
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                                                                                                                                                                                     APPLICANT: Heegaard, Peter Mikael Helweg
APPLICANT: Jakobsen, Palle Hoy
TITLE OF INVENTON: Non-Dendrittc Backbone Peptide Carrier
FILE REFERENCE: 2316.1009-000
CURRENT APPLICATION NUMBER: US/09/165,878B
CURRENT FILING DATE: 1998-10-02
EARLIER APPLICATION NUMBER: PCT/DK97/00146
EARLIER APPLICATION NUMBER: DG 1089/96
EARLIER FILING DATE: 1996-04-03
EARLIER FILING DATE: 1996-04-03
SACFUARE: FastSEQ for Windows Version 3.0
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                                                                                                                                                Sequence 60, Application US/09165878B GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 8; Conservative
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RESULT 9
PCT-USO0-26524B-4656
Sequence 4656. Application PC/TUS0026524B
Sequence 4656. Application PC/TUS0026524B
GENERAL INFORMATION:
TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypept
FILE REFERENCE: PA005PCT
CURRENT FILIANG DAFE: 2000-09-28
PRIOR FILING DATE: 1999-09-29
PRIOR FILING DATE: 1999-09-29
PRIOR FILING DATE: 1999-11-03
PRIOR FILING DATE: 1999-11-03
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTE
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 7160
LENGTH: 806
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TITLE OF INVENTION: ISOLATED SECRETED PROTEINS, NUCLEIC ACID
TITLE OF INVENTION: MOLECULES ENCODING SECRETED PROFEINS, AND USES THEREOF
FILE REFERENCE: CLOOMO67
CURRENT APPLICATION NUMBER: US/60/146,055
CURRENT FILING DATE: 1999-07-28
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Pred. No. 4.5e+02;
2; Mismatches 0
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SOFTWARE: FastSEQ for Windows Version 3.0
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75.0%;
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SOFTWARE: Patentin Ver. 2.0
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Best Local Similarity 75.07
E. Local 6; Conservative
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Best Local Similarity 75.0
Matches 6; Conservative
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ORGANISM: Homo sapiens
PCT-US00-26524B-4656
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    272 TPLEELY 278
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LENGTH: 284
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GENERAL INFORMATION:
APPLICANT: Jiang, Bo
APPLICANT: Zamudio, Carlos
APPLICANT: Zamudio, Carlos
APPLICANT: Zamudio, Carlos
TITLE OF INVENTION: Identification of Essential Genes of Aspergillus fumigatus and Me
TITLE OF INVENTION: USe
TITLE OF INVENTION: USe
CURRENT APPLICATION NUMBER: US/60/316,362
CURRENT FILING DATE: 2001-08-31
NUMBER OF SEQ ID NOS: 4037
SEQ ID NOS: 4037
SEQ ID NO 3517
LENGTH: 310
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Sequence 4430, Application US/09543681A
Sequence 4430, Application US/09543681A
GENERAL INFORMATION:
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709-1002-001
CURRENT FILING DATE: 1200-04-05
PRIOR APPLICATION NUMBER: US 60/128,706
PRIOR FILING DATE: 1999-04-09
SEQ ID NOS: 8344
SEQ ID NOS: 8344
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                                                                                                                                     90.2%; Score 37; DB 18; Length 88; 100.0%; Pred. No. 18; ive 0; Mismatches 0; Indels
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95;
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100.0%; Pred. No. 86;
tive 0; Mismatches
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US-60-316-362-3517
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; ORGANISM: Proteus mirabilis
US-09-543-681A-4430
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Best Local Similarity 100.
Matches 7; Conservative
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Best Local Similarity 100.
Matches 7; Conservative
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Best Local Similarity 100.
Matches 7; Conservative
                                                       ; ORGANISM: A.fumigatus
US-09-417-507-35531
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| 123 TPLEELY 129
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| 59 TPLEELY 65
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SEQ ID NO 35531
                    LENGTH: 88
                                       TYPE: PRT
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105 TPLEEIY 111
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105 TPLEEIY 111
        US-09-270-849B-189381
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US-09-270-767-44698
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Sequence 849, Application US/60147189
SEGUENCE INFORMATION:
APPLICANT: Bonazzi, Vivien
TITLE OF INVENTION: MOLECULES ENCODING SECRETED PROTEINS, AND USES THEREOF
FILE REFERENCE: CL000072
CURRENT APPLICATION NUMBER: US/60/147,189
CURRENT FILING DATE: 1999-08-08
NUMBER OF SEQ ID NOS: 1115
SSETWARE: FastSEQ for Windows Version 3.0
SSQ ID NO 849
LENGTH: 71
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APPLICANT: Homburger et al.

TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REPERENCE: File Reference: 7326-094

CURRENT APPLICATION NUMBER: US/09/270,767

CURRENT FILING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 62517

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 60152

LENGTH: 148
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Pred. No. 36;
2; Mismatches 0; Indels
                                                                                                             Score 35; DB 24; Length 71;
Pred. No. 36;
2; Mismatches 0; Indels
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Pred. No. 89;
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Sequence 00152
GENERAL INFORMATION:
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ORGANISM: Drosophila melanogaster
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75.0%;
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Best Local Similarity 75.0%;
Matches 6; Conservative
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Best Local Similarity 85.7
Matches 6; Conservative
                                                                                                                  Query Match 85.4
Best Local Similarity 75.0
Matches 6; Conservative
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US-60-147-189-849
                               TYPE: PRT;
ORGANISM: Drosophila
US-60-146-055-775
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46 ITPLEELF 53
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SEQ ID NO 775
LENGTH: 71
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Sequence 44698 Application US/09270767

GENERAL INFORMATION:
APPLICANT: Homburger et al.
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster;
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 44698
LENGTH: 329
                                                                                                                                                                                                                                                                                            OTHER INFORMATION: Description of Artificial Sequence: Synthetic; CTHER INFORMATION: at any location having Xaa, Xaa means any amino acid US-09-270-849B-189381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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Pred. No. 2.4e+02;
1; Mismatches 0; Indels
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89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
Sequence 189381, Application US/09270849B
GENERAL INFORMATION:
APPLICANT: SWITTON:
TITLE OF INVERTION: Insect genome survey devices
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/09/270,849B
CURRENT APPLICATION NUMBER: 1999-03-17
NUMBER OF SEQ ID NOS: 195450
SOFTWARE: Patentin Ver. 2.0
SSOFTWARE: Patentin Ver. 2.0
SEQ ID NO 189381
LENGTH: 148
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Mismatches
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Pred. No. 8
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Best Local Similarity 85.7.
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Matches 6; Conserv
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Title: Perfect score:

Sequence:

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Run on:

Scoring table:

Searched:

Minimum DB Maximum DB

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Sequence 3470, Application US/09620394B

GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai
APPLICANT: BROVER, Vyacheslav
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptid
TITLE OF INVENTION: Thereby
FILE REFERENCE: 2750-1067P
CORRENT APPLICATION NUMBER: US/09/620,394B
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 9131
SEQ ID NO 3470
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TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID
TITLE OF INVENTION: THEREBY
FILE REFERENCE: 2750-1243P
CURRENT PEPLICATION NUMBER: US/09/708,427
CURRENT PILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: Patentin version 3.1
SEQ ID NO 40050
LENGTH: 106
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7797, Ap
58997, A
7796, Ap
58996, A
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                US-09-916-790-7
US-60-335-352-4
US-09-922-138-11
US-60-338-690-8
US-09-922-138-18
US-09-922-138-18
US-09-922-138-18
US-09-910-150-17
US-09-910-150-17
US-09-910-150-17
US-09-620-394B-7799
US-09-620-394B-7795
US-09-620-394B-7796
US-09-620-394B-7796
US-09-620-394B-7796
US-09-620-394B-7796
US-09-620-394B-7796
US-09-620-394B-7796
US-09-620-394B-7796
US-09-620-394B-7796
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; LOCATION: 1..89
; OTHER INFORMATION: Ceres Seq. ID 1386864
0S-09-620-394B-3470
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100.0%; Pred. No.
:ive 0; Mismatc
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NAME/KEY: misc_feature
LOCATION: 1..89
OTHER INFORMATION: Xaa is
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US-09-708-427-40050
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LENGTH: 89
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2.421 Million cell updates/sec
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1: /cgn2_6/ptcdata/2/paa/USO6_NEW_COMB.pep:*

2: /cgn2_6/ptcdata/2/paa/USO6_NEW_COMB.pep:*

3: /cgn2_6/ptcdata/2/paa/USO7_NEW_COMB.pep:*

4: /cgn2_6/ptcdata/2/paa/USO8_NEW_COMB.pep:*

5: /cgn2_6/ptcdata/2/paa/USO8_NEW_COMB.pep:*

6: /cgn2_6/ptcdata/2/paa/USO8_NEW_COMB.pep:*

7: /cgn2_6/ptcdata/2/paa/USO8_NEW_COMB.pep:*
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Compugen Ltd.
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US-09-708-427-40054
US-09-620-394B-3469
US-09-708-427-40049
US-09-708-427-40049
US-09-708-427-40053
US-09-708-427-40052
US-09-708-427-40053
US-09-708-427-40053
US-09-708-427-40053
US-09-708-427-40053
US-09-995-542-10
US-09-995-542-10
US-09-708-427-26083
US-09-708-427-26083
US-09-815-242-10068
US-09-815-342-10068
US-09-815-343-10068
US-09-815-343-10068
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US-09-708-427-13382
US-09-708-427-13381
US-09-910-150-14
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Maximum Match 100%
Listing first 45 summaries
                                                                                                             sw model
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Gapop 10.0 , Gapext 0.5
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Copyright (c) 1993
                                                                                                           protein search, using
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seq length: 200000000
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US-09-708-427-40049

US-09-708-427-40049

Sequence 40049, Application US/09708427

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID
TITLE OF INVENTION: THEREBY
FILLE REFERENCE: 2750-1243P

CURRENT APPLICATION NUMBER: US/09/708,427

CURRENT FILING DATE: 2000-11-09

NUMBER OF SEQ ID NOS: 85564

SEQ ID NO 40049

LENGTH: 134
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Sequence 3466, Application US/09620394B

GENERAL INFORMATION:

APPLICANT: ALEXANDROV, Nickolai

APPLICANT: BROWER, Vyacheslav

TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptid

TITLE OF INVENTION: Thereby

FILE REFERENCE: 2750-1067P

CURRENT FILING DATE: 2000-07-21

NUMBER OF SEQ ID NOS: 9131

SEQ ID NO 3468

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Pred. No. 15;
0; Mismatches
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Pred. No. 14;
0; Mismatches
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LOCATION: 1..134
OTHER INFORMATION: Xaa is any amino acid
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| LOCATION: 1.122
| OTHER INFORMATION: Ceres Seq. ID 1386862
US-09-620-3948-3468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc_feature
; LOCATION: 1..117
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc_feature
; LOCATION: 1..117
; OTHER INFORMATION: Ceres Seq. ID 1386863
US-09-620-394B-3469
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100.0%; Pre
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                                                                                                                                                                                                                                                             78.0%;
100.0%;
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Best Local Similarity luv.
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Best Local Similarity
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34 PLEELY 39
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TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
TITLE OF INVENTION: Thereby
TITLE OF INVENTION: Thereby
TITLE OF INVENTION: Thereby
TITLE OF INVENTION: Thereby
CURRENT APPLICATION NUMBER: US/09/620,394B
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 9131
SEQ ID NOS: 9131
LENGTH: 117
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GENERAL INFORMATION:
APPLICANT: N ALEXANDROV et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: THEREBY
FILE REFERENCE: 2750-1243P
CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: Patentin version 3.1
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100.0%; Pred. No. 13;
iive 0; Mismatches
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; LOCATION: 1..106
; CTHER INFORMATION: Ceres Seq. ID 1842101
0S-09-708-427-40054
                                                                                                      NAME/KEY: misc_feature
COCATION: 1..106
CTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc_feature
COCATION: 1..106
COCATION: 1..106
US-09-708-427-40050
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US-09-620-394B-3469
Sequence 3469, Application US/09620394B
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, NICKOLai
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ORGANISM: Arabidopsis thaliana
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                                          ORGANISM: Arabidopsis thaliana FEATURE:
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Best Local Similarity 100.0
Local 6; Conservative
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OTHER INFORMATION: Xaa is
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Matches 6; Conserv
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LENGTH: 106
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APPLICANT: N. ALEXANDROV et al.

TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID
TITLE OF INVENTION: THEREBY
TITLE OF INVENTION: THEREBY
FILE REFERENCE: 2750-1243P
CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SEQ ID NO 40052
LENGTH: 139
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APPLICANT: Summers, Eric
TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungi
FILE REFERENCE: 109272.147
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100.0%; Pred. No. 18;
iive 0; Mismatches (
                                                      78.0%; Score 32; DB 5; 100.0%; Pred. No. 18; iive 0; Mismatches
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PRIOR FILING DATE: 2000-01-19
PRIOR APPLICATION NUMBER: US 60/160,587
PRIOR FILING DATE: 1999-10-20
NUMBER OF SEQ ID NOS: 440
                                                                                                                                                                                                                                                               Sequence 40052, Application US/09708427 GENERAL INFORMATION:
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APPLICANT: Call, Brian
APPLICANT: Hecht, Peter
APPLICANT: Holtzman, Doug
APPLICANT: Madden, Kevin
                                      Ouery Match
Best Local Similarity 100..
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Best Local Similarity 100.
Matches 6; Conservative
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Royer, John
Salama, Sofie
Sherman, Amir
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 US-09-708-427-40048
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39 PLEELY 44
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US-09-708-427-40052
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APPLICANT:
APPLICANT:
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APPLICANT:
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GENERAL INFORMATION:
APPLICAMY: N. ALEXANDROV et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: THEREBY
CURRENCE: 2750-1243P
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SEQ TO NOS: 85364
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GENERAL INFORMATION:
APPLICAMENTON:
APPLICAMENTON: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: THEREBY
TITLE OF INVENTION: THEREBY
CURRENCE: 2750-1243P
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SECTION OF 40048
LENGTH: 139
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                                                                                                             78.0%; Score 32; DB 5; Length 134; 100.0%; Pred. No. 17; Live 0; Mismatches 0; Indels
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17;
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CCATION: 1..134
COTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc_feature
LCCATION: 1..134
COTHER INFORMATION: Ceres Seq. ID 1842100
US-09-708-427-40053
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OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc_feature
LOCATION: 1..139
OTHER INFORMATION: Ceres Seq. ID 1842095
; NAME/KEY: misc_feature
; LOCATION: 1..134
; CTHER INFORMATION: Ceres Seq. ID 1842096
US-09-708-427-40049
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Best Local Similarity luv..
6; Conservative
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LOCATION: 1..139
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34 PLEELY 39
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US-09-708-427-40053
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US-09-708-427-40048
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NAME/KEY: misc_feature
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US-09-620-394B-3777
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APPLICANT: Summers, Eric
TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production
TITLE OF INVENTION: in Fungi
FILE REPERENCE: 109272-147
CURRENT APPLICATION NUMBER: US/09/487,558
CURRENT FILING DATE: 2000-01-19
PRIOR APPLICATION NUMBER: US/09/801,368
PRIOR FILING DATE: 2001-03-07
PRIOR PAPLICATION NUMBER: US/09/487,558
PRIOR FILING DATE: 2000-01-19
PRIOR FILING DATE: 2000-01-19
PRIOR FILING DATE: 1999-10-20
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APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
TITLE OF INVENTION: Sphingomonas elodea genome sequences and uses thereof FILE REFERENCE: 38-10(15806)
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Pred. No. 70;
3; Mismatches 0; Indele
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Pred. No. 70;
3; Mismatches 0; Indels
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                                                                         ORGANISM: Saccharomyces cerevisiae US-09-801-368-150
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62.58;
SOFTWARE: PatentIn version 3.0
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Best Local Similarity 62.5%;
Matches 5; Conservative
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Best Local Similarity 62.5
Matches 5; Conservative
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Holtzman, Doug
Madden, Kevin
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Salama, Sofie
Sherman, Amir
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90 LSPLEDIY 97
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90 LSPLEDIY 97
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US-10-015-127-11693
                SEQ ID NO 150
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                                       LENGTH:
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Sequence 3777, Application US/09620394B

Sequence 3777, Application US/09620394B

GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai
APPLICANT: BROVER, Vyacheslav

TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptid

TITLE OF INVENTION: Thereby
FILE REFERENCE: 2750-1067P
CURRENT APPLICATION NUMBER: US/09/620,394B

CURRENT PILING DATE: 2000-07-21

NUMBER OF SEQ ID NOS: 9131
SEQ ID NOS: 9131
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ITILE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID
TITLE OF INVENTION: THEREBY
FILE REFERENCE: 2750-1243P
CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: Patentin version 3.1
ENGTHREE: 295
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Pred. No. 63;
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Pred. No. 50;
0; Mismatches
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PRIOR FILING DATE: 2000-11-22
NUMBER OF SEQ ID NOS: 14357
LENGTH: 224
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Second 27-18806
; Sequence 18806, Application US/09708427
; GENERAL INFORMATION:
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75.0%;
                                                                                                                        ; TYPE: PRT
; ORGANISM: Sphingomonas elodea
US-10-015-127-11693
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85.7%;
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Best Local Similarity 85.7
Matches 6; Conservative
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LOCATION: 1..271
OTHER INFORMATION: Xaa
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69 ITTLEELY 76
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187 TPWEELY 193
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19-09-995-542-12

Sequence 12, Application US/09995542

GENERAL INFORMATION:

APPLICANT: Shutter, John

APPLICANT: Shutter, John

TITLE OF INVENTION: ATP-Blinding Cassette Transporter-Like Molecules and

TITLE OF INVENTION: Uses Thereof

FILE REFERENCE: 00-658-A

CURRENT APPLICATION NUMBER: US/09/995,542

CURRENT FILING DATE: 2001-11-28

PRIOR FILING DATE: 2000-11-28

NUMBER OF SEQ ID NOS: 24

SOCTHARE: Patentin Ver. 2.0

SEQ ID NO 12

LENGTH: 2273

TTPE: PATENT HOMO Sapiens

US-09-995-542-12
                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                     Query Match 75.6%; Score 31; DB 5; Length 295; Best Local Similarity 75.0%; Pred. No. 70; Matches 6; Conservative 1; Mismatches 1; Indels
; LOCATION: 1..295
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc_feature
; LOCATION: 1..295
; OTHER INFORMATION: Ceres Seq. ID 1834879
US-09-708-427-18806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ||||||::
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Search completed: January 29, 2002, 10:58:18 Job time: 2514 sec

Sequence 2, Appl1
Sequence 4, Appl1
Sequence 3, Appl1
Sequence 3, Appl1
Sequence 13, Appl1
Sequence 120, Appl
Sequence 1207, Appl
Sequence 1707, Appl
Sequence 1707, Appl
Sequence 173, Appl
Sequence 174, Appl
Sequence 175, Appl
Sequence 177, Appl

US-08-849-375-13 US-60-312-544-8632 PCT-US01-00663-26532

US-09-864-761-33581 US-60-236-359-14953 US-09-328-352-7022 PCT-US01-14827-14972

ALIGNMENTS

```
APPLICANT: Sim. Betty K
APPLICANT: Sim. Betty K
APPLICANT: Haynes, David J
APPLICANT: Haynes, David J
APPLICANT: Orlandi, Palmar A
APPLICANT: Collandi, Palmar A
APPLICANT: Carter, John M
APPLICANT: Carter, John M
APPLICANT: Canus, Daniel
CONTY: Frederick
STATE: HQ. USAMROC, FORT DETRICK
STATE: HQ. USAMROC, FORT DETRICK
STATE: HQ. USAMROC, FORT DETRICK
STATE: HQ.
COUNTRY: US
COMPUTER READBLE FORM:
MEDIUM TYPE: Chopy disk
COMPUTER: LBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
SOFTWARR: Patentin Release #1.0, Version #1.25
CURSIFICATION UNMER: Q4-Aug-1994
APPLICATION NUMBER: Q4-Aug-1994
APPLICATION NUMBER: Q4-Aug-1994
APPLICATION NUMBER: LBM PC-CARENT INFORMATION: AAPPLICATION AND ATTAINS
APPLICATION NUMBER: Q4-Aug-1994
APPLICATION NUMBER: Q4-Aug-1994
APPLICATION AND ATTAINS
APPLICATION NUMBER: Q4-Aug-1994
                                            US-09-210-288-4

US-08-09-210-288-4

US-08-105-878-39

US-09-165-878-39

US-09-165-878-39

US-09-165-878-39

US-09-165-878-39

US-09-165-878-30

US-09-165-878-30

US-00-1140-27-1764

US-00-137-464-18047

US-00-137-464-18047

US-00-137-464-18047

US-09-228538-173

US-09-228538-173

US-09-228538-173

US-09-228538-173

US-09-228538-173

US-09-228538-173

US-09-228538-173

US-09-284-020-14

US-09-281-447-37

US-08-591-447-40

US-08-591-447-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 5, Application US/08295164 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION
US-08-295-164-5
   J, Appl
Appli
Appli
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                                                                                                           ; Search time 1760.55 Seconds (without alignments)
2.996 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 20, 18 Sequence 3, App Sequence 4, App Sequence 2, As Sequence 2, As Sequence 4, App Sequence 4, App Sequence 4, App
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 5,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pending_Patents_AA_Main:*

| cgn2_6/ptodata/2/paa/PCTUS_COMB.pep:*
| cgn2_6/ptodata/2/paa/USOG_COMB.pep:*
| cgn2_6/ptodata/2/paa/USOG_COMB.pep:*
| cgn2_6/ptodata/2/paa/USOB_COMB.pep:*
                GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-763-397A-20
US-08-295-164-3
US-08-295-164-4
US-09-763-397A-2
PCT-US94-10330-4
US-08-487-826-4
US-08-568-459-4
                                                                                                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                       3148936 segs, 277657034 residues
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                                                                                                           January 29, 2002, 10:56:12
                                                                                                                                                                                                                                                                                                                                                                                                 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                             OM protein – protein search, using sw model
                                                                                                                                                                                                       1 NEREDERTLIKEYEDIVLK 19
                                                                                                                                                                                                                                       BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                US-09-763-397A-20
96
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Maximum DB seq length: 2000000000
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19
42
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350
1426
1426
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Match 1
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100.0
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                                                                                                                                                                                                         sednence:
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                                                                                                           Run on:
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                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/295,164
FILING DATE: 24-AUG-1994
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 96; DB 6; 100.0%; Pred. No. 6.5e-07; Live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: ORLANDI, Palmer A.
APPLICANT: HAYNES, JR., John David
APPLICANT: KLOTZ, Francis W.
APPLICANT: KLOTZ, Francis W.
APPLICANT: CARTER, John Mark
APPLICANT: CARUS, Daniel
APPLICANT: CEGRANS, Michael E.
APPLICANT: CHULAY, Jeffrey David
APPLICANT: HADLEY, Terence J.
TITLE OF INVENTION: Malaria Vaccine
NUMBER OF INVENTION: Malaria Vaccine
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                  STREET: JOhn Morank
STREET: HQ. USAMRDC, FORT DETRICK
CITY: Frederick
STARE: ""
                                                                               APPLICANT: Zegans, Michael E
APPLICANT: Chulcy, Jeffrey D
APPLICANT: Hadley, Teenore J
TITLE OF INVENTION: Malaria Vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : Plasmodium falciparum EBA-175
                                                                                                                                                                                                                                                                                       COUNTRY: US
ZIP: 21702-5012
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 5, Application US/07606259
GENERAL INFORMATION:
APPLICANT: SIM, Betty Kim Lee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY AGENT INFORMATION:
NAME: Hendricks, Glenna M
REGISTRATION NUMBER: 32,535
REFERENCE/CDCKET NUMBER: Sims
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 619-7807
  Orlandi, Palmar A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 NEREDERTLIKEYEDIVLK 19
                       Klotz, Francis W
Carter, John M
Camus, Daniel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9 NEREDERTLIKEYEDIVLK 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (301) 619-7714
INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 42 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 unknown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FRAGMENT TYPE: NORIGINAL SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM:
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US-08-295-164-3
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US-07-606-259-5
                                                                APPLICANT:
APPLICANT:
                                                 APPLICANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         δλ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: The Government of the United States of America, as represented by the APPLICANT: Secretary of the Department of Health and Human Services, Centers for Dis APPLICANT: Secretary of the Department of Health and Human Services, Centers for Dis APPLICANT: Control and Prevention
APPLICANT: Lal, Altaf A.
APPLICANT: Ping Shl, Ya
APPLICANT: Hasnain, Seyed E.
APPLICANT: Hasnain, Seyed E.
APPLICANT: Basnain, Seyed E.
APPLICANT: Bornain, Seyed E.
CURRENT FILING DATE: 2001-02-16
PRIOR APPLICATION NUMBER: US 60/097,703
PRIOR PLING DATE: 1999-08-19
PRIOR PLING DATE: 1999-08-19
PRIOR PLING DATE: 1999-08-19
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patentin Version 3.1
SEQ ID NO 20
LENGTH: 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 96; DB 21; 100.0%; Pred. No. 2.3e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 96; DB 6; 1
100.0%; Pred. No. 2.3e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
REGISTRATION NUMBER: 32,535
REFERENCE/DOCKET NUMBER: 51ms
TELEPOMNUNICATION INFORMATION:
TELEPHONE: (301) 619-7807
TELEPAX: (301) 619-7714
INPORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERESTICS:
LENGTH: 19 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 2
US-09-763-397A-20
; Sequence 20, Application US/09763397A
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Plasmodium falciparum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 3, Application US/08295164 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ), ORGANISM: Plasmodium falciparum US-09-763-397A-20
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APPLICANT: Haynes, David J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 NEREDERTLIKEYEDIVLK 19
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                                                                                                                                                                                                                                                                                                    ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 100.
Best Local Similarity 100.
Matches 19; Conservative
                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 19; Conserva
                                                                                                                                                                                                                                                                                                                                                                                   ; STRAIN: EBA-175
US-08-295-164-5
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ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 7
PCT-US94-10230-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 96; DB 3; Length 43; 100.0%; Pred. No. 6.7e-07;
ADDRESSEE: U.S. Army Medical Research and Development ADDRESSEE: Command
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                             ADDRESSE: Command
STREET: Fort Detrick
CITY: Frederick
STATE: Maryland
COUNTR: USA
ZIP: 21702-5012
COMPUTER: USA
MEDIUM TYPE: FORD:
MEDIUM TYPE: POPOPY disk
COMPUTER: IBM PC COMPATIBLE
OFFRATION NUMBER: WS/07/606,259
FILING DATE: 19901031
CLASSIFICATION NUMBER: US/07/606,259
FILING DATE: 27-SEP-1985
ATTOREY/AGENT INFORMATION:
MAME: MORAN JOHN F.
REGISTATION NUMBER: 26,313
TELEPHONE: (301)619-2416
INFORMATION FOR SED ID NO: 5:
INFORMATION FOR SED ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Haynes, David J
APPLICANT: Orlandi, Palmar A
APPLICANT: Orlandi, Palmar A
APPLICANT: Carter, John M
APPLICANT: Camus, Daniel
APPLICANT: Cagans, Michael E
APPLICANT: Chuley, Jeffrey D
APPLICANT: Hadley, Terence J
APPLICANT: Hadley, Terence J
APPLICANT: Hadley, Terence J
APPLICANT: Hadley, Terence J
APPLICANT: Malaria Vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: John Morank
STREET: HQ. USAMRDC, FORT DETRICK
CITY: Frederick
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/295,164
FILING DATE: 24-AUG-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 4, Application US/08295164
GENERAL INFORMATION:
APPLICANT: Sim, Betty K
APPLICANT: Haynes, David J
APPLICANT: Orlandi, Palmar A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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Best Local Similarity 100.
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           43 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 21702-5012
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: John Mora
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 24-AUG
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   S
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COUNTRY: L
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US-08-295-164-4
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APPLICANT: The Government of the United States of America, as represented by the APPLICANT: Control and Prevention
APPLICANT: Secretary of the Department of Health and Human Services, Centers for APPLICANT: Control and Prevention
APPLICANT: Lal, Altaf A.
APPLICANT: Lal, Altaf A.
APPLICANT: Ping Shi, Ya
APPLICANT: Ping Shi, Ya
APPLICANT: Hasnain, Seyed B.
TILE REFERENCE: 6395-57049
FILE REFERENCE: 6395-57049
FILE REFERENCE: 6395-57049
FILE REFERENCE: 2001-02-16
PRIOR APPLICATION NUMBER: US 60/097,703
FRIOR FILING DATE: 1998-08-21
PRIOR FILING DATE: 1998-08-19
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 350
MANCHEN DATE
SEQ ID NO 2
LENGTH: 350
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 96; DB 6;
Pred. No. 6.7e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: Recombinant DNA/Protein US-09-763-397A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 4, Application PC/TUS9410230
                                                                                                                                                                                                                                                                                                                                                                                      Plasmodium falciparum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/09763397A GENERAL INFORMATION:
NAME: Hendricks, Glenna M
REGISTRATION UNDRER: 32,535
REFERENCE/DOCKET NUMBER: Sims
TELECOMMUNICATION INFORMATION:
TELEFONE: (301) 619-7807
TELEFONE: (301) 619-7714
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE GHARACTERISTICS:
LEMOTH: 43 anino acids
TYPE: amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%;
100.0%;
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ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                            N-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 100.
Best Local Similarity 100.
Matches 19; Conservative
                                                                                                                                                                                                                                               TOPOLOGY: unknown
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-termina
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 19; Conserv
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US-08-295-164-4
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Sequence 4, Application US/08568459

APPLICANT: Sim, Kim L.

APPLICANT: Construction David S.

APPLICANT: Wellens, Tahonas E.

TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX

TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend Khourie and Crew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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ZIP: 94105-1493
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/568,459
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 96; DB 8; I
100.0%; Pred. No. 6.2e-05;
Live 0; Mismatches 0;
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: ISRAELOSE, Ned
REGISTRATION NUMBER: 29,655
REGISTRATION NUMBER: 29,655
TELECOMMUNICATION INFORMATION:
TELEPRONE: (619) 235-8550:
TELEPRONE: (619) 235-8550:
TELEPRONE: (619) 235-0176
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/119,677
                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: Plasmodium falciparum
US-08-487-826-4
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ATTORNEY/AGENT INFORMATION:
NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 15
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1066 NEREDERTLTKEYEDIVLK 1084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 1426 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 NEREDERTLIKEYEDIVLK 19
                                                                                                                                                                                                                                                                     LENGTH: 1426 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: Steuart Stre
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                              ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                 HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 9
US-08-568-459-4
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GENERAL INFORMATION:
APPLICANT: Sim, Kim L.
APPLICANT: Chitnis, Chetan
APPLICANT: Miller, Louis H.
APPLICANT: Peterson, David S.
APPLICANT: Peterson, David S.
APPLICANT: Wellems, Tin-Thomas E.
TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
NUMBER OF SEQUENCES: 45
CORRESPONDENCE: ADDRESS:
ADDRESSEE: Knobbe Mattens Olson & Bear
                                                        BINDING DONAINS FROM PLASMODIUM VIVAX
AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
12
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                                                        TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHH NUMBER OF SEQUENCES: 12 COMPUTER FRADABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IFN PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: PCT/US94/10230 FILING DATE: 07-SEP-1994
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MEDIUM TYPE: Floppy disk
COMBUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 96; DB 1; L
100.0%; Pred. No. 6.2e-05;
vative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Knobbe Martens Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
STATE: Callfornia
                                                                                                                                                                                                                                                                                                                              CLASSIFCATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 10-SEP-193
ATTORNEY, AGENT INFORMATION:
NAME: Bastian, Kevin L.
RECISTRATION NUMBER: 34,774
RECISTRATION NUMBER: 34,774
RECISTRATION NUMBER: 34,774
REPERENCE/DOCKET NUMBER: 15280-139000
TELEPHONE: (415) 543-9600
TELEPAX: (415) 543-9600
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1426 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Plasmodium falciparum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1066 NEREDERTLIKEYEDIVLK 1084
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Best Local Similarity 100.0%;
Matches 19; Conservative C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein HYPOTHETICAL: NO
            GENERAL INFORMATION:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORIGINAL SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             92660
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 8
US-08-487-826-4
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Gaps
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100.0%; Pred. No. 6.3e-05; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: US
ZIP: 21702-5012
ZIP: 21702-5012
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                         APPLICANT: Zegans, Michael E
APPLICANT: Chuley, Jeffrey D
APPLICANT: Hadley, Terence J
TITLE OF INVENTION: Malaria Vaccine
NUMBER OF SEQUENCES: 8
                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: John Morank
STREET: HQ. USAMRDC, FORT DETRICK
CITY: Frederick
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US/08/295,164
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APPLICANT: Sim, Kim L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Hendricks, Glenna M
REGISTRATION UNDRER: 32,535
REFERENCE/COCKET UNDRER: Sims
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 619-7707
TELEFAX: (301) 619-7714
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                              RESULT 11
US-08-295-164-2
Sequence 2, Application US/08295164
; GENERAL INFORMATION:
                                                                                                                                                                          Sim, Betty K
Haynes, David J
Orlandi, Palmar A
Klotz, Francis W
Carter, John M
Camus, Daniel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Db 1069 NEREDERTLTKEYEDIVLK 1087
1 NEREDERTLIKEYEDIVLK 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1435 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/0
FILING DATE: 24-AUG-1994
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-terminal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: unknown
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: John Mora
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 19; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; STRAIN: EBA-175
US-08-295-164-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ANTI-SENSE: NO
FRAGMENT TYPE: N
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM:
                                                                                                                                                                                                                                    APPLICANT:
APPLICANT:
APPLICANT:
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US-08-487-826A-4
                                                                                                                                                                                               APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGIH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE:
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                                                                                                                                                                                             Length 1426;
                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Malaria Vaccine
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: U.S. Army Medical Research and Development
ADDRESSEE: Command
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 21702-5012
COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/606,259
FILING DATE: 19901031
                                                                                                                                                                                             Query Match 100.0%; Score 96; DB 9; I
Best Local Similarity 100.0%; Pred. No. 6.2e-05;
Matches 19; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 06/780,750
FILING DATE: 27.5EP-1985
ATTORNEY/AGENT INFORMATION:
NAME: MORAN, John F.
REGISTRATION NUMBER: 26,313
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301)619-2016
TELEFAX: (301)619-2416
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: SIM, Betty Kim Lee
APPLICANT: ORLANDI, Palmer A.
APPLICANT: HAYNES, JR., John David
APPLICANT: KLOTZ, Francis W.
APPLICANT: CARTER, John Mark
APPLICANT: CARNES, Daniel
APPLICANT: ZEGHANS, Michael E.
APPLICANT: CHULAY, Jeffrey David
APPLICANT: HADLEY, Terence J.
                                                                                            ORIGINAL SOURCE:
ORGANISM: Plasmodium falciparum
US-08-568-459-4
                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application US/07606259 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                               1066 NEREDERTLTKEYEDIVLK 1084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 1435 amino acids
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                         1 NEREDERTLIKEYEDIVLK 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.8
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; MOLECULE TYPE: protein US-07-606-259-2
                STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: Fort Detrick
CITY: Frederick
STATE: Maryland
                                                   MOLECULE TYPE: protein
HYPOTHETICAL: NO
amino acid
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/605,185
PRIOR APPLICATION NUMBER: WO PCT/GB94/01900
APPLICATION NUMBER: GB 93 18350.7
FILING DATE: 03-5EP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 94 17021.4
FILING DATE: 23-AuG-1994
INFORMATION FOR SEQ 1D NO: 3: SEQUENCE CHARACTERISTICS:
LENGTH: 1604 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                  SOFTWARE: PC-DOS/MS-DOS SOFTWARE: PC-DOS/MS-DOS CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/210,288 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.0%; Pred. No. 7.2e-05;
Matches 19; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 96; DB 16;
100.0%; Pred. No. 6.3e-05;
Live 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
ATTORNEY_AGENT INFORMATION:
NAME: FULLE, Michael
REGISTRATION NUMBER: 36,516
REFERENCE/DOCKET NUMBER: NIH121.1FWDV1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: Plasmodium falciparum US-09-210-288-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 3, Application US/08605185 GENERAL INFORMATION: APPLICANT:
                                                                                                                                 E: Floppy disk
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (619) 235-8550
TELEFAX: (619) 235-0176
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 NEREDERTLIKEYEDIVLK 19
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Best Local Similarity 100.0
Matches 19; Conservative
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YES
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linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein
                                                                                                         COMPUTER READABLE FORM:
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, HYPOTHETICAL:
US-08-605-185-3
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US-08-605-185-3
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APPLICANT: Peterson, David S.
APPLICANT: Peterson, David S.
APPLICANT: Wellems, Thomas E.
TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe Martens Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
STATE: California
COUNTRY: US
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Sequence 4, Application US/09210288
Sequence 4, Application:

APPLICANT: Sim, Kim L.

APPLICANT: Chitchis, Chetan
APPLICANT: Miller, Louis H.

APPLICANT: Peterson, David S.

APPLICANT: Potenson, David S.

APPLICANT: Wellems, Thomas E.

TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
NUMBER OF SEQUENCES: 37

CORRESPONDENCE ADDRESS:

ADDRESSES: Knobbe Martens Olson & Bear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
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SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/487,826A
FILING DATE: 10-SEP-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Israelsen, Ned
REGISTRATION NUMBER: 29,655
REFERENCE/DOCKET NUMBER: NIH121.001CP1
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 235-0176
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 96; DB 8; 100.0%; Pred. No. 6.3e-05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 1435 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.
Matches 19; Conservative
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MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORIGINAL SOURCE
ORGANISM: Pla
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                                            RESULT 15

US-08-307-742-3

Sequence 3, Application US/08307742

GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: ANTI-VIRAL FUSION PEPTIDES
NUMBER OF SEQUENCES: 6
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC COMPATIDLE
CORNEUTER: TBM PC COMPATIDLE
CORNEUTER: PAPELICATION DATA:
APPLICATION NUMBER: WO PCTY(GB93/00505

PRIOR APPLICATION NUMBER: WO PCTY(GB93/00505

PRIOR APPLICATION NUMBER: GB 9205276.0

FILING DATE: 11 MAR-1992
PRIOR APPLICATION NUMBER: GB 9205276.0

FILING DATE: 11 MAR-1992
PRIOR APPLICATION NUMBER: GB 9205276.0

FILING DATE: 16-8EP-1992
PRIOR APPLICATION NUMBER: GB 9215829.4

FILING DATE: 16-SEP-1992
PRIOR APPLICATION NUMBER: GB 9219562.7

PRIOR APPLICATION NUMBER: GB 9304311.5

FILING DATE: 16-SEP-1993

INFORMATION POR SEQ INO: 3

SEQUENCE CHARACTERISTICS:
LENGTH: 1786 amino acids

TYPE: amino acids

TYPE: amino acids

TYPE: AMINO acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
100.0%; Score 96; DB 7; Length 1786;
Best Local Similarity 100.0%; Pred. No. 8.3e-05;
Matches 19; Conservative 0; Mismatches 0; Indels
DD 1238 NEREDERTLTKEYEDIVLK 1256
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Search completed: January 29, 2002, 10:56:13 Job time: 2409 sec

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Perfect score:
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     Pred. No.
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DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein search, using sw mode.
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length: 2000000000
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1: /cgn2_6/ptodata/2/paa/PCT_NEW_COMB.pep:*

2: /cgn2_6/ptodata/2/paa/US06_NEW_COMB.pep:*

3: /cgn2_6/ptodata/2/paa/US07_NEW_COMB.pep:*

4: /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep:*

5: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep:*

6: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep:*

7: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep:*
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US-09-708-427-32945
US-09-708-427-24697
US-09-708-427-24697
US-09-708-427-24695
US-09-708-427-13441
US-09-708-427-13440
US-09-708-427-13440
US-09-708-427-13440
US-09-708-427-13440
US-09-897-516-7022
US-09-897-516-7022
US-09-801-358-298
US-09-801-358-298
US-09-708-427-32122
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US-09-708-427-32121
US-09-708-427-28019
US-09-708-427-28018
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Sequence 32947, A
Sequence 32946, A
Sequence 24697, A
Sequence 24696, A
Sequence 24696, A
Sequence 13441, A
Sequence 13441, A
Sequence 13449, A
Sequence 14, Appli
Sequence 7,02, Ap
Sequence 298, Appl
Sequence 298, App
Sequence 32121, A
Sequence 28018, A
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	108, App	76307, A	20901, A	901, App	10904, A	76308, A	20902, A	902, App	10293, A	6224, Ap	84, Appl	7370, Ap	7367, Ap	2194, Ap	15452, A	15453, A	15454, A	24/61, A

ALIGNMENTS

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RESULT 2
US-09-708-427-32946
; Sequence 32946, Application US/09708427
; GENERAL INFORMATION:
APPLICANT: N. ALEXANDROV et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA
TITLE OF INVENTION: THEREBY
FILE REFERENCE: 2750-1243P
CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 83364
SOFTWARE: Patentin version 3.1
SEQ ID NO 32946
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Best Local Similarity
""" 9; Conserve
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; LCCATION: 1..256
; OTHER INFORMATION: Ceres Seq.
US-09-708-427-32947
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US-09-708-427-32947
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GENERAL IMFORMATION:
APPLICANT: N. ALEXANDROV et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID TITLE OF INVENTION: THEREBY
FILE REFERENCE: 2750-1243P
CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: Patentin version 3.1
SEQ ID NO 32947
LENGTH: 256
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FEATURE:
NAME/KEY: misc_feature
LOCATION: 1..256
LOCHER INFORMATION: Xaa is any NAME/KEY.
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56.2%;
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; NAME/KEY: misc_feature; LOCATION: 1..362; OTHER INFORMATION: Ceres Seq. ID 1835390 US-09-708-427-32946
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Best Local S
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 32945, Application US/09708427 GENERAL INFORMATION:
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GENERAL INFORMATION:
APPLICANT: N. ALEXANDROV et al.
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                                                                  SEQ ID NO 24697
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                                                                           TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES TITLE OF INVENTION: THEREBY FILE REFERENCE: 2750-1243P CURRENT APPLICATION NUMBER: US/09/708,427 CURRENT FILING DATE: 2000-11-09 NUMBER OF SEQ ID NOS: 85364 SOFTWARE: PATENTIAL VERSION 3.1
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LOCATION: 1..362
OTHER INFORMATION: Xaa is any
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ORGANISM: Arabidopsis thaliana
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LOCATION: 1..368
OTHER INFORMATION: Xaa is any amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Arabidopsis thalians
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LOCATION: 1..368
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                ORGANISM: Arabidopsis thaliana
                                TYPE: PRT
FEATURE:
                                             ENGTH: 376
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les 9; Conservative
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56.2%;
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Pred. No.
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Pred. No. 4.1;
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: NAME/KEY: misc_feature
: LOCATION: 1..376
: OTHER INFORMATION: Xaa is any amino acid
: NAME/KEY: misc_feature
: LOCATION: 1..376
: OTHER INFORMATION: Ceres Seq. ID 1812577
US-09-708-427-24697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc_feature
LOCATION: 1..377
COTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc_feature
LOCATION: 1..377
COTHER INFORMATION: Ceres Seq. ID 1812576
US-09-708-427-24696
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                                                                                                TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS:
TITLE OF INVENTION: THEREBY
FILE REFERENCE: 2750-12439
CURRENT APPLICATION UNMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: Patentin version 3.1
SEQ ID NO 24695
LEBGTH: 384
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LENGTH: 377
TYPE: PRT
ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 57.1%;
Matches 8; Conservative
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CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn version 3.1
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             NAME/KEY: misc_feature LOCATION: 1..384
                                                                   ORGANISM: Arabidopsis thaliana
                                                  FEATURE:
OTHER INFORMATION: Xaa is any amino
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165 NRKEDQRSLTRETE 178
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57.1%;
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Pred. No.
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17;
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US-09-708-427-13441

Sequence 13441, Application US/09708427

GENERAL INFORMATION:

APPLICANT: N. ALEXANDROV et al.
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US-09-897-516-7722
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Best Local Similarity
Thes 8; Conserva
                                                                                                                                                       CURRENT APPLICATION UNBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09.
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: Patentin version 3.1
SEQ ID NO 13441
LENGTH: 1035
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Best Local Similarity

Matches 8; Conserv
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SEQ ID NO 7722
LENGTH: 974
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                                                                                                                                                                                                                                                              TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES TITLE OF INVENTION: THEREBY FILE REFERENCE: 2750-1243P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/897,516
CURRENT FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US 60/215, 161
PRIOR FILING DATE: 2000-06-30
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                NAME/KEY: misc_feature LOCATION: 1..1035
OTHER INFORMATION: Xaa is any amino acid NAME/KEY: misc_feature LOCATION: 1..1035
                                                                                                       ORGANISM: Arabidopsis thaliana FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc_feature
LOCATION: 1.384
                                                                                                                                          TYPE: PRT
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OTHER INFORMATION: Ceres Seq. ID 1826362
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Hinkle, Gregory J.
Huesing, Joseph E.
Krasomil-Osterfeld, Karina C.
Malvar, Thomas M.
Slater, Steven C.
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57.18;
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Pred. No.
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Pred. No.
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; FEATURE: misc_feature ; NAME/KEY: misc_feature ; LOCATION: 1..1104 ; OTHER INFORMATION: Xaa is ; NAME/KEY: misc_feature ; LOCATION: 1..1104 ; OTHER INFORMATION: Ceres S. US-09-708-427-13439
                                                                                                                                                                                                                                                                                                                       US-09-708-427-13439, Application US/09708427; Sequence 13439, Application US/09708427; GENERAL INFORMATION:
APPLICANT: N. ALEXANDROV et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID TITLE OF INVENTION: THERREBY
FILE REFERENCE: 2750-1243P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             B
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LOCATION: 1..1072
OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc_feature
LOCATION: 1..1072
OTHER INFORMATION: Ceres Seq. ID 1826361
US-09-708-427-13440
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Sequence 13440, Application US/09708427

GENERAL INFORMATION:

APPLICANT: N. ALEXANDROV et al.

TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID TITLE OF INVENTION: TERREBY

FILE REFERENCE: 2750-1243P
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                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: Patentin version 3.1
SEQ ID NO 13439
LENGTH: 1104
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CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85384
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 13440
LENGTH: 1072
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Best Local Similarity
Matches 10; Conserv
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Best Local Similarity
Matches 10; Conserv
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                                                                                                                                                           ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                  TYPE: PRT
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62.5%;
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                      Seq. ID 1826360
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Pred. No. 1.9e+02;
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Pred. No. 1.9e+02;
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US-09-897-516-7022
                                               Query Match
Best Local Similarity
"hes 8; Conserva
В
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                                                                                                                                         ; ORGANISM: Homo sapiens US-09-825-882-14
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PRIOR FILING DATE: 2000-06-30
NUMBER OF SEQ ID NOS: 8409
SEQ ID NO 7022
LENGTH: 198
TYPE: DEM
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Best Local S
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GENERAL INFORMATION:
APPLICANT: ADLER, JON EILIOT
TITLE OF INVENTION: 72R TASTE RECEPTORS AND GENES ENCODING SAME
FILE REFERENCE: 078003/0279152/RXT
CURRENT FILING DATE: 2001-04-05
PRIOR APPLICATION NUMBER: 05/09/825,882
CURRENT FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: 60/195,532
PRIOR APPLICATION NUMBER: 60/247,014
PRIOR FILING DATE: 2000-01-13
NUMBER: 05 SEQ. ID NOS: 31
NUMBER: 05 SEQ. ID NOS: 31
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Best Local :
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GENERAL INFORMATION:
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LENGTH: 299
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                                                                                                                                                                          TYPE: PRT
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150 DERVWTKEYE 159
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                             5 DERTLTKEYE 14
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Slater, Steven C.
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Hinkle, Gregory J.
Toseph E.
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Krasomil-Osterfeld, Karina
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80.0%;
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Pred. No.
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                                                                             Score 41; DB Pred. No. 74;
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46;
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PRIOR APPLICATION NUMBER: US 09/487,558
PRIOR FILING DATE: 2000-01-19
PRIOR APPLICATION NUMBER: US 60/160,587
PRIOR ETLING DATE: 1999-10-20
NUMBER OF SEQ ID NOS: 440
SOFTWARE: Patentin version 3.0
SEQ ID NO 298
LENGTH: 1770
TYPE: PRT
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Qy
                       Query Match
Best Local Similarity
"-+~hes 8; Conserv
                                                                                                                                    ; ORGANISM: Saccharomyces cerevisiae US-09-801-368-298
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LENGTH: 871
TYPE: PRT
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GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: NOVEL HUMAN NUCLEIC ACID MOLECULES AND POLYPEPTIDES ENCODING A
TITLE OF INVENTION: HUMAN ION CHANNEL EXPRESSED IN SPINAL CORD AND BRAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
...+~hes 8; Conserv
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PRIOR APPLICATION NUMBER: 60/250,587
PRIOR FILING DATE: 2000-12-01
NUMBER OF SEQ ID NOS: 31
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
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CURRENT APPLICATION NUMBER: US/10/000,823
CURRENT FILING DATE: 2001-11-30
                                                                                                                                                                                                                                                                                                                                       APPLICANT: Sherman, Amir AppLICANT: Silva, Jeff APPLICANT: Silva, Jeff APPLICANT: Summers, Eric TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungi FILE REFERENCE: 109272.147 for Improving Secondary Metabolite Production in Fungi CURRENT APPLICATION NUMBER: US/09/801,368 CURRENT FILING DATE: 2001-03-07
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| ||: : :|| |: ::||
334 NTRENTKFVTKMYDLLLLK 352
 1 NEREDERTLTKEYEDIVLK 19
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Milne, Todd
Norman, Thea
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Salama, Sofie
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Holtzman, Doug
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42.1%;
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Pred. No. 2.6e+02;
                                         Score 41; DB 5; Length 1770; Pred. No. 5.9e+02; 4; Mismatches 7; Indels
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US-09-487-589-298
US-09-487-588-298
US-09-487-58
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us-09-763-397a-19.rapm

Mon Feb

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Sequence 19, Appl
Sequence 2, Appli
Sequence 8, Appli
Sequence 8, Appli
Sequence 9, Appli
Sequence 9, Appli
Sequence 606, App
Sequence 606, App
                                                                                                                                                                                                                                 (without alignments)
3.470 Million cell updates/sec
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                                                                                                                                                                                               ; Search time 1760.55 Seconds
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    /cgn2_6/ptodate12/paa/US06_COMB.pep:*
    /cgn2_6/ptodate12/paa/US01_COMB.pep:*
    /cgn2_6/ptodate12/paa/US08_COMB.pep:*
    /cgn2_6/ptodate12/paa/US081_COMB.pep:*
    /cgn2_6/ptodate12/paa/US081_COMB.pep:*
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    /cgn2_6/ptodate12/paa/US081_COMB.pep:*
    /cgn2_6/ptodate12/paa/US091_COMB.pep:*
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/cgn2_6/ptodata/2/paa/US096_COMB.pep:*
/cgn2_6/ptodata/2/paa/US097_COMB.pep:*
/cgn2_6/ptodata/2/paa/US098_COMB.pep:*
/cgn2_6/ptodata/2/paa/US099_COMB.pep:*
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-09-763-397A-2
PCT-US92-02207-8
US-07-672-183A-8
US-08-072-867-8
US-08-075-783-9
US-08-075-783-9
US-08-013-01-01307-606
PCT-US01-01307-6859
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3148936 segs, 277657034 residues
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                                                                                                                                                                                           January 29, 2002, 10:56:11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                              OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                               131
1 EFTYMINFGRGONYWEHPYOKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pending_Patents_AA_Main:*
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                                                                                                                                                                                                                                                                                                                          US-09-763-397A-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Match Length DB
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                                                                                                                                                                                                                                                                                                                                                            Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Scoring table:
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Sequence 48408, A Sequence 31002, A Sequence 775, App Sequence 775, App Sequence 42572, A Sequence 42572, A Sequence 19616, A Sequence 24449, A Sequence 526, App Sequence 11315, A Sequence 11315, A Sequence 2627, App Sequence 24383, A Sequence 24777, A Sequence 24183, A Sequence 24183, A Sequence 2419, App Sequence 719, App Sequence 719, App Sequence 119, App Sequence 1	
US-60-324-109-31002 US-60-324-109-31002 US-60-172-468-72 US-60-173-468-72 US-60-173-468-75 US-60-196-710-5435 US-60-196-710-5435 US-60-191-637-23927 US-60-191-637-23927 US-60-191-637-23927 US-60-191-637-23927 US-60-191-637-2449 US-60-197-87-2449 US-60-197-87-2449 US-60-191-637-31024 US-60-113-637-31024 US-60-113-637-31024 US-60-114-862-719 US-60-114-862-719 US-60-114-863-713 US-60-114-863-713 US-60-114-863-713 US-60-114-863-713 US-60-114-863-713 US-60-114-863-713 US-60-114-863-713 US-60-113-637-933-1275 US-60-114-863-713 US-60-113-643-374-527	
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8 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9	
444	
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## ALIGNMENTS

Sequence 19, Application US/09763397A GENERAL INFORMATION:

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APPLICANT: The Government of the United States of America, as represented by the APPLICANT: The Government of the Department of Health and Human Services. Centers for APPLICANT: Control and Prevention APPLICANT: Lal, Altaf A. APPLICANT: ping Shi, Ya APPLICANT: Hasnain, Seyed E. TITLE OF INVENTION Recombinant Multivalent Malarial Vaccine Against Plasmodium Fa FILE REFERENCE: 6395-57049
CUBRENT FILING DATE: 2001-02-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 131; DB 21;
Pred. No. 6.4e-13;
; Mismatches 0;
                                                                                                                                                                                                                                                       CURRENT FILING DATE: 2001-02-16
PRIOR APPLICATION NUMBER: US 60/097,703
PRIOR FILING DATE: 1998-08-21
PRIOR PELING DATE: 1999-08-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match ' 100.0%; So
Best Local Similarity 100.0%; Pi
Matches 22; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Plasmodium falciparum
                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 26
SOFTWARE: PatentIn version 3.1
SEQ ID NO 19
LENGTH: 22
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Gaps

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Indels

1 EFTYMINFGRGONYWEHPYOKS 22

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Pred. No. 1.3e-10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Paoletti, Enzo
APPLICANT: de Taisne, Charles
APPLICANT: Tine, John A.
APPLICANT: Tine, John A.
APPLICANT: Tine, John A.
ALARIA RECOMBINANT POXVIRUS VACCINE
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/07/672,183A FILING DATE: 19910320 CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: William S. Frommer ADDRESSEE: c/o Curtis, Morris & Safford, P.C. STREET: 530 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 126; DB 3;
Pred. No. 1.3e-10;
0; Mismatches 1;
                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Frommer, William S.
REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 454310-2300
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 8, Application US/07672183A GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 5
US-08-072-867-8
; Sequence 8, Application US/08072867
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14 EFTYMINFGRGONYWEHPYONS 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 EFTYMINFGRGONYWEHPYOKS 22
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                                                                                                                                                                                                                                                                                                  1 EFTYMINFGRGONYWEHPYOKS 22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (212) 840-0712 INFORMATION FOR SEQ ID NO: 8:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 622 amino acids
TYPE: AMINO ACID
STRANDEDNESS: Single
TOPOLOGY: linear
                                             LENGTH: 622 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: New York
COUNTRY: United States
ZIP: 10036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 95.5
Matches 21; Conservative
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                                                                                                                                                                                                        Query Match 96.2
Best Local Similarity 95.5
Matches 21; Conservative
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 622 amino acid
                                                                                          single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                  ; TOPOLOGY: linear
PCT-US92-02207-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New York
                                                                                          STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 4
US-07-672-183A-8
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                                                                                                                                                                           APPLICANT: The Government of the United States of America, as represented by the APPLICANT: Secretary of the Department of Health and Human Services, Centers for Dis APPLICANT: Control and Prevention
APPLICANT: Lal, Altaf A. APPLICANT: Lal, Altaf A. APPLICANT: Lal, Altaf A. APPLICANT: Hashain, Seyed E. TITLE OF INVENTION: Recombinant Multivalent Malarial Vaccine Against Plasmodium Falci FILE REFERENCE: 6395-57049
CURRENT APPLICATION NUMBER: US/09/763,397A
CURRENT PILING DATE: 1098-08-21
PRIOR PILING DATE: 1998-08-21
PRIOR PILING DATE: 1999-08-19
PRIOR FILING DATE: 1999-08-19
PRIOR FILING DATE: 1999-08-19
PRIOR FILING DATE: 1990-08-19
PRIOR FILING DATE: 1990-08-19
PRIOR FILING DATE: 1990-08-19
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patentin version 3.1
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PCT-0292-02207-8

PCT-0292-02207

Sequence 8, Application PC/TUS9202207

GENERAL INFORMATION:
APPLICANT: VIROSENETICS, CORPORATION

TILLE OF INVANTION: MALARIA RECOMBINANT POXVIRUS VACCINE
NUMBER OF SEQUENCES: 74

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 100.0%; Score 131; DB 21; Best Local Similarity 100.0%; Pred. No. 1.1e-11; Matches 22; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Curtis, Morris, and Safford
ADDRESSEE: c/o William S. Frommer
STREET: 300 Fifth Avenue
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTHER INFORMATION: Recombinant DNA/Protein US-09-763-397A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Frommer, William S.
REGISTATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 454310-2411
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         омыЕК: PCT/US92/02207
19-MAR-1992
                                                                                                                                       Sequence 2, Application US/09763397A GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 EFTYMINFGRGQNYWEHPYQKS 22
    1 EFTYMINFGRGONYWEHPYOKS 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT ORGANISM: Artificial Sequence
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(212) 840-0712
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE:
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LENGTH: 350
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Sequence 871, Application US/60207216
GENERAL INFORMATION:
APPLICANT: Beasley, Ellen
TITLE OF INVENTION: ISOLATED HUMAN DRUG TARGET PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN DRUG TARGET PROTEINS,
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: CLO00580
CURRENT APPLICATION NUMBER: US/60/207,216
CURRENT APPLICATION NUMBER: US/60/207,216
CURRENT FILING DATE: 2000-05-26
NUMBER OF SEQ ID NOS: 898
SEQ ID NO 871
LENGTH: 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc., et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PT218PCT
CURRENT PILING DATE: 2001-01-17
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 1040
SCOTWARE: Patentin Ver. 2.0
SEQ ID NO 606
LENGTH: 99
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Pred. No. 1.3e-10;
0; Mismatches 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: VARIANT
LOCATION: (1)...(89)
OTHER INFORMATION: Xaa = Any Amino Acid
                                        NAME: Fromer, William S.
REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 45431
TELECOMMUNICATION INPORMATION:
TELEFAX: (212) 840-3333
TELEFAX: (212) 840-0712
INPORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 622 amino acids
TYPE: amino acid
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14 EFTYMINEGRGONYWEHPYONS 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 EFTYMINFGRGONYWEHPYOKS 22
                                                                                                                                                                                                                                                                                                                                                                      96.28;
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    CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
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Best Local Similarity 95.5
Matches 21; Conservative
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Best Local Similarity 44.4
Matches 8; Conservative
                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
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Pred. No. 1.3e-10;
0; Mismatches 1; Indels
APPLICANT: Paoletti, et al
TITLE OF INVENTION: MALARIA RECOMBINANT POXVIRUS VACCINE
NUMBER OF SEQUENCES: 74
CORRESPONDENCE ADDRESS:
ADDRESSEE: Curtis, Morris, and Safford
ADDRESSEE: C/O William S. Frommer
STREET: 530 Fifth Avenue
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 9, Application US/08075783
GENERAL INFORMATION:
APPLICANT: Paoletti, Enzo
APPLICANT: Tine, John A.
TITLE OF INVENTION: MALARIA RECOMBINANT POXVIRUS VACCINE
NUMBER OF SEQUENCES: 124
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUTLIS, MORTIS & Safford
ADDRESSEE: COV Milliam S. Frommer
STREET: 530 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/075,783
FILING DATE: 11-JUN-1993
                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/072,867
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Frommer, William S.
REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 454310-2410
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 840-3333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: United States of America ZIP: 10036
                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/852,305
FILING DATE: 18-MAR-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | TELEPHONE: (212) 840-3333
| TELEFAX: (212) 840-0712
| INFORMATION FOR SEQ ID NO: 8:
| SEQUENCE CHARACTERISTICS:
| LENGTH: 622 amino acids
| TYPE: amino acid
| STRANDEDNESS: single
| US-08-072-867-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14 EFTYMINFGRGONYWEHPYONS 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 EFTYMINFGRGONYWEHPYOKS 22
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95.5%;
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Best Local Similarity 95.55, Conservative
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MEDIUM TYPE: Floppy
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                                                                                                                                                                                               USA
                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                 10036
                                                                                                                                                                      STATE: NA
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ORGANISM: Glycine max
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Matches 8; Conserv
NAME/KEY: DOMAIN
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LENGTH: 313
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US-09-672-785-2
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LENGTH: 506
                                                                                                                                        Query Match
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LOCATION: (15)..(330)
OTHER INFORMATION: WW DOMAIN SIGNATURE domain identified by eMAIRIX, accession OTHER INFORMATION: number PR00403B, p-value=3.898e-09, raw score of 12.19
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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                                                                                                                                          Gaps
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GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc., et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PT18PCT
CURRENT APPLICATION NUMBER: PCT/US01/01307
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 1040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 48408, Application PC/TUS0108631
; Sequence 48408, Application PC/TUS0108631
; GENERAL INFORMATION:
APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES;
FILE REFERENCE: 21272-049
; CURRENT APPLICATION NUMBER: PCT/US01/08631
CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
PRIOR FILING DATE: 2000-03-31
; PRIOR FILING DATE: 2000-03-31
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1; Length 103; 1.1;
                                                                                                 Score 57; DB 1; Length 99;
Pred. No. 1.1;
2; Mismatches 5; Indels
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Pred. No. 1.1;
2; Mismatches
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Best Local Similarity 53.3%;
Matches 8; Conservative
                                                                                                     43.5%;
                                                                                  Ouery Match
Best Local Similarity 53.3.
Post Local 8; Conservative
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                                                                                                                                                                               4 YMINFGRGQNYWEHP 18
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54 YYENFANGQSMWDHP 68
    ; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US01-01307-606
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                                                                                                                                                                                                                                                                              RESULT 9
PCT-US01-01307-859
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: SITE
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TYPE: PRT
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. LOCATION: (82)..(149)
. OTHER INFORMATION: Subtilase family domain identified by PFam, accession name pcr-usol.08631-48408
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Liu, Jingdong
APPLICANT: Liu, Jingdong
APPLICANT: Liu, Jingdong
APPLICANT: Stein, Joshua
TITLE OF INVENTION: CDNA SEQUENCES AND USES FOR PLANT IMPROVEMENT
FILE REPERENCE: 38-10(52726)B
CURRENT APPLICATION NUMBER: US/60/324,109
CURRENT FILING DATE: 2001-09-21
NUMBER OF SEQ ID NOS: 33196
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                                                                                                                                    Score 57; DB 1; Length 374;
Pred. No. 4.3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2, Application US/09672785
GENERAL INFORMATION:
APPLICANT: Mizuteni, Masako
APPLICANT: Ayabe, Shin-ichi
APPLICANT: Asami, Takaaki
APPLICANT: Ayabe, Shin-ichi
APPLICANT: Ayabe, Shin-ichi
APPLICANT: Ayabe, Shin-ichi
APPLICANT: Akami, Tomoyoshi
TITLE OF INVENTION: Genes Coding for Flavone Synthases
FILE REFERENCE: 001560-383
CURRENT PAPLICATION NUMBER: US/09/672,785
CURRENT FILING DATE: 2000-09-29
PRIOR APPLICATION NUMBER: PCT/JP00/04379
PRIOR APPLICATION NUMBER: PCT/JP00/0490
PRIOR PILING DATE: 1999-01-28
PRIOR FILING DATE: 1999-01-18
PRIOR FILING DATE: 1999-01-19
PRIOR FILING DATE: 1999-01-19
PRIOR FILING DATE: 1999-01-19
NUMBER OF FEO ID NOS: 8
SOFTWARE: Patentin version 3.0
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Pred. No. 22;
0; Mismatches
                                                                                                                                                                                               2; Mismatches
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                                                                                                                                                  43.5%;
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Best Local Similarity 34.4
Matches 11; Conservative
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                                                                                                                                                                                                                                                                            315 YYFNFANGQSMWDHP 329
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NUCLEIC ACID MOLECULES ENCODING HUMAN DRUG TARGET PROTEINS,
AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                        Sequence 775, Application US/60173468
GRERAL INFORMATION:
GREERL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN DRUG TARGET PROTIENS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN DRUG TARGET PROTIENS
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: CL000181
CURRENT APPLICATION NUMBER: US/60/173,468
CURRENT FILING DATE: 1999-12-29
NUMBER OF SEQ ID NOS: 1418
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 775
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  ; FEATURE:
; OTHER INFORMATION: Amino acid sequence of a protein having an activity to
; OTHER INFORMATION: directly convert flavanone to flavone
US-09-672-785-2
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42.1%; Pred. No. 36;
tive 4; Mismatches 7; Indels
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Pred. No. 3.9;
2; Mismatches 6; Indels
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GENERAL INFORMATION:
APPLICANT: BONAZZI, VIVIEN:
TITLE OF INVENTION: ISOLATED HUMAN DRUG TARRY TITLE OF INVENTION: AND USES THEREOF
FILE REPERENCE: CL000450
CURRENT APPLICATION NUMBER: US/60/196,710
CURRENT FILING DATE: 2000-04-13
NUMBER OF SEQ ID NOS: 7166
SOFTWARE FASTESE for Windows Version 4.0
SEQ ID NO 5435
LENGTH: 30
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ilarity 46.7%;
Conservative
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ORGANISM: Antirrhinum majus
                                                                                                                                                                                       Conservative
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Best Local Similarity 46.7
Matches 7; Conservative
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16 YFFNFANRQSIWDHP 30
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                                                                                                                                              Query Match
Best Local Similarity
Matches 8; Conserv
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Best Local Similarity
Matches 7; Conserv
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US-60-196-710-5435
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Sequence 4. Application US/09672785

Sequence 4. Application US/09672785

Sequence 4. Application US/09672785

Sequence 4. Application US/09672785

Sequence 4. Application US/0967285

Sequence 4. Application US/0967285

APPLICANT: Masumi, Tranky Masaki

APPLICANT: Akashi, Tomoyani

TITLE 0F INVANTION Genes Cooling for Flavone Synthases

TITLE 0F INVANTION Genes COOL-09

SURRENT APPLICATION NUMBER: US/09/672,785

CURRENT APPLICATION NUMBER: US/09/672,785

SROR TILING DATE: 1200-01-30

PRIOR FILING DATE: 1300-01-30

PRIOR PLILOR DATE: 1309-01-29

PRIOR PLILOR DATE: 1399-01-29

NUMBER OF SEQ ID NOS: 8

SOFTWARE: PATOR PLILOR DATE: 1999-01-29

NUMBER OF SEQ ID NOS: 8

SEQ ID NO 4

LENGTH: 512

TYPE: PRT

OFFANTIS: 12

TYPE: PRT

OFFANTIS: 1
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7; Conservative
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Best Local Similarity
Matches 7; Conserv
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US-09-708-427-15235
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US-09-708-427-15234
FEATURE:
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25013, A
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15743, A
                                                                                                                                                (without alignments)
6.657 Million cell updates/sec
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                                                                                                                              ; Search time 120.95 Seconds
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Sequence 1
Sequence 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pending_Patents_AA_New:*

1. /cgn12_6/ptodata/2/paa/USO6_NEW_COMB.pep:*

2. /cgn2_6/ptodata/2/paa/USO6_NEW_COMB.pep:*

3. /cgn2_6/ptodata/2/paa/USO7_NEW_COMB.pep:*

4. /cgn2_6/ptodata/2/paa/USO8_NEW_COMB.pep:*

5. /cgn2_6/ptodata/2/paa/USO8_NEW_COMB.pep:*

5. /cgn2_6/ptodata/2/paa/USO8_NEW_COMB.pep:*

6. /cgn2_6/ptodata/2/paa/USO8_NEW_COMB.pep:*
                 GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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US-09-708-427-1523

US-09-108-427-1523

US-09-108-427-21795

US-09-708-427-21795

US-09-108-427-21795

US-09-108-427-15512

US-09-108-427-1958

US-09-108-427-19513

US-09-108-427-15513
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1 EFTYMINFGRGQNYWEHPYQKS 22
                                                                                                                            January 29, 2002, 10:58:16
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Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Match 1
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                                                                                          OM protein
                                                                                                                                                                                                                                               Sequence:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Database
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Sequence 15235, Application US/09708427

GENERAL INFORMATION:
APPLICANT:
APPLICANT:
TITLE OF INVENTION: THEREBY
FILLE REFERENCE: 2750-1243P
CURRENT APPLICATION NUMBER: US/09/708,427

CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SEQ ID NO 15235
LENGTH: 292
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TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID
TITLE OF INVENTION: THEREBY
FILE REFERENCE: 2750-1243P
CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: PatentIn version 3.1
SEQ ID NO 15234
LENGTH: 341
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                                           10593, A
10592, A
10591, A
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31, Appl
31, Appl
20343, A
23930, A
20342, A
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2, Appli
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27392, A
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Pred. No. 7.6;
US-09-708-427-15541

US-09-708-427-10593

US-09-708-427-10592

US-09-708-427-10592

US-09-976-594-757

US-09-976-594-757

US-09-689-731

US-09-688-731

US-09-688-731

US-09-688-731

US-09-708-427-20343

US-09-708-427-20342

US-09-50-3948-1036

US-09-708-427-27391

US-09-708-427-27391

US-09-708-427-27391

US-09-708-427-27391

US-09-708-427-27391

US-09-708-427-27391
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LOCATION: 1..292
COTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc_feature
LOCATION: 1..292
COTHER INFORMATION: Ceres Seq. ID 1828911
US-09-708-427-15235
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ORGANISM: Arabidopsis thaliana
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70.0%;
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; Sequence 21795, Application US/09708427; GENERAL INFORMATION: APPLICANT: N. ALEXANDROV et al. TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 21796, Application US/09708427

GENERAL INFORMATION:
APPLICANT: N. ALEXANDROV et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID
TITLE OF INVENTION: THEREBY
FILE REFERENCE: 2750-1243P
CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: PATENTIN VETSION 3.1
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Pred. No. 4.8;
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Mismatches
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR PLING DATE: 2000-11-27
PRIOR PLING DATE: 2000-11-27
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2001-22
PRIOR FILING DATE: 2001-22
PRIOR FILING DATE: 2001-26
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: PASLSEQ for Windows Version 4.0
SOFTWARE: 1620
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LOCATION: 1..133
OTHER INFORMATION: Xaa is any amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Pseudomonas aeruginosa
US-09-815-242-5126
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LOCATION: 1..133
CTHER INFORMATION: Ceres Seq.
0S-09-708-427-21796
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46.2%;
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36.8%;
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Best Local Similarity 36.0.
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13 GSGEAFWEHEWEK 25
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Matches 6; Conserv
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US-09-708-427-21795
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LENGTH: 133
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TITLE OF INVENTION: THEREX
FILE REFERENCE: 2750-1243P
CURRENT APPLICATION NUMBER: 108/09/708,427
CURRENT APPLICATION NUMBER: 2000-11-09
NUMBER OF SEQ ID NOS: 85564
SOFTWARE: Patentin version 3.1
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                                                                                                                                                                                                                                                                                                                                                                     DB 5; Length 341;
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APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
ITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
FILE REPERENCE: BLITRA 011A
CURRENT FILING DATE: 2001-03-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 47; DB 5;
Pred. No. 12;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                      .2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: Ceres Seq. ID 1828909
US-09-708-427-15233
                                                                                                                     LOCATION: 1..341
OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc_feature
LOCATION: 1..341
OTHER INFORMATION: Ceres Seq. ID 1828910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: Xaa is any amino acid
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 15233, Application US/09708427 GENERAL INFORMATION:
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APPLICANT: Ohlsen, Kari L.
APPLICANT: Oylsen, Wail L.
APPLICANT: Syskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Arabidopsis thaliana
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70.0%;
                          ORGANISM: Arabidopsis thaliana
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70.0%;
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Best Local Similarity 70.0
Matches 7; Conservative
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Best Local Similarity 70.0
Matches 7; Conservative
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LOCATION: 1..452
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                                                                                        NAME/KEY: misc_feature
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US-09-815-242-5126
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LENGTH: 452
                                                              FEATURE:
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Sequence 17, Application US/09689730
GENERAL INFORMATION:
APPLICANT: SERIN. Mothbaru
APPLICANT: SATO, Hiroshi
APPLICANT: SHINACAWA, Akira
TITLE OF INVENTION: NOVEL METALLOPROTEINASE AND ENCODING DNA THEREFOR
FILE REFERENCE: 55-290P
CURRENT APPLICATION NUMBER: US/09/689,730
CURRENT FILING DATE: 2000-10-13
PRIOR PAPLICATION NUMBER: US/08/448,489
PRIOR APPLICATION NUMBER: US/08/448,489
PRIOR PILING DATE: 1995-06-07
NUMBER OF SEQ ID NOS: 19
SOFTWARE PATENTING DATE: 2000-10-13
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APPLICANT Oblisen, Kari L.
APPLICANT: Oblisen, Kari L.
APPLICANT: Oblisen, Kari L.
APPLICANT: Oblisen, Jodith W.
APPLICANT: Zyskind, Judith W.
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Tamamoto, Robert T.
APPLICANT: Tamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: 1000011A
CURRENT FILING DATE: 2001-03-21
PRIOR PELING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR PELICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/253,931
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-10-22
PRIOR PILING DATE: 2000-10-22
PRIOR PILING DATE: 2000-10-22
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17;
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PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4997
LENGTH: 467
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Pred. No.
                                                                                                                                                                                                         Sequence 4997, Application US/09815242 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Enterococcus faecalis US-09-815-242-4997
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Best Local Similarity 50.0%;
Matches 7; Conservative
                                        1:||| |: ||::
28 GKGQNIWDFWYQEA 41
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   9 GRGQNYWEHPYQKS 22
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ORGANISM: Unknown
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US-09-689-730-17
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APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Yammanco, Robert T.
APPLICANT: Yammanco, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVEWTION: Identification of Essential Genes in TITLE OF INVEWTION: Protaryotes
FILE REFERENCE: ELITRA.01A
CURRENT APPLICATION NUMBER: 60/201,078
FRIOR PLING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR PLICATION NUMBER: 60/207,727
PRIOR PLICATION NUMBER: 60/207,727
PRIOR PLICATION NUMBER: 60/205,93
PRIOR FLING DATE: 2000-05-23
PRIOR FLING DATE: 2000-05-37
PRIOR FLING DATE: 2000-10-23
PRIOR FLING DATE: 2000-12-27
PRIOR FLING DATE: 2000-12-27
PRIOR FLING DATE: 2000-12-27
PRIOR FLING DATE: 2000-12-22
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Pred. No. 8.4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4; Mismatches
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                     FILE REFERENCE: 2750-1243P
CURRENT PEPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: PatentIn version 3.1
SEQ ID NO 21795
LENGTH: 230
                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc_feature
CCCATION: 1..230
OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc_feature
CCCATION: 1..230
US-09-708-427-21795
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ohlsen, Kari L.
Zyskind, Judith W.
Wall, Daniel
Trawick, John D.
Carr, Grant J.
Yamamoto, Robert T.
                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  35.1%;
46.2%;
   THEREBY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 46.2
Matches 6; Conservative
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Best Local Similarity 50.0
Matches 7; Conservative
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110 GSGEAFWEHEWEK 122
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TITLE OF INVENTION:
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Sequence 3, Application US/09876225
Sequence 3, Application US/09876225
GENERAL INFORMATION
APPLICANT: Baylor College of Medicine
APPLICANT: Thompson, Timothy C.
APPLICANT: Ren, Chengalen
TITLE OF INVENTION: RTVP Based Compositions and Methods for the Treatment of Prost
FILE REFERENCE: 38594.0027
CURRENT APPLICATION NUMBER: US/09/876,225
CURRENT PILING DATE: 2001-06-08
PRIOR FILING DATE: 2000-06-08
PRIOR FILING DATE: 2000-06-08
SOFTWARE: PATENTING DATE: 2000-06-08
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APPLICANT: Shimkets, Richard A
APPLICANT: Shimkets, Richard A
APPLICANT: Herrmann, John L
APPLICANT: Majuwder, Kund
APPLICANT: Majuwder, Kund
APPLICANT: Majuwder, Kund
APPLICANT: Mazes, Peter S
APPLICANT: Rastelli, Luca
TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
FILE REFERRENCE: 15966-697
CURRENT FILING DATE: 2001-03-05
PRIOR APPLICATION NUMBER: 60/186,596
PRIOR APPLICATION NUMBER: 60/186,596
PRIOR PLING DATE: 2000-03-03
NUMBER OF SEQ ID NOS: 98
SOFTWARE: Patentin Ver. 2.1
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                                                                                                                        Length 219;
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                                                                                                                                                                                    6; Indels
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28;
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Pred. No. 28;
5; Mismatches
                                                                                                                           DB 5;
                                                                                                                           Score 43; DB Pred. No. 23; 5; Mismatches
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Pred. No. 2
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38.9%;
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Best Local Similarity 38.9%;
Matches 7; Conservative 5
                                                                                                                              32.8%;
38.9%;
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                                                                                                                                                                                                                                                4 YMINFGRGONYWEHPYOK 21
                                                                                               TYPE: PRT
CRGANISM: Homo sapiens
US-09-876-225-3
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US-09-800-198-90
; ORGANISM: Homo sapiens
US-09-800-198-91
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Best Local Similarity
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SEQ ID NO 90
LENGTH: 266
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Sequence 15512, Application US/09708427

GENERAL INFORMATION:
APPLICANT: N. ALEXANDROV et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: THEREBY
FILE REFERENCE: 2750-1243P

CURRENT APPLICATION NUMBER: US/09/708,427

CURRENT FILING DATE: 2000-11-09

NUMBER OF SEQ ID NOS: 85364

SEQ ID NO 15512
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APPLICANT: Fernandes, Elma
APPLICANT: Fernandes, Elma
APPLICANT: Stankets, Richard A
APPLICANT: Herrmann, John L
APPLICANT: Majumder, Kumud
APPLICANT: Majumder, Kumud
APPLICANT: Majumder, Kumud
APPLICANT: Rastelli, Luca
APP
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                                         CTHER INFORMATION: Description of Unknown Organism: Known Member of CTHER INFORMATION: Matrix Metalloproteinase Family US-09-689-730-17
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                                                                                                                                                                                              Score 45; DB 5; Length 631;
Pred. No. 34;
0; Mismatches 3; Indels
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LOCATION: 1..228
OTHER INFORMATION: Xaa is any amino acid
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CCATION: 1.228

CTHER INFORMATION: Ceres Seq. ID 1829311

US-09-708-427-15512
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                 34.4%;
58.8%;
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| 137 EADIMINEGR----WEH 149
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Best Local Similarity 54.59
Matches 6; Conservative
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                                                                                                                                                                                                       Query Match 34.4
Best Local Similarity 58.8
Matches 10; Conservative
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US-09-800-198-91
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SEQ ID NO 91
LENGTH: 219
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Search completed: January 29, 2002, 10:58:17 Job time: 2513 sec
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120 KGKRVWEHPF 129
  10 RGQNYWEHPY 19
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Sequence 67426 Application US/09708427

GRNERAL INFORMATION:
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES TITLE OF INVENTION: THEREBY
FILE REFERENCE: 2750-1243P

CURRENT APPLICATION NUMBER: US/09/708,427

CURRENT FILING DATE: 2000-11-09

NUMBER OF SEQ ID NOS: 85364

SEQ ID NOS: 85364

SEQ ID NO 64426

LENGTH: 135
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APPLICANT: Fernandes, Elma
APPLICANT: Fernandes, Elma
APPLICANT: Richard A
APPLICANT: Majumder, Richard A
APPLICANT: Majumder, Kumud
APPLICANT: Majumder, Kumud
APPLICANT: Majumder, Kumud
APPLICANT: Majumder, Vishna
APPLICANT: Mastelli, Luca
APPLICANT: Rastelli, Luca
APPLICANT: Rastelli, Luca
APPLICANTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: 1596-697
CURRENT APPLICATION NUMBER: US/09/800,198
CURRENT APPLICATION NUMBER: 00/186,596
PRIOR APPLICATION NUMBER: 60/186,596
PRIOR FILING DATE: 2000-03-03
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 89
LENGHH: 415
  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 43; DB 5; Length 415;
Pred. No. 44;
2; Mismatches 4; Indels
  6; Indels
  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc_feature

LOCATION: 1..135

OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc_feature

LOCATION: 1..135

OTHER INFORMATION: Ceres Seq. ID 1932516
US-09-708-427-67426
                                                                                                                                                                    US-09-800-198-89; Sequence 89, Application US/09800198; GENERAL INFORMATION:
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ORGANISM: Zea mays subsp. mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: PRT
; ORGANISM: Halocynthia roretzi
US-09-800-198-89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match 32.8%;
Best Local Similarity 53.8%;
Matches 7; Conservative
                                                                   171 FICNYGPGGNYPTWPYKR 188
                                        4 YMINFGRGQNYWEHPYOK 21
7; Conservative
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268 NYGPGGNYPTHPF 280
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/ cgn2_6/ptodata/2/paa/US08_COMB.pep: *
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1: /cgn2_6/ptcdata/2/paa/PCTUS_COMB.pep:*

2: /cgn2_6/ptcdata/2/paa/USO6_COMB.pep:*

3: /cgn2_6/ptcdata/2/paa/USO8_COMB.pep:*

4: /cgn2_6/ptcdata/2/paa/USO8_COMB.pep:*

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3148936 seqs, 277657034 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                       OM protein - protein search, using sw model
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1 DQPKQYEQHLTDYEKIKEG 19
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Gapop 10.0 , Gapext 0.5
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Sequence 808, App Sequence 1.76, Ap Sequence 1176, Ap Sequence 4, Appli Sequence 8, Appli Sequence 8, Appli Sequence 8, Appli	Sequence 4, Appliance 2, Appliance 6, Appliance 6, Appliance 6, Appliance 1, Appliance 2, Applia	6,200		Sequence 20, Appl Sequence 20, Appl Sequence 35, Appl Sequence 34118, A Sequence 24239, A Sequence 24239, A Sequence 24511, A
24 US-60-194-106-808 24 US-60-231-679-2 24 US-60-213-847-1176 1 PCT-US00-02544-4 1 PCT-US00-30542-8 1 US-09-371-674-4 21 US-09-371-674-4	US-09-855-1459 US-09-855-1459 PCT-US00-02544 PCT-US00-30542 US-09-152-814 US-09-371-674 US-09-706-426	13 US-08-984-099-3 18 US-09-44-810-2 18 US-09-44-810A-2 24 US-60-126-214-2 18 US-09-489-039A-9599 17 US-09-328-352-5693 24 US-60-215-161-6793	PCT-USO1-08631-370 US-09-573-655A-17 US-09-898-554-17 US-09-888-554-26 US-60-324-109-257 US-60-334-109-261 US-60-334-109-261	22 US-00-324-109-26/08 22 US-09-989-554-20 24 US-60-173-466-55 1 PCT-US01-08631-34518 24 US-60-173-464-24239 24 US-60-191-631-24571
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## ALIGNMENTS

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Sequence 18, Application US/09763397A

Sequence 18, Application US/09763397A

Sequence 18, Application US/09763397A

GENERAL INFORMATION:
APPLICANT: The Government of the United States of America, as represented by the APPLICANT: Control and Prevention
APPLICANT: Lal, Altaf A.
APPLICANT: Hasnain, Seyed E.
TITLE OF INVENTION: Recombinant Multivalent Malarial Vaccine Against Plasmodium Fa FILE REFERENCE: 6395-57049

TITLE OF INVENTION: Recombinant Multivalent Malarial Vaccine Against Plasmodium Fa FILE REFERENCE: 6395-57049

CURRENT FILING DATE: 2001-02-16

PRIOR APPLICATION NUMBER: US 60/097,703

PRIOR APPLICATION NUMBER: POT / US99/18869

PRIOR APPLICATION NUMBER: POT / US99/18869
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 19;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Plasmodium falciparum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 26
SOFTWARE: PatentIn version 3.1
SEQ ID NO 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ) ORGANISM: Plas
US-09-763-397A-18
US-09-763-397A-18
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                                                                                                                                                                         Length 622;
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Sequence 8, Application US/07672183A

Sequence 8, Application US/07672183A

Sequence 8, Application US/07672183A

Sequence 8, Application US/07672183A

APPLICANT: Pancy Charles

APPLICANT: de Taisne, Charles

APPLICANT: Tine, John A.

APPLICANT: Tine, John A.

TITLE OF INVENTION: MALARIA RECOMBINANT POXVIRUS VACCINE

NUMBER OF SEQUENCES: 19

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/672,183A FILING DATE: 19910320 CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 105; DB 3;
Pred. No. 3.8e-07;
                                                                                                                                                                         Score 105; DB 1;
Pred. No. 3.8e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: William S. Frommer ADDRESSEE: c/o Curtis, Morris & Safford, P.C. STREET: 530 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 5
US-08-072-867-8
; Sequence 8, Application US/08072867
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Frommer, William S.
REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 454.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 840-3333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .;
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100.0%;
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TELERAX: (212) 840-0712
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                             100.0%;
100.0%;
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                                                                                                                                                                                                                                                          19
                                       622 amino acids
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INFORMATION FOR SEQ ID NO:
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                      SEQUENCE CHARACTERISTICS
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Best Local Similarity
Matches 19; Conserva
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Best Local Similarity
Matches 19; Conserva'
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                                                     TYPE: amino acid
STRANDEDNESS: sir
                                                                                                   TOPOLOGY: linear
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                                       LENGTH:
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                                                                                                           Sequence 2, Application US/09763397A

Sequence 2, Application US/09763397A

Sequence 2, Application US/09763397A

GENERAL INFORMATION:

APPLICANT: The Government of the United States of America, as represented by the APPLICANT: Secretary of the Department of Health and Human Services, Centers for Dis APPLICANT: Control and Prevention

APPLICANT: Hasnahi, Seyde E.

APPLICANT: Hasnahi, Seyde E.

APPLICANT: Hasnahi, Seyde E.

APPLICANT: Hasnahi, Seyde E.

CURRENT APPLICATION NUMBER: US/09/763,397A

CURRENT APPLICATION NUMBER: US/06/097,703

PRIOR FILING DATE: 1998-08-11

PRIOR FILING DATE: 1998-08-12

PRIOR FILING DATE: 1998-08-13

NUMBER OF SEQ ID NOS: 26

SOFTHARE: PATENTIN VERSION 3.1

SOFTHARE: PATENTIN VERSION 3.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 350;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 8, Application PC/TUS920207
GENERAL INFORMATION:
APPLICANT: VIROSENETICS, CORPORATION
APPLICANT: VIROSENETICS, CORPORATION
NUMBER OF SEQUENCES: 74
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.25
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Pred. No. 1.8e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Curtis, Morris, and Safford ADDRESSEE: c/o William S. Frommer STREET: 530 Fifth Avenue CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: Recombinant DNA/Protein US-09-763-397A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Frommer, Millam S.
REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 454310-2411
TELEPHONE: (212) 840-3333
TELEPHONE: (212) 840-0712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          имьек: РСТ/US92/02207
19-мак-1992
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MEDUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
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100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Artificial Sequence
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            1 DQPKQYEQHLTDYEKIKEG 19
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: PC
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Best Local Similarity 100.
Matches 19; Conservative
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CLASSIFICATION:
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PCT-US92-02207-8
                                                                                                               US-09-763-397A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 2
LENGTH: 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
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Sequence 1135, Application US/60192737

Sequence 1135, Application US/60192737

GENERAL INFORMATION:

APPLICANT: Bonazzi, Vivien

APPLICANT: Bonazzi, Vivien

TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS OF THE

TITLE OF INVENTION: SER/THR AND TYR FAMILY OF KINASES, NUCLEIC ACID MOLECULES

TITLE OF INVENTION: ENCODING THESE HUMAN KINASE PROTEINS, AND USES THEREOF

TITLE OF INVENTION: ENCODING THESE HUMAN KINASE PROTEINS, AND USES THEREOF

CURRENT PAPLICATION NUMBER: US/60/192,737

CURRENT FILING DATE: 2000-03-28

NUMBER OF SEQ ID NOS: 1342

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 1135

LENGTH: 149
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US-60-194-106-704
US-60-194-106-704
US-60-194-106-704
GENERAL INFORMATION:
APPLICANT: Bonazzi, Vivien
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MCLECULES ENCODING HUMAN KINASE PROTEINS, AND USES;
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
CURRENT FILING DATE: 2000-04-03
NUMBER OF SEQ ID NOS: 826
SOCTHARE: FastSEQ for Windows Version 4.0
SEQ ID NO 704
LENGTH: 149
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Pred. No. 6.7;
3; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                               Score 105; DB 4;
Pred. No. 3.8e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                           454310-2500
                ATTORNEY/AGENT INFORMATION:
NAME: Frommer William S.
REGISTATION NUMBER: 25,506
REPERENCE/DOCKET NUMBER: 45431
TELECOMMUNICATION INFORMATION:
TELEFRAM: (212) 840-333
TELEFRAM: (212) 840-333
TELEFRAM: (212) 840-0712
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 622 mmino acids
TYPE: amino acids
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100.0%;
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Best Local Similarity 100.
Matches 19; Conservative
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68 KQYKHHLTAYEKLE 81
                                                                                                                                                                                                                                                                                                    ; TOPOLOGY: linear
US-08-075-783-9
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Best Local Similarity
Matches 9; Conserv
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; ORGANISM: HUMAN
US-60-192-737-1135
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; ORGANISM: HUMAN
US-60-194-106-704
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10S-08-075-783-9

1 Sequence 9, Application US/08075783

1 Sequence 9, Application US/08075783

2 Sequence 9, Application:

2 APPLICANT: Paoletti, Enzo

3 APPLICANT: Tine, John A.

3 TITLE OF INVENTION: MALARIA RECOMBINANT POXVIRUS VACCINE

3 NUMBER OF SEQUENCES: 124

3 CORRESPONDENCE ADDRESS:

4 ADDRESSEE: Curtis, Morris & Safford

5 ADDRESSEE: C/O William S. Frommer

5 STREET: 530 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 622;
APPLICANT: Paoletti, et al TTLE OF INVENTION MALARIA RECOMBINANT POXVIRUS VACCINE NUMBER OF SEQUENCES: 74 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/072,867
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 105; DB 4;
100.0%; Pred. No. 3.8e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 07/852,305
FILING DATE: 18-MAR-1992
ATTORNEY,AGENT INFORMATION:
NAME: Frommer, William S.
REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 45,4310-2410
TELECHONE: (212) 840-3333
                                                                                      ADDRESSEE: Curtis, Morris, and Safford ADDRESSEE: c/o William S. Frommer STREET: 530 Fifth Avenue CITY: New York STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New York
: United States of America
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FILING DATE: 11-JUN-1993
                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (212) 840-3333
TELEFAX: (212) 840-0712
INFORMATION FOR SEQ ID NO: 8:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.0%;
Matches 19; Conservative C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 622 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
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                                                                                                                                                                                                           USA
                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                               10036
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                                                                                                                                                                                                    COUNTRY:
ZIP: 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE:
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Sequence 1317, Application US/60192737

Sequence 1317, Application US/60192737

Sequence 1317, Application US/60192737

SERNEMATION:
SENTHATION:
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS OF THE
TITLE OF INVENTION: ERRYTHR AND TYR FAMILY OF KINASES, NUCLEIC ACID MOLECULES
TITLE OF INVENTION: ENCODING THESE HUMAN KINASE PROTEINS, AND USES THEREOF
FILE REFERENCE: CLO00402

CURRENT APPLICATION NUMBER: US/60/192,737

CURRENT APPLICATION NOWBER: US/60/192,737

CURRENT FILING DATE: 2000-03-28

NUMBER OF SEQ ID NOS: 1342

SOFTWARE: FastSEQ for Windows Version 4.0
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Sequence 808, Application US/60194106
GENERAL INFORMATION:
APPLICANT: BONAZZI, VIVIEN
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
TITLE OF INVENTION: THEREOF
FILLE REFERENCE: CLOOMAGER: US/60/194,106
CURRENT APPLICATION NUMBER: US/60/194,106
CURRENT FILMO DATE: 2000-04-03
NUMBER OF SEQ ID NOS: 826
SOFTWARE: FRASEQ for Windows Version 4.0
SEQ ID NO 808
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 53; DB 24; Length 160; pred. No. 7.3; 3; Mismatches 2; Indels
                              DB 24; Length 149;
6.7;
                                                                                     2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3; Mismatches
                                             Score 53; DB;
Pred. No. 6.7;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; LOCATION: (1)...(160)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-60-194-106-808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: VARIANT
COCATION: (1)...(160)
COTHER INFORMATION: Xaa = Any Amino Acid
US-60-192-737-1317
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64.3%;
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64.3%;
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Best Local Similarity 64.3
Matches 9; Conservative
                                                   Query Match 50.5
Best Local Similarity 64.3
Matches 9; Conservative
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85 KQYKHHLTAYEKLE 98
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68 KQYKHHLTAYEKLE 81
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Best Local Similarity
Matches 9; Conserv
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US-60-194-106-808
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4 KQYEQHLTDYEKIK 17

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NESCOLATION OF APPLICATION US/60213847

Sequence 1176, Application US/60213847

GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION:
SER/THR AND TYR FAMILY OF KINASES, NUCLEIC ACID MOLECULES;
TITLE OF INVENTION:
SER/THR AND TYR FAMILY OF KINASES, NUCLEIC ACID MOLECULES;
TITLE OF INVENTION:
CURRENT FAPILCATION NUMBER: US/60/213,847

CURRENT FILING DATE: 2000-06-23

NUMBER OF SEQ ID NOS: 1824

SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 53; DB 24; Length 360; pred. No. 20; A; Indels 2; Mismatches 4; Indels
                                       Lao, Monique G.

APPLICANT: Burford, Neil
APPLICANT: Stewart, Elizabeth A.
APPLICANT: Stewart, Elizabeth A.
APPLICANT: Gradhi, Amean R.
APPLICANT: Patterson, Chandra
APPLICANT: Lee, Ernestine A.
APPLICANT: Lee, Ernestine A.
APPLICANT: Lu, Dyung Ain M.
TITLE OF INVENTION: PROTEIN PHOSPHATASES
FILE REFRENCE: PI-0173 P.
CURRENT FILING DATE: 2000-07-28
CURRENT FILING DATE: 2000-07-28
SEQ ID NO 2
SEQ ID NO 2
LENGTH: 360
TYPE: PRT
COPPT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc_feature
CTHER INFORMATION: Incyte ID No: 7476908CD1
US-60-221-679-2
Sequence 2, Application US/60221679 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          50.5%;
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144 PEALKQHLQDYEKDKE 159
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Best Local Similarity 64.3
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 50.5
Best Local Similarity 62.5
Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 1176
LENGTH: 471
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APPLICANT: SMITHKLINE BEECHAM CORPORATION
TITLE OF INVENTION: SPECIFIC PEPTIDE SUBSTRATE FOR HUMAN
TITLE OF INVENTION: SPECIFIC PEPTIDE SUBSTRATE FOR HUMAN
TITLE OF INVENTION: YAK3A, AND YAK3B AND YEAST YAK1 PROTEIN KINASES
FILE REFERENCE: GH-70650W
CURRENT APPLICATION NUMBER: PCT/0400/330542
CURRENT FILING DATE: 1999-11-05
PRIOR APPLICATION NUMBER: TO BE ASSIGNED
PRIOR FILING DATE: 2000-11-03
NUMBER OF SEQ ID NOS: 18
SOFTWARE: FEASISEQ for Windows Version 3.0
SEQ ID NO 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 50.5%; Score 53; DB 1; Length 568; Best Local Similarity 64.3%; Pred. No. 35; Matches 9; Conservative 3; Mismatches 2; Indels
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                                                                 APPLICAMT: SmithKilne Beecham Corporation
TITLE OF INVENTION: A METHOD OF TREATING ANEMIA
FILE REFERENCE: GH-50041
CURRENT APPLICATION NUMBER: PCT/US00/02544
CURRENT FILING DATE: 2000-02-01
EARLIER APPLICATION NUMBER: 09/440,236
EARLIER APPLICATION NUMBER: 09/371,674
EARLIER FILING DATE: 1999-08-10
EARLIER FILING DATE: 1999-08-10
EARLIER FILING DATE: 1999-08-10
EARLIER FILING DATE: 1999-08-10
SERIER FILING DATE: 1999-08-10
NUMBER OF SEO ID NOS: 9
SOFTWARE: FASTESO for Windows Version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 8, Application PC/TUS0030542 GENERAL INFORMATION:
                        Sequence 4, Application PC/TUS0002544 GENERAL INFORMATION:
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APPLICANT: Lord, Kenneth A.
APPLICANT: Dillion, Susan B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: HOMO SAPIENS
PCT-US00-30542-8
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PCT-US00-02544-4
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Best Local Similarity
Matches 9; Conserv
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PCT-US00-30542-8
PCT-US00-02544-4
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US-09-371-674-4
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Run on:

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Sequence 7930, AP
Sequence 26645, A
Sequence 10604, A
Sequence 26644, A
Sequence 5544, Ap
Sequence 4042, Ap
Sequence 4041, Ap
Sequence 26643, A
Sequence 5543, Ap
                 Sequence 25, Appl
Sequence 26150, A
Sequence 1152, Ap
Sequence 2192, Ap
Sequence 214, App
Sequence 154, App
                                 US-09-708-427-50450
US-09-708-427-50450
US-09-708-427-50449
US-09-801-368-154
US-09-807-518-154
US-09-897-518-154
US-09-897-518-164
US-09-708-427-26645
US-09-708-427-26644
US-09-708-427-26644
US-09-708-427-4042
US-09-708-427-4042
                                                                                                                                                                                                                                                                                                       US-09-708-427-26643
US-09-708-427-5543
US-09-708-427-5542
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                                                                                                                                                                                                                                                                                                                                                                                                      ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 34
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 24
LENGTH: 551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/10/016,333 CURRENT FILING DATE: 2001-12-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 24, Application US/10016333
GENERAL INFORMATION:
APPLICANT: Ian Edward James
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Michael N. Cook
Kathleen T. Gallagher
Kristine Kay Kikly
David Michalovich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Brian Michael Burns
Kimberly A. Brun
Richard James Chenery
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Randall Forrest Smith
Xiaotong Li
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alexander H. Taylor
Donald M. Wojchowski
Stephen A. Hughes
David J. Powell
Gary Christie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tania Tamson Testa
John Anthony Feild
Caretha Lee Creasy
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Peter C. McDonnell
Wendy S. Halsey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Warren J. Leonard
Katsutoshi Ozaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Zunxuan Chen
Todd Fredrickson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ian Edward James
Michael W. Lark
Han N. Trinh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Harma Ellens
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US-10-016-333-24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Yuan Zhu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lin Yue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-016-333-24
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APPLICANT:
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APPLICANT:
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APPLICANT:
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APPLICANT:
APPLICANT:
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APPLICANT:
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 Sequence 6793, Apple Sequence 30615, A Sequence 33993, A Sequence 33993, A Sequence 13993, A Sequence 181, Apple Sequence 12540, Apple Sequence 12540, Apple Sequence 12540, Apple Sequence 2980, Apple Sequence 21965, Apple Sequence 21965, Apple Sequence 21965, Apple Sequence 1306, Apple Sequence 15014, Apple Sequence 15016, Apple Sequence
                                                                                                                                                   (without alignments)
5.749 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                 ; Search time 120.95 Seconds
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pending_Patents_AA_New:*

1: /cgn2_6/ptcdata/2/paa/US06_NEW_COMB.pep:*

3: /cgn2_6/ptcdata/2/paa/US06_NEW_COMB.pep:*

3: /cgn2_6/ptcdata/2/paa/US07_NEW_COMB.pep:*

4: /cgn2_6/ptcdata/2/paa/US08_NEW_COMB.pep:*

5: /cgn2_6/ptcdata/2/paa/US08_NEW_COMB.pep:*

5: /cgn2_6/ptcdata/2/paa/US08_NEW_COMB.pep:*

7: /cgn2_6/ptcdata/2/paa/US08_NEW_COMB.pep:*
                 GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-09-897-516-6793
US-09-708-427-30615
US-09-708-427-30615
US-09-708-427-30615
US-09-708-427-33993
US-09-708-427-33993
US-09-708-427-33993
US-09-815-242-5240
US-09-815-242-5240
US-09-815-242-5240
US-09-815-242-5240
US-09-815-242-12892
US-09-815-242-12892
US-09-815-242-12892
US-09-61-1526-2980
US-09-61-1526-2980
US-09-708-427-21965
US-09-708-427-21965
US-09-708-427-21965
US-09-708-427-1306
US-09-708-427-1306
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US-09-108-427-1306
US-09-108-427-1306
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US-09-108-427-1306
US-09-108-427-1306
US-09-108-427-1306
US-09-108-427-1306
US-09-108-427-1306
US-09-815-242-5250
US-09-815-242-5250
US-09-708-427-15015
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                                                                                                                                                                                                                                                                                                                                            173191 segs, 36597120 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUMMARIES
                                                                                                                             January 29, 2002, 10:58:16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Match
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39.5
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                                                                                             OM protein
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Result

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APPLICANT: N. ALEXANDROW et al.
APPLICANT: N. ALEXANDROW et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID
TITLE OF INVENTION: THEREBY
FILLE REFERENCE: 2750-1248
CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILLING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85564
SSCTWARE: Patentin version 3.1
ENGTH: 222
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APPLICANT: Bower, Stanley G.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
TITLE ON INSTAUTION: Sphingomonas elodea genome sequences and uses thereof FILE REFERENCE: 38-10(15806)B
CURRENT APPLICATION NUMBER: US/10/015,127
CURRENT FILING DATE: 2001-10-29
PRIOR FILING DATE: 2001-11-22
NUMBER OF SEQ ID NOS: 14357
SEQ ID NO 13974
LENGTH: 575
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pred. No. 52;
6; Mismatches 5; Indels
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13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc_feature
LOCATION: 1.222
OTHER INFORMATION: Ceres Seq. ID 1829599
US-09-708-427-30614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 46;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 5
0/S-10-015-127-13974
; Sequence 13974, Application US/10015127
; GENERAL INFORMATION:
                                                                                                                                                                                                              Sequence 30614, Application US/09708427; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             43.8%;
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; ORGANISM: Sphingomonas elodea
US-10-015-127-13974
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Best Local Similarity 38.9%;
Matches 7; Conservative
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Best Local Similarity 61.55
Matches 8; Conservative
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176 YAQHWTDYDQSKE 188
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                 6 YEQHLTDYEKIKE 18
                                                  RESULT 6
US-09-708-427-33993
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US-09-708-427-30615
US-09-708-427-30615
SQUENCE 30615, Application US/09708427
GENERAL INFORMATION:
APPLICANT: N. ALEXANDROV et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: THERENY
FILE REFERENCE: 2750-1243P
CURRENT APPLICATION UNMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 30615
LENGTH: 130
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APPLICANT: Corbin, David R.
APPLICANT: Goldman, Barry S.
APPLICANT: Hoshing, Joseph E.
APPLICANT: Hueshing, Joseph E.
APPLICANT: Hasomil-Osterfeld, Karina C.
APPLICANT: Arsomil-Osterfeld, Karina C.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Sla
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Length 551;
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                                                        2; Indels
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43.8%; Score 46; DB 5;
Best Local Similarity 61.5%; Pred. No. 6.9;
Matches 8; Conservative 2; Mismatches
  DB 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 46; DB Pred. No. 3.8; 5; Mismatches
                                                           Mismatches
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LOCATION: 1..130
CTHER INFORMATION: Xaa is any amino acid;
NAME/KEY: misc_feature
LOCATION: 1..130
COTHER INFORMATION: Ceres Seq. ID 1829600
US-09-708-427-30615
     Score 53;
Pred. No.
                                                                                                                                                                                                                                                                                                                    Sequence 6793, Application US/09897516 GENERAL INFORMATION:
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50.0%;
  Query Match
Best Local Similarity 64.3%;
Matches 9; Conservative
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Best Local Similarity 50.0
Matches 7; Conservative
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                                                                                                                                                        112 KQYKHHLTAYEKLE 125
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55 YKKHSTDFMKIRQG 68
                                                                                                                    4 KQYEQHLTDYEKIK 17
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Matches
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APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Hulasing, Joseph E.
APPLICANT: Huesing, Joseph E.
APPLICANT: Malvar, Thomas M.
APPLICANT: Staven C.
APPLICANT: Staven C.
APPLICANT: Spiridonov, Sergei
TITLE OF INVENTION: Xenorhabdus sp. Genome Sequences And Uses Thereof
FILE REPERENCE: 38-21(51847)8
CURRENT APPLICATION NUMBER: US/09/897,516
CURRENT FILING DATE: 2001-06-29
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                       TITLE OF INVENTION: Methods for Analyzing Biological Elements FILE REFERENCE: 16517.246/38-10(52045)A
CURRENT APPLICATION NUMBER: US/60/325,537
CURRENT FILING DATE: 2001-10-01
NUMBER OF SEQ ID NOS: 40
SOFTWARE: PatentIn version 3.1
SEQ ID NO 18
LENGTH: 715
                                                                                                                                                                                                                                                                                    Score 42; DB 7; Length 715;
Pred. No. 1.9e+02;
3; Mismatches 5; Indels
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APPLICANT: Zyskind, Judith W.
APPLICANT: Zyskind, Judith W.
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Xu, H. Howard
TITLE OF INVERTION: Identification of Essential Genes
TITLE OF INVERTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 41; DB Pred. No. 81; 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: US 60/215, 161
PRIOR FILING DATE: 2000-06-30
NUMBER OF SEQ ID NOS: 8409
SEQ ID NO 8110
LENGTH: 256
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 8110, Application US/09897516 GENERAL INFORMATION:
                                                                                                                                                                               TYPE: PRT
ORGANISM: Arabidopsis thaliana
US-60-325-537-18
                                                                                                                                                                                                                                                                                        40.0%;
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53.8%;
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Best Local Similarity 53.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                           Best Local Similarity 46.7
Matches 7; Conservative
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142 QYQQHVAEMEAAKAG 156
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; ORGANISM: Xenorhabdus sp.
US-09-897-516-8110
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48 RQYDQMLADYNQI 60
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US-09-815-242-5240
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Sequence 33993, Application US/09708427
GENERAL INFORMATION:
APPLICANT: N. ALEXANDROV et al.
APPLICANT: N. ALEXANDROV et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES TITLE OF INVENTION: THEREBY FILE REFERENCE: 2750-1243P
CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85564
SOFTWARE: PATENTI VERSION 3.1
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GENERAL INFORMATION:
APPLICAMENTON:
APPLICAMENTON: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: THEREBY
TITLE OF INVENTION: THEREBY
CURRENCE: 2750-1243P
CURRENT FAPLICATION UNDMER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SEQ ID NO 33992
LENGTH: 655
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Pred. No. 1.5e+02;
2; Mismatches 7; Indels
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Pred. No. 1.7e+02;
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LOCATION: 1..655
OTHER INFORMATION: Xaa is any amino acid
                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc_feature
| LOCATION: 1.587
| OTHER INFORMATION: Ceres Seq. ID 1837602
US-09-708-427-33993
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COCATION: 1..655
COTHER INFORMATION: Ceres Seq. ID 1837601
US-09-708-427-33992
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Sequence 18, Application US/60325537
GENERAL INFORMATION:
                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Arabidopsis thaliana
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Best Local Similarity 50.07
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LOCATION: 1..587
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Best Local Similarity
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LENGTH: 587
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Length 445;

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WAKAMATSU, AI
SUGIYAMA, TOMOYASU
NAGAI, KEIICHI
KOJIMA, SHINICHI
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33.3%;
  39.0%;
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HAYASHI, KOJI
ISHII, SHIZUKO
KAWAI, YURI
                                                                                                                                   286 EQQRKHVEHLSSYYKFKQ 303
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Best Local Similarity 33.3.
Best Local 6; Conservative
                                                                                                 1 DQPKQYEQHLTDYEKIKE 18
  Query Match
Best Local Similarity 33.33
Matches 6; Conservative
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US-09-611-526-2980
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APPLICANT:
APPLICANT:
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APPLICANT: Cart, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TTTLE OF INVENTION: Identification of Essential Genes in
TTTLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITARA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2000-03-21
PRIOR PELICATION NUMBER: 60/191,078
PRIOR PELICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-03-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
PRIOR PELICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/253,931
PRIOR FILING DATE: 2000-110-23
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2001-10-16
PRIOR FILING DATE: 2001-10-16
SOFTWARE: RastesQ for Windows Version 4.0
SEQ ID NO 12582
LENGTH: LANGTH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 39.0%; Score 41; DB 5; Length 438; Best Local Similarity 33.3%; Pred. No. 1.5e+02; Matches 6; Conservative 7; Mismatches 5; Indels
          CUCRRENT AFFLICATION NUMBER: 05/05/011/42

PRIOR APPLICATION NUMBER: 60/191,078

PRIOR FILING DATE: 2001-03-21

PRIOR PELICATION NUMBER: 60/201

PRIOR PELICATION NUMBER: 60/205,848

PRIOR PELICATION NUMBER: 60/207,727

PRIOR PELING DATE: 2000-05-26

PRIOR FILING DATE: 2000-05-26

PRIOR FILING DATE: 2000-10-23

PRIOR FILING DATE: 2000-11-27

PRIOR PELICATION NUMBER: 60/253,625

PRIOR PELING DATE: 2000-11-27

PRIOR APPLICATION NUMBER: 60/257,931

PRIOR PILING DATE: 2000-12-22

PRIOR PELING DATE: 2000-12-22

PRIOR PELING DATE: 2000-12-22

PRIOR PELING DATE: 2001-02-16

NUMBER OF SED ID NOS: 14110

SOFTWARE: FASSES FOR WINDGWS VERSION 4.0
CURRENT APPLICATION NUMBER: US/09/815,242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-815-242-12582
; Sequence 12582, Application US/09815242
; GENERAL INFORMATION:
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US-09-815-242-12582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Staphylococcus aureus US-09-815-242-5240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Ohlsen, Kari L.
APPLICANT: Syskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         :| ::::||: | |: 283 EQQRKHVEHLSSYYKFKQ 300
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APPLICANT: Oblisen, Kari L.
APPLICANT: Syskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Tranick, John D.
APPLICANT: Tranick, John D.
APPLICANT: Tranick, John D.
APPLICANT: Tammorco, Robert T.
APPLICANT: Yammorco, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
TITLE OF INVENTION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR PILICATION NUMBER: 60/207,727
PRIOR PILICATION NUMBER: 60/207,727
PRIOR PILICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-36
PRIOR FILING DATE: 2000-12-36
PRIOR FILING DATE: 2000-13-30
PRIOR PRIOR FILING DATE: 2000-13-30
PRIOR PRIOR FILING DATE: 2000-13-30
PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRI
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Pred. No. 1.5e+02;
7; Mismatches 5.
Score 41; DB 5; I Pred. No. 1.5e+02;
                                                                                           7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2980, Application US/09611526 GENERAL INFORMATION:
APPLICANT: OTA, TOSHIO
APPLICANT: NISHIKAWA, TETSUO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 12940, Application US/09815242; GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
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US-09-815-242-12940
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Zelder, Oskar
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APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Halvar, Thomas M.
APPLICANT: Malvar, Thomas M.
APPLICANT: Slater, Steven C.
APPLICANT: Splitdonov, Sergei
TITLE OF INVENTION: Xenorhabdus sp. Genome Sequences And Uses Thereof
FILE REBERBENCE: 38-21(51847)B
CURRENT APPLICATION NUMBER: US(9/9/897,516
CURRENT FILING DATE: 2001-06-29
PRIOR FILING DATE: 2000-06-30
NUMBER OF SEQ ID NOS: 8409
SEQ ID NO 7774
FEATURE OF SEQ ID NOS: 8409
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          APPLICANT: CLEAR AT A PERMENS FOR SYNTHESIS OF FULL LENGTH CDNAS TITLE OF INVENTION: PRIMERS FOR SYNTHESIS OF FULL LENGTH CDNAS TITLE OF INVENTION: AND THEIR USES TITLE OF INVENTION: AND THEIR USES TITLE PRIMERS. 0400-07-07 CURRENT APPLICATION NUMBER: US/09/611,526 CURRENT FILING DATE: 2000-07-07 PRIOR APPLICATION NUMBER: US/09/1874 PRIOR FILING DATE: 1999-07-08 PRIOR FILING DATE: 1999-07-08 PRIOR APPLICATION NUMBER: US/00-01-11 PRIOR APPLICATION NUMBER: US/00-01-11 PRIOR PRIOR APPLICATION NUMBER: US/00-01-11 PRIOR FILING DATE: 2000-05-02 NUMBER OF SEQ ID NOS: 4484 SOFTWARE: PALENT NET. 2000-05-02 NUMBER OF SEQ ID NOS: 4484 SOFTWARE: PALENT NET. 2000-05-02 NUMBER OF SEQ ID NOS: 4484 SOFTWARE: DATE: 2000-05-02 NUMBER OF SEQ ID NOS: 4484 SOFTWARE: PALENTIN VET. 2.1
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Pred. No. 6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 540;
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GENERAL INFORMATION:
APPLICANT: Pompejus, Markus
APPLICANT: Schroder, Burkhard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 7774, Application US/09897516 GENERAL INFORMATION:
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50.0%;
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53.3%;
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Best Local Similarity 50.0%
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Best Local Similarity 53.3
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Xenorhabdus sp. US-09-897-516-7774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           933 PRQHEQLQRDYEMAK 947
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                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Homo sapiens
US-09-611-526-2980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 15
US-09-605-703B-2270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-897-516-7774
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## APPLICANT: Haberhauer, Gregor
TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING NOVEL
TITLE OF INVENTION: PROTEINS
FILE REFERENCE: BG1-129CP
CURRENT APPLICATION NUMBER: US/09/605,703B
CURRENT APPLICATION NUMBER: 60/12,764
PRIOR PILING DATE: 1999-07-08
PRIOR RPLING DATE: 1999-07-08
PRIOR PILING DATE: 1999-07-08
PRIOR RPLING DATE: 1999-07-08
PRIOR RPLING DATE: 1999-07-08
PRIOR RPLING DATE: 1999-07-08
PRIOR RPLING DATE: 1999-07-08
PRIOR PILING DATE: 1999-07-08
PRIOR APPLICATION NUMBER: 60/152,318
PRIOR PILING DATE: 1999-07-08
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Sequence 24400, A Sequence 24400, A Sequence 6098, Ap Sequence 27679, A Sequence 22289, A Sequence 11724, A Sequence 11652, A Sequence 1362, A Sequence 263, Ap Sequence 263, Ap Sequence 263, Ap Sequence 2126, A Sequence 2126, A Sequence 2126, A Sequence 19397, A Sequence 2126, A Sequence 2123, A Sequence 2124, A Sequence

Run on:

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US-09-270-849B-1B9090
US-09-270-767-4400
US-09-270-767-4400
US-09-270-767-4400
US-09-270-34B2
US-60-316-362-34B2
US-60-131-637-27679
US-60-191-637-27679
US-60-191-637-278BB
US-60-191-637-278BB
US-60-191-637-37777
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US-60-191-637-37777
US-60-191-637-37777
US-60-191-637-37777
US-60-191-637-37777
US-60-191-637-37777
US-60-191-64-312-681397
US-09-32B-352-9700
                                                                                                                                                                                                                                                                                                                                                                                             US-09-328-352-6123
US-60-312-544-8243
US-60-312-544-8901
US-09-270-767-43442
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                                                                                                                                                                       US-09-763-397A-17
  40.5
40.5
40.5
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LENGTH: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
   Sequence 17, Appl
Sequence 2, Appli
Sequence 8, Appli
Sequence 8, Appli
Sequence 9, Appli
Sequence 1218, Ap
Sequence 1218, Ap
                                                                                 Search time 1760.55 Seconds (without alignments)
2.839 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Description
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| cgn2_6/ptodata/2/paa/PCTUS_COMB.pep:*
2: /cgn2_6/ptodata/2/paa/USOG_COMB.pep:*
3: /cgn2_6/ptodata/2/paa/USOG_COMB.pep:*
4: /cgn2_6/ptodata/2/paa/USOB_COMB.pep:*
5: /cgn2_6/ptodata/2/paa/USOB_COMB.pep:*
7: /cgn2_6/ptodata/2/paa/USOB_COMB.pep:*
8: /cgn2_6/ptodata/2/paa/USOB_COMB.pep:*
9: /cgn2_6/ptodata/2/paa/USOB_COMB.pep:*
10: /cgn2_6/ptodata/2/paa/USOB_COMB.pep:*
11: /cgn2_6/ptodata/2/paa/USOB_COMB.pep:*
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13: /cgn2_6/ptodata/2/paa/USOB_COMB.pep:*
14: /cgn2_6/ptodata/2/paa/USOB_COMB.pep:*
15: /cgn2_6/ptodata/2/paa/USOB_COMB.pep:*
16: /cgn2_6/ptodata/2/paa/USOB_COMB.pep:*
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19: /cgn2_6/ptodata/2/paa/USOB_COMB.pep:*
10: /cgn2_6/ptodata/2/paa/USOB_COMB.pep:*
11: /cgn2_6/ptodata/2/paa/USOB_COMB.pep:*
12: /cgn2_6/ptodata/2/paa/USOB_COMB.pep:*
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17: /cgn2_6/ptodata/2/paa/USOB_COMB.pep:*
18: /cgn2_6/ptodata/2/paa/USOB_COMB.pep:*
19: /cgn2_6/ptodata/2/paa/USOB_COMB.pep:*
21: /cgn2_6/ptodata/2/paa/USOB_COMB.pep:*
22: /cgn2_6/ptodata/2/paa/USOB_COMB.pep:*
             4.5
Compugen Ltd
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1 US-09-763-397A-2
PCT-US92-02207-8
US-07-672-183A-8
US-08-072-867-8
US-08-075-783-9
US-08-075-783-9
US-09-171-507-36491
US-09-417-507-36491
                                                                                                                                                                                                                                            Potal number of hits satisfying chosen parameters:
                                                                                                                                                                                                                      3148936 seqs, 277657034 residues
                                                                                      ٠.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUMMARIES
            GenCore version
Copyright (c) 1993 - 2000
                                                                                   January 29, 2002, 10:56:09
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Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

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Gapop 10.0 , Gapext 0.5
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Match 1
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91.2
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46.1
43.1
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Maximum DB :
                                                             OM protein
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APPLICANT: The Government of the United States of America, as represented by the APPLICANT: The Government of the Department of Health and Human Services, Centers for APPLICANT: Control and Prevention
APPLICANT: Lal, Altaf A.
APPLICANT: Lal, Altaf A.
APPLICANT: Ping Shi, Ya
APPLICANT: Hasnain, Seyed E.
TITLE OF INVENTION: Recombinant Multivalent Malarial Vaccine Against Plasmodium Fa
FILE REPERENCE: 6395-57049
CURRENT FILING DATE: 2001-02-16
PRIOR APPLICATION NUMBER: US 60/097,703
PRIOR APPLICATION NUMBER: US 60/097,703
PRIOR APPLICATION NUMBER: PCT / US99/18869
PRIOR FILING DATE: 1998-08-19
PRIOR FILING DATE: 1999-08-19
PRIOR FILING DATE: 1999-08-19
PRIOR FILING DATE: 1999-08-19
PRIOR FILING PATE: 1099-08-19
PRIOR FILING DATE: 1099-08-19
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Pred. No. 2.6e-09;
Mismatches 0;
ALIGNMENTS
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Sequence 8, Application US/07672183A
Sequence 8, Application US/07672183A
Sequence 8, Application Sequence 8, Applicant Posterial Sequence 9, Applicant Palex, Dana Applicant de Taisne, Charles
Applicant Tine, John A.
Applicant OF INVENTION: MALARIA RECOMBINANT POXVIRUS VACCINE NUMBER OF SEQUENCES: 19
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 93; DB 3; Length 622
Pred. No. 5.7e-06;
0; Mismatches 1; Indels
                                                                                                                                                                                               DB 1; Length 622;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: 0S/07/672,183A FILING DATE: 19910320 CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: William S. Frommer ADDRESSEE: c/o Curtis, Morris & Safford, P.C. STREET: 530 Fifth Avenue
                                                                                                                                                                                             Score 93; DB 1; 1
Pred. No. 5.7e-06;
0; Mismatches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AUTORNEY/AGENT INFORMATION:
NAME: Frommer, William S.
REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 454310-2300
REFERENCE/DOCKET NUMBER: 454310-2300
TELECHONE: (212) 840-3333
TELERAX: (212) 840-0712
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 8, Application US/08072867 GENERAL INFORMATION:
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AMINO ACID
                                                                                                                                                                                                                                                                                                                571 GNAEKYDKMDEPQDYGKS 588
                                           LENGTH: 622 amino acids
TYPE: amino acid
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
PCT-US92-02207-8
                                                                                                                                                                                                                                                                                       1 GNAEKYDKMDEPQHYGKS 18
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Best Local Similarity 94.4
Matches 17; Conservative
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 17; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New York
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US-07-672-183A-8
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US-08-072-867-8
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                                                                                                                                                                        APPLICANT: The Government of the United States of America, as represented by the APPLICANT: The Government of the United States of America, as represented by the APPLICANT: Secretary of the Department of Health and Human Services, Centers for Dis APPLICANT: Control and Prevention
APPLICANT: Lal, Altaf A.
APPLICANT: Ping Shi, Seyed E.
TITLE OF INVENTION: Recombinant Multivalent Malarial Vaccine Against Plasmodium Falci FILE REFERENCE: 6395-57049
CURRENT APPLICATION NUMBER: US/09/763,397A
CURRENT APPLICATION NUMBER: US 60/097,703
PRIOR APPLICATION NUMBER: PCT / US99/18869
PRIOR APPLICATION NUMBER: PCT / US99/18869
PRIOR RILING DATE: 1999-08-19
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patentin Version 3.1
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GENERAL INFORMATION:
APPLICANT: VIROGENETICS, CORPORATION
TITLE OF INVENTION: MALARIA RECOMBINANT POXVIRUS VACCINE
NUMBER OF SEQUENCES: 74
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.25
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100.0%; Pred. No. 9.9e-08;
+ive 0: Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: Recombinant DNA/Protein US-09-763-397A-2
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REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 454310-2411
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 840-3333
TELEFAX: (212) 840-0712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                UMBER: PCT/US92/02207
19-MAR-1992
                                                                                                                                                   Sequence 2, Application US/09763397A GENERAL INFORMATION:
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COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-
SOFTWARE: PATENTIN Release #
CURRENT APPLICATION DATA:
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                       1 GNAEKYDKMDEPQHYGKS 18
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Best Local Similarity 100.
Matches 18; Conservative
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FILING DATE: 19-MAF
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STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
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PCT-US92-02207-8
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LENGTH: 350
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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICAMT: REITH G. WEINSTOCK ET AL.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ASPERGILLUS:
TITLE OF INVENTION: FUMIGATUS FOR DIAGNOSTICS AND THERAPEUTICS
FILLE REFERENCE: PAPH199-10
CURRENT APPLICATION NUMBER: US/09/417,507
CURRENT APPLICATION NUMBER: US/09/417,507
NUMBER OF SEQ ID NOS: 44312
SEQ ID NO 36491
LENGTH: 393
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Sequence 1218, Application US/60171489
Sequence 1218, Application US/60171489
GENERAL INFORMATION:
TERMINEL INFORMATION:
TITLE OF INVENTION: USCLATED HUMAN DRUG TARGET PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN DRUG TARGET PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN DRUG TARGET PROTEINS,
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: CL000165
CURRENT APPLICATION NUMBER: US/60/171,489
CURRENT FILING DATE: 1999-12-22
NUMBER OF SEQ ID NOS: 1412
SEQ ID NO 1218
SEQ ID NO 1218
LENGTH: 104
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Pred. No. 5.7e-06;
0; Mismatches 1; Indels
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2; Mismatches
                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Frommer, William S.
REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 454310-2500
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 840-3333
TELEPAX: (212) 840-3733
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 622 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-075-783-9
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61.58;
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Best Local Similarity 94.4
Matches 17; Conservative
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Best Local Similarity 61.5
Matches 8; Conservative
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LOCATION: (44),(53)
                                                                                                                                            CLASSIFICATION:
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US-60-171-489-1218
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US-09-417-507-36491
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TITLE OF INVENTION: MALARIA RECOMBINANT POXVIRUS VACCINE
NUMBER OF SEQUENCES: 74
CORRESPONDENCE ADDRESS:
ADDRESSEE: Curtis, Morris, and Safford
ADRESSEE: C/O William S. Frommer
STREET: S30 Fifth Avenue
CITY: New York
STATE: New York
ZIP:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Paoletti, Enzo
APPLICANT: Tine, John A.
TITLE OF INVENTION: MALARIA RECOMBINANT POXVIRUS VACCINE
TITLE OF INVENTION: MALARIA RECOMBINANT POXVIRUS VACCINE
NUMBER OF SEQUENCES: 124
CORRESPONDENCE ADDRESS:
ADDRESSEE: Curtis, Morris & Safford
ADDRESSEE: C/O William S. Frommer
STREET: S30 Fifth Avenue
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 622;
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/075,783
FILING DATE: 11-JUN-1993
                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/072,867
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Pred. No. 5.7e-06;
0; Mismatches 1;
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION DATA:
FILLING DATE: 18-MAR-1992
ATTORNEY AGENT INFORMATION:
NAME: Frommer, William S.
REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 454310-2410
TELEPHONE: (212) 840-3333
TELEPHONE: (212) 840-3333
TELEPHONE: (212) 840-3333
TELEPHONE: (212) 840-3712
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 622 amino acids
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; STRANDENESS: single
; TOPOLOGY: linear
US-08-072-867-8
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Best Local Similarity 94.4
Matches 17; Conservative
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Sequence 24400, Application US/09252991A GENERAL INFORMATION:
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|515 YDRFERPQHY 524
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Matches 7; Conser
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 US-09-252-991A-24400
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US-09-270-767-44609
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US-60-316-362-3482
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; OTHER INFORMATION: Identity of amino acid sequences at the above locations are unknd
US-09-417-507-36491
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Sequence 60056, Application US/09270767

GENERAL INFORMATION:

APPLICANT: Homburger et al.

TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster.

FILE REFERENCE: File Reference: 7326-094

CURRENT APPLICATION NUMBER: US/09/270,767

NUMBER OF SEQ ID NOS: 62517

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 60056

LENGTH: 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHTER INFORMATION: Description of Artificial Sequence: Synthetic CTHER INFORMATION: at any location having Xaa, Xaa means any amino acid US-09-270-849B-189090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                            Length 393;
                                                                                                                  2; Indels
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US-09-270-849B-189090
; Sequence 189090, Application US/09270849B
; GeneRal INFORMATION:
    TILL OF INVENTION:
    TILLE OF INVENTION:
    TILLE REFERENCE:
    CURRENT AFPLICATION NUMBER: US/09/270,849B
    CURRENT FILING DATE: 1999-03-17
    NUMBER OF SEQ ID NOS: 195450
    SOFTWARE: Patentin Ver. 2.0
    SEQ ID NO 189090
    LENGTH: 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 44; DB 16; Le
Pred, No. 3.5e+02;
                                                                            43.1%; Score 44; DB 18;
ilarity 53.8%; Pred. No. 2.7e+02;
Conservative 4; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-60056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Artificial Sequence
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Best Local Similarity
Matches 6; Conserv
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                                                                                                     Best Local Similarity
Matches 7; Conserv
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                                                                                    Query Match
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RESULT

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Sequence 3482, Application US/60316362
Sequence 3482, Application US/60316362
GENERAL INFORMATION:
APPLICANT: Tishkoff, Daniel
APPLICANT: Zamudio, Carlos
APPLICANT: Eroshkin, Alexey M.
TITLE OF INVENTION: Identification of Essential Genes of Aspergillus fumigatus and
TITLE OF INVENTION: USe
FILE REFERENCE: 10182-012-888
CURRENT APPLICATION NUMBER: US/60/316,362
CURRENT FILING DATE: 2001-08-31
NUMBER OF SEQ ID NOS: 4037
APPLICANT: Marc J: Rubenfield et al.

APPLICANT: Marc J: Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 24400
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Sequence 44609, Application US/09270767

GENERAL INFORMATION

APPLICANT: Homburger et al.

TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILE REFERENCE: FILE REFERENCE: FILE REFERENCE: THE REF
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Pred. No. 5e+02;
2; Mismatches 2; Indels
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Pred. No. 4.9e+02;
1; Mismatches 2;
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Best Local Similarity 60.0
Matches 6; Conservative
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CURRENT APPLICATION NUMBER: US/60/215,161
CURRENT FILING DATE: 2000-06-30
NUMBER OF SEQ ID NOS: 84.09
SEQ ID NO 6098
LENGTH: 133
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                                                                                                                                                       Score 44; DB 24; Length 740; Pred. No. 6e+02;
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Pred. No. 1.1e+02;
4; Mismatches 5; Indels
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                                                                                                                                                                                              2; Indels
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GENERAL INFORMATION:
APPLICANT: Douglas, James O.
TITLE OF INVENTION: Hypothalamic-Secreted Polypeptide
FILE REFERENCE: 01017/36937
CURRENT APPLICATION NUMBER: US/09/723,229
CURRENT FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-04-06
NUMBER OF SEQ ID NOS: 6
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                       Ouery Match 43.1%; Score 44; DB Best Local Similarity 53.8%; Pred. No. 6e+0 Matches 7; Conservative 4; Mismatches
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Huesing, Joseph E.
Krasomil-Osterfeld, Karina C.
                                                                                                                                                                                                                                                                                                                                                                        Sequence 6098, Application US/60215161 GENERAL INFORMATION:
APPLICANT:
Corbin, David R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Huesing, Joseph E. APPLICANT: Krasomil-Osterfeld, I APPLICANT: Malvar, Thomas M. APPLICANT: Slater, Steven C. APPLICANT: Spiridonov, Sergei APPLICANT: Hinkle, Gregory J. TITLE OF INVENTION:
                                                                           ; ORGANISM: Aspergillus fumigatus US-60-316-362-3482
SOFTWARE: Patentin version 3.1
SEQ ID NO 3482
LENGTH: 740
TYPE: PRT
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Best Local Similarity 43.8%;
Matches 7; Conservative
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| 548 GNAEKYAQVENPE 560
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; ORGANISM: Homo sapiens
US-09-723-229-2
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LENGTH: 196
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Search completed: January 29, 2002, 10:56:10 Job time: 2406 sec

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Result
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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         900
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seq length:
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1: /cgn2_6/ptodata/2/paa/PCT_NEW_COMB.pep:*

2: /cgn2_6/ptodata/2/paa/US06_NEW_COMB.pep:*

3: /cgn2_6/ptodata/2/paa/US07_NEW_COMB.pep:*

4: /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep:*

5: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep:*

6: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep:*

7: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep:*
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Gapop 10.0 , Gapext 0.5
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102
1 GNAEKYDKMDEPQHY
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US-09-648-004-8
US-09-897-516-6098
US-09-708-427-55948
US-09-708-427-55948
US-09-708-427-55946
US-09-832-292-31
US-09-815-242-12798
US-09-708-427-75548
US-09-708-427-75448
US-09-708-427-73363
US-09-708-427-73362
US-09-708-427-65583
US-09-708-427-65583
US-09-708-427-17879
US-09-708-427-17879
US-09-708-427-1258
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200, Appl

12798, Appl

12798, Appl

12798, Appl

12798, Appl

10504, A

11863, A

11863, A

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11863, A

11878, Appl

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115046, Appl

15046, A
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             RESULT 2
US-09-897-516-6098
US-09-897-516-6098
Sequence 6098, Application US/09897516
GEMERAL INFORMATION:
APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Krasomil-osterfeld, Karina C.
APPLICANT: Malvar, Thomas M.
APPLICANT: Slater, Steven C.
APPLICANT: Spiridonov, Sergei
TITLE OF INVENTION: Xenorhabdus sp. Genome Sequences And Uses Thereof
FILE REFERENCE: 38-21(51847)B
CURRENT APPLICATION NUMBER: US/09/897,516
CURRENT FILING DATE: 2001-06-29
CURRENT FILING DATE: US/09/897,516
    PRIOR APPLICATION NUMBER: US
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Query Match Best Local Matches 5 KY- 11 206 KYN	RESULT 1 US-09-648-004- Sequence 8, GENERAL INFO APPLICANT: APPLICANT: APPLICANT: TITLE OF IN TITLE OF IN TITLE OF IN FILE REFERE CURRENT APPL CURRENT FIL PRIOR APPLI PRIOR APPLI PRIOR FILN UMBER OF S SOFTWARE: M SEO ID NO SEO		22226666666666666666666666666666666666
atch cal Si 9; KYD	SULT 1 :09-648-004-8 :-09-648-004-8 Sequence 8, Application GENERAL INFORMATION: APPLICANT: CHEN, QION APPLICANT: HOMAS,: APPLICANT: NAGARAJAN TITLE OF INVENTION: FILE REFERENCE: CL-1: CURRENT APPLICATION NUI FILEN APPLICATION NUI FILE REFERENCE: DATE: PRIOR APPLICATION NUI PRIOR FILING DATE: PRIOR SEQ ID NOS SOFTWARE: MICTOSOFT IN 08 SEQ ID NO SOFTWARE: MICTOSOFT ORGANISM: Acinetobae ORGANISM: Acinetobae ORGANISM: Acinetobae		38 37 37 37 37 37 37 37 37 37
tch al Similarity 9; Conserv KYDKMDEPQHYG	-8 Application CHEM, QIONG CHEM, QIONG CHEM, QIONG CHEM, QIONG CHEM, QIONG CHEM, QIONG THOMAS, ST MAGARAJAN, NVENTION: BI NVENTION: BI NVENTION: BI INVENTION: BI ENCE: CL-134		
larity 64. Conservative DEPQHYG 16 :      sDPQHYG 219	O9-648-004-8 09-648-004-8 109-648-004-8 ENERAL INFORMATION: APPLICANT: CHEN, QIONG APPLICANT: THOMAS, STUART TITLE OF INVENTION: INTERMED TITLE OF INVENTION: INTERMED FILE REFERENCE: CL-1341-A CURRENT APPLICATION UNMBER: 09/ PRIOR APPLICATION UNMBER: 09/ PRIOR FILING DATE: 2000-04 PRIOR FILING DATE: 2000-02 PRIOR FILING DATE: 2000-02 PRIOR FILING DATE: 2000-03 PRIOR FILING DATE: 2000-04 PRIOR FILING DATE: 1999-02-19 NUMBER OF SEQ ID NOS: 32 SOFTMARE: MICROSOFT OFFICE 97 EQ ID NO 8 LENGTH: 572 TYPE: PRT ORGANISM: Acinetobacter sp. 09-648-004-8		1304 1313 124 232 232 237 361 361 361 344 412 412 412 410 390 390 390 390 390 390 390 390 390 39
13.1%; 64.3%; Lve	7 7 7 SAN		~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
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44; No. smatc	DD FOR 18,004	ALIGNMENTS	99900000000000000000000000000000000000
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ORGANISM: Xenorhabdus sp. US-09-897-516-6098
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NUMBER OF SEQ ID NOS
SEQ ID NO 6098
LENGTH: 133
TYPE: PRT
                                                                                                                                                                                                                                                US-09-708-427-55947
; Sequence 55947, Application US/09708427
; GENERAL INFORMATION:
; APPLICANT: N. ALEXANDROV et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: THEREBY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc_feature; LOCATION: 1..269
COTHER INFORMATION: Ceres Seq. ID 1936382
US-09-708-427-55948
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: N. ALEXANDROV et al.
APPLICANT: N. ALEXANDROV et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: THEREBY
FILE REFERENCE: 2750-1143P
CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT APPLICATION APPLICATION OF SEQUENCE OF SEQUENCE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 55948
LENGTH: 269
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Best Local Similarity
Matches 7; Conserv
                                                                                                           FILE REFERENCE: 2750-1243P
CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: PATCHIIN VERSION 3.1
SEQ ID NO 55947
LENGTH: 281
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Best Local
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LOCATION: 1..269
OTHER INFORMATION: Xaa is any amino acid
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                    NAME/KEY: misc_feature LOCATION: 1..281
                                                      FEATURE:
                                                                          ORGANISM: Zea mays subsp. mays
OTHER INFORMATION: Xaa is any amino acid
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os: 8409
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Pred. No. 5
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Pred. No. 17;
2; Mismatches
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5.2;
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CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: Patentin version 3.1
SEQ ID NO 55946
LENGTH: 384
TYPE: PRT
ORGANISM: Zea mays subsp. mays
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; LCCATION: 1..281
; OTHER INFORMATION: Ceres Seq.
US-09-708-427-55947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc_feature
LOCATION: 1..384
NAME/KEY: misc_feature
LOCATION: 1..384
OTHER INFORMATION: Ceres Seq. ID 1936380
US-09-708-427-55946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-708-427-55946; Sequence 55946, Application US/09708427; GENERAL INFORMATION:
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Best Local Similarity
Whiches 7; Conserve
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                                            CURRENT APPLICATION NUMBER: US/09/897,516
CURRENT FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US 60/215, 161
PRIOR FILING DATE: 2000-06-30
NUMBER OF SEQ ID NOS: 8409
SEQ ID NO 6859
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Best Local Similarity 41.
Matches 7; Conservative
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TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID TITLE OF INVENTION: THEREBY
FILE REFERENCE: 2750-1243P
                                                                                                                                                                                                                                  APPLICANT:
APPLICANT:
                                                                                                                                               APPLICANT: Malvar, Thomas M.
APPLICANT: Slater, Steven C.
APPLICANT: Spiridonov, Sergei
TITLE OF INVENTION: Xenorhabdus sp. Genome
FILE REFERENCE: 38-21(51847)B
                                                                                                                                                                                                                                                                                  APPLICANT: Corbin, David R. APPLICANT: Goldman, Barry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
ORGANISM: Xenorhabdus sp
                              LENGTH: 519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              160 GEGDKYDROAEKDHLSK 176
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Hinkle, Gregory J.
Huesing, Joseph E.
Krasomil-Osterfeld,
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41.2%;
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Pred. No. 18;
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Pred. No.
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26;
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APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: 05/09/815,242
CURRENT APPLICATION NUMBER: 05/191,078
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR PRICING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-11-29
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
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; ORGANISM: Homo sapiens
US-09-832-292-31
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: 09/632,131
PRIOR FILING DATE: 2001-08-03
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FILING DATE
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Yamamoto, Robert T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Zyskind, Judith W.
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                     60/269,308
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; Sequence 75548, Application US/0
; GENERAL INFORMATION:
; APPLICANT: N. ALEXANDROV et al.
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                                                                                                                                                                                                                                                                                                                                     US-09-708-427-74488
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                                                                                                                          FILE REFERENCE: 2750-1243P
CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEO ID NOS: 85364
SOFTWARE: PatentIn version 3.1
SEO ID NO 74488
                                                                                                                                                                                                                                                                             Sequence 74488, Application US/09708427 GENERAL INFORMATION:
APPLICANT: N. ALEXANDROV et al.
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SOFTWARE: FRASTSEQ for Windows Version 4.0
SEO ID NO 12798
LENGTH: 697
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Best Local Similarity
Matches 7; Conserv
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Best Local 9
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                                                      TYPE: PRT ORGANISM: Zea mays subsp. mays FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: mlsc_feature
LOCATION: 1..53
OTHER INFORMATION: Ceres Seq. ID 1946917
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ORGANISM: Zea mays subsp. mays
FEATURE:
                   NAME/KEY: misc_feature LOCATION: 1..139
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OTHER INFORMATION: Xaa is any amino acid
                                                                                                              LENGTH: 139
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les 7; Conserv
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Pred. No.
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Pred. No.
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; NAME/KEY: misc_feature
; LOCATION: 1..139
; OTHER INFORMATION: Ceres Seq. ID 1945476
US-09-708-427-74488
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US-09-708-427-84690
Sequence 84690, Application US/09708427
Sequence 11 ALEXANDROV et al.
APPLICANT: N. ALEXANDROV et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: THEREBY
TITLE OF INVENTION: THEREBY
FILE REFERENCE: 2750-1243P
FILE REFERENCE: 2750-1243P
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US-09-708-427-73364
; Sequence 73364, Appl
; GENERAL INFORMATION:
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CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: Patentin version 3.1
SEQ ID NO 84690
LENGTH: 139
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Best Local Similarity
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TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: THEREBY
FILE REFERENCE: 2750-1243P
CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: Patentin version 3.1
SEQ ID NO 73364
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Best Local :
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LOCATION: 1..139
OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc_feature
LOCATION: 1..139
OTHER INFORMATION: Ceres Seq. ID 1964740
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                                                  NAME/KEY: misc_feature
LOCATION: 1..158
OTHER INFORMATION: Xaa is
                                                                                                                           ORGANISM: Zea mays subsp.
                                                                                                                                                TYPE: PRT
                   NAME/KEY: misc_feature LOCATION: 1..158
                                                                                                           FEATURE:
                                                                                                                                                               LENGTH: 158
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nes 7; Conservative
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INFORMATION: Ceres Seq. ID 1943726
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53.8%;
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Pred. No.
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Pred. No.
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CORRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: Patentin version 3.1
SEQ ID NO 73363
LENGTH: 212
TYPE: PRT
ORGANISM: Zee mays subsp. mays
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Best Local Similarity
""" hes 7; Conserv
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LOCATION: 1..212
OTHER INFORMATION: Ceres Seq.
US-09-708-427-73363
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US-09-708-427-73362
SEQUENCE 73362, Application US/09708427
SEQUENCE TI INFORMATION:
GENERAL INFORMATION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID TITLE OF INVENTION: THEREBY
TITLE OF INVENTION: THEREBY
FILE REFERENCE: 2750-1243P
CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT ETLING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
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GENERAL INFORMATION:
APPLICANT: N. ALEXANDROV et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID
TITLE OF INVENTION: THEREBY
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Best Local S
Matches 7
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NAME/KEY: misc_feature
LOCATION: 1..212
OTHER INFORMATION: Xaa
                                                                                                   TYPE: PRT ORGANISM: Zea mays subsp. mays FEATURE:
                                                   NAME/KEY: misc_feature
LOCATION: 1..246
OTHER INFORMATION: Xaa
                   NAME/KEY: misc_feature LOCATION: 1..246
OTHER INFORMATION: Ceres Seq. ID 1943724
                                                                                                                                                    LENGTH: 246
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53.8%;
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Pred. No.
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RESULT 15
US:09-708-427-66583
Sequence 66583, Application US/09708427
GENERAL INFORMATION:
APPLICANT: N. ALEXANDROV et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: THERRBY
FILE REFERENCE: 2750-1243P
CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 66583
LENGTH: 316
                                                                                                                                                                                                                                                                               TYPE: PRT
ORCANISM: Zea mays subsp. mays
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1..316
OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc_feature
LOCATION: 1..316
COCATION: 1..316
OTHER INFORMATION: Ceres Seq. ID 1930901
US-09-708-427-66583
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Search completed: January 29, 2002, 10:58:16 Job time: 2512 sec
                                                                                                                                                                                 Query Match
Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 38.2%; Score 39; DB 5; Length 246; Best Local Similarity 53.8%; Pred. No. 49; Matches 7; Conservative 2; Mismatches 4; Indels
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120 HAESYDWVDIPDH 132
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                                                                                                                                                                                 38.2%; Score 39; DB 5; Length 316; 66.7%; Pred. No. 65; tive 1; Mismatches 2; Indels
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Sequence 2, Appli
Sequence 8, Appli
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Sequence 9, Appli
Sequence 9, Appli
Sequence 783, Appli
Sequence 7648, Appli
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2.839 Million cell updates/sec
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                                                                                                                              Search time 1760.55 Seconds
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version 4.5
- 2000 Compugen Ltd.
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1 US-09-763-397A-2

PCT-US92-02207-8

US-07-672-183A-8

US-08-072-867-8

US-08-075-783-9

US-09-248-796-18857

US-09-248-796-18857

US-09-314-050-7648
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                                                                                                                                                                                                                                                                                                                                                              3148936 seqs, 277657034 residues
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                                                                                                                          January 29, 2002, 10:56:08
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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      GenCore
Copyright (c) 1993
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Perfect score:
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## ALIGNMENTS

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US-09-763-397A-16

Sequence 16, Application US/09763397A

SERERAL INFORMATION:

APPLICANT: The Government of the United States of America, as represented by the APPLICANT: The Government of the United States of America, as represented by the APPLICANT: Secretary of the Department of Health and Human Services, Centers for APPLICANT: Control and Prevention

APPLICANT: Lal, Altaf A.

APPLICANT: Divided Shi, Ya.

APPLICANT: Paing Shi, Ya.

APPLICANT: ASSENCE: 8395-57049

CURRENT FILE OF INVENTION: Recombinant Multivalent Malarial Vaccine Against Plasmodium Fair TILE OF INVENTION: NUMBER: US/09/763,397A

CURRENT FILING DATE: 2001-02-16

PRIOR APPLICATION NUMBER: US 60/097,703

PRIOR APPLICATION NUMBER: PCT / US99/18869

PRIOR APPLICATION NUMBER: US98-08-10

PRIOR APPLICATION NUMBER: US99/18869

PRIOR APPLI
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                                                                                                                                                                                                                                                                                                                                                                           US-07-672-183A-8
Sequence 8, Application US/07672183A
Sequence 8, Application US/07672183A
GENERAL INFORMATION:
APPLICANT: Paoletti, Enzo
APPLICANT: de Taisne, Charles
APPLICANT: Tine, John A.
TITLE OF INVENTION: MALARIA RECOMBINANT POXVIRUS VACCINE
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: New York
COUNTRY: United States
ZIP: 10036
COMPUTER READABLE FORM:
MEDTUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/672,183A
FILING DATE: 19910320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: William S. Frommer ADDRESSEE: c/o Curtis, Morris & Safford, P.C. STREET: 530 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4.3e-07;
                                                                                                                                                                          Score 95; DB 1; Pred. No. 4.3e-07;
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 840-3333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 95;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-072-867-8; Sequence 8, Application US/08072867; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Frommer, William S.
REGISTRATION NUMBER: 25,506
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94.48;
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94.4%;
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INFORMATION FOR SEQ ID NO: 8
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                   317 DGNCEDIPHVNEFPAIDL 334
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                                       622 amino acids
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INFORMATION FOR SEQ ID NO:
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                     SEQUENCE CHARACTERISTICS
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Matches 17; Conserv
                                                          amino acid
                                                                                                    linear
                                                                                                                                                                            Query Match
Best Local Similarity
Matches 17; Conserv
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TOPOLOGY: lin
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US-07-672-183A-8
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PCT-US92-02207-8
                                     LENGTH:
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                                                                                                                                                         APPLICANT: The Government of the United States of America, as represented by the APPLICANT: The Government of the Department of Health and Human Services, Centers for Dis APPLICANT: Control and Prevention APPLICANT: Call, Altaf A. APPLICANT: Lail, Altaf A. APPLICANT: Ping Shi, Ya APPLICANT: Hashain, Seyed E. TITLE OF INVENTION: Recombinant Multivalent Malarial Vaccine Against Plasmodium Falci FILE OF TREERENCE: 6395-57049 CURRENT APPLICATION NUMBER: US/09/763,397A
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GENERAL INFORMATION:
APPLICANT: VIROGENETICS, CORPORATION
TITLE OF INVENTION: MALARIA RECOMBINANT POXVIRUS VACCINE
NUMBER OF SEQUENCES: 74
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPENATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 21;
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100.0%; Pred. No. 3e-08;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: Recombinant DNA/Protein US-09-763-397A-2
                                                                                                                                                                                                                                                                                                                                              CURRENT FILING DATE: 2001-02-16
PRIOR APPLICATION NUMBER: US 60/097,703
PRIOR FILING DATE: 1998-08-21
PRIOR APPLICATION NUMBER: PCT / US99/1869
PRIOR FILING DATE: 1999-08-19
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Frommer, William S.
REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 454310-2411
TELECOMUNICATION INFORMATION:
TELEPHONE: (212) 840-3333
TELEFAX: (212) 840-0712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            омыЕR: PCT/US92/02207
19-MAR-1992
1.
                                                                                                                         Sequence 2, Application US/09763397A GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Artificial Sequence
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          1 DGNCEDIPHVNEFSAIDL 18
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Best Local Similarity 100
Matches 18; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 10036
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PCT-US92-02207-8
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                                                                                                             US-09-763-397A-2
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US-09-248-796-18857
Sequence 18857. Application US/09248796
Sequence 18857. Application US/09248796
Sequence 18857. Application US/09248796
TOTAL INCRAMATION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBI
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERRENCE: 107196-132
CURRENT APPLICATION NUMBER: US/09/248,796
CURRENT FILING DATE: 1999-02-12
NUMBER OF SEQ ID NOS: 28206
SEQ ID NO 18857
LENGTH: 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COCATION: (221),(244); OTHER INFORMATION: Identity of amino acid sequences at the above locations are un US-09-248-796-18857
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GENERAL INFORMATION:
APPLICANT: Roemer, Terry
APPLICANT: Boone, Charles
APPLICANT: Boone, Charles
APPLICANT: Done, Charles
APPLICANT: Done, Charles
APPLICANT: Done, Charles
APPLICANT: Bussey, Howard
APPLICANT: Ohisen, Kari L.
TITLE OF INVENTION: GENE DISRUPTION METHODOLOGIES FOR DRUG TARGET DISCOVERY
FILE REFERENCE: 10182-013-888
CURRENT APPLICATION NUMBER: US/60/314,050
CURRENT FILING DATE: 2001-08-22
NUMBER OF SEQ ID NOS: 7834
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Pred. No. 4.3e-07;
0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 51.5%; Score 51.5; DB 16; Best Local Similarity 52.4%; Pred. No. 5.5; Matches 11; Conservative 2; Mismatches 3;
                                    NAME: Frommer, William S.
REGISTRATION NUMBER: 25,506
REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 454310-2500
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 840-3333
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 622 amino acids
TYPE: amino acids
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                89 DFNCQDIPEFFEDHMNELMAI 109
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                                                                                                                                                                                                                                                                                                                                                                                                  95.0%;
                          ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          317 DGNCEDIPHVNEFPAIDL 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 DGNCEDIPHVNEFSAIDL 18
                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 94.4
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Candida albicans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: UNSURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-60-314-050-7648
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GENERAL INFORMATION:
APPLICANT: Paoletti, Enzo
APPLICANT: De Taisne, Charles
APPLICANT: Tine, John A.
TITLE OF INVENTION: MALARIA RECOMBINANT POXVIRUS VACCINE
NUMBER OF SEQUENCES: 124
CORRESPONDENCE ADDRESS:
APPLICANT: Paoletti, et al TITLE OF INVENTION MALARIA RECOMBINANT POXVIRUS VACCINE NUMBER OF SEQUENCES: 74 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 622;
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MEDIUM TYPE: Floppy disk
COMPUTER: ELDA PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
AURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/075,783
FILING DATE: 11-JUN-1993
                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
AURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/072,867
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 95; DB 4; 1
Pred. No. 4.3e-07;
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                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/852,305
FILING DATE: 18-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Frommer, William S.
REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 25,506
TELECOMMUNICATION INFORMATION:
                                                                                        ADDRESSEE: Curtis, Morris, and Safford ADDRESSEE: c/o William S. Frommer STREET: 330 Fifth Avenue CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Curtis, Morris & Safford
ADDRESSEE: c/o William S. Frommer
STREET: 530 Fifth Avenue
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: United States of America ZIP: 10036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (212) 840-3333
TELEFAX: (212) 840-0712
INFORMATION FOR SEQ ID NO: 8: SEQUENCE CHARACTERISTICS:
LENGTH: 622 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             95.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                317 DGNCEDIPHVNEFPAIDL 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 DGNCEDIPHVNEFSAIDL 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDENESS: single ; TOPOLOGY: linear US-08-072-867-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 94.4 Matches 17; Conservative
                                                                                                                                                                                                                                 ZIP: 10036
COMPUTER READABLE FORM:
                                                                                                                                                                                          New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New York
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US-08-075-783-9
                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                               CITY: N
STATE:
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STATE:
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Gaps
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APPLICANT: Gao, Yongwei
APPLICANT: Bdgerton, Michael D
APPLICANT: Hinkle, Gredory J.
APPLICANT: Kovalic, David K.
APPLICANT: Lu, Jingdong
APPLICANT: Stein, Joshua
TITLE OF INVENTION: CDNA SEQUENCES AND USES FOR PLANT IMPROVEMENT
FILE REFREENCE: 38-10(52726)8
CURRENT APPLICANT: 2001-09-21
NUMBER OF SEQ ID NOS: 33196
SEQ ID NO 25459
LENGTH: 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Gao, Yongwei
APPLICANT: Bdgerton, Michael D
APPLICANT: Edgerton, Michael D
APPLICANT: Hinkle, Gregory J.
APPLICANT: Howalic, David K.
APPLICANT: Liu, Jingdong
APPLICANT: Liu, Jingdong
APPLICANT: Stein, Joshua
TITLE OF INVENTION: cDNA SEQUENCES AND USES FOR PLANT IMPROVEMENT
FILE REPRENCE: 38-10(5276)B
CURRENT APPLICATION NUMBER: US/60/324,109
CURRENT FILING DATE: 2001-09-21
NUMBER OF SEQ ID NOS: 33196
SEQ ID NO 18127
LENGTH: 160
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                                                                                                                                                                                                                                                                                        Score 47.5; DE
Pred. No. 13;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2; Mismatches
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Pred. No. 13
                                                                                              NAME/KEY: misc_feature
LOCATION: 1..160
COTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc_feature
LOCATION: 1..160
COTHER INFORMATION: Ceres Seq. ID 1597432
US-09-689-980-1245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 25459, Application US/60324109; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 18127, Application US/60324109; GENERAL INFORMATION:
                                         TYPE: RRT
ORGANISM: Arabidopsis thaliana
FEATURE:
                                                                                                                                                                                                                                                                                          47.5%;
61.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     47.58;
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81 NC-DIPHVNRTEYQLIDI 97
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Best Local Similarity 61.15
Matches 11; Conservative
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Best Local Similarity 61.1
Matches 11; Conservative
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ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 11
US-60-324-109-18127
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SEQ ID NO 1245
LENGTH: 160
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TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
TITLE OF INVENTION: Thereby
FILE REFERENCE: 2750-1237P
CURRENT APPLICATION NUMBER: US/09/689,980
CURRENT FILING DATE: 2000-10-13
**QUBBER CF-SEQ ID NOS: 3877
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Sequence 753, Application US/09538092

Sequence 753, Application US/09538092

GENERAL INFORMATION

APPLICANT: Glot, Loic

APPLICANT: Mansfield, Traci A.

TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same

FILE REFERENCE: 15966-542

CURRENT APPLICATION NUMBER: US/09/538,092

CURRENT FILING DATE: 2000-03-29

PRIOR PILING DATE: 1999-04-01

PRIOR FILING DATE: 1999-04-01

PRIOR FILING DATE: 2000-02-01

NUMBER OF SEQ ID NOS: 1387

SEQ ID NO 753

LENGTH: 347
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 51; DB 19; Length 347;
Pred. No. 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COCATION: (0)...(0); OTHER INFORMATION: Polypeptide Accession Number YOR262W US-09-538-092-753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                       CCATION: (584)...(586)

COTHER INFORMATION: X=any amino acid
NAME/KEY: MISC_FEATURE

LOCATION: (617)...(617)

OTHER INFORMATION: X=any amino acid
NAME/KEY: MISC_FEATURE

LOCATION: (625)...(625)

US-60-314-050-7648
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APPLICANT: ALEXANDROV, Nickolai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                  7
                                                                                                                                                                                                                                                                                                                                                                                                                                                         220 DFNCQDIPEFFEDHMNELMAI 240
                                                                                                                                                                                                                                                                                                                                                                                                                                1 DGNCEDIP----HVNEFSAI 16
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61.5%;
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Best Local Similarity 61.5.
                                                                                                                                                                                                                                                                                                                                                                                       11; Conservative
                                                ORGANISM: Candida albicans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |:||:| || ||:
167 DLPHINVESKIDM 179
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                                                                                        NAME/KEY: MISC_FEATURE
                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
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        LENGTH: 1042
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Gaps

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RESULT 15
US-09-858-546-4
Sequence 4, Application US/09858546
Sequence 4, Application US/09858546
Sequence 4, Application US/09858546
SERBEAL INFORMATION:
APPLICANT: SHAO, Wei et al
TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
TITLE OF INVENTION: USES THEREOF
FILE REPRENCE: CLOOL232
CURRENT APPLICATION NUMBER: US/09/858,546
CURRENT APPLIATING DATE: 2001-05-17
NUMBER OF SEQ ID NOS: 5
SOCTHANDER: PASLED FOR Windows Version 4.0
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62;
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Pred. No. 62;
0; Mismatches
  61.1%; Pred. No. 16;
tive 2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          47.0%;
                                                                                    113 NC-DIPHVNRTEYQLIDI 129
                                                             3 NCEDIPHVN--EFSAIDL 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 47.0
Best Local Similarity 58.8
Matches 10; Conservative
  Best Local Similarity 61.1
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Mus musculus
US-09-858-546-4
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APPLICANT: BROVER, Vyacheslav
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
TITLE OF INVENTION: Thereby
FILE OF INVENTION: Thereby
CURRENT APPLICATION NUMBER: US/09/689,980
CURRENT APPLICATION NUMBER: US/09/689,980
CURRENT FILING DATE: 2000-10-13
NUMBER OF SEQ ID NOS: 3877
LENGTH: 192
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                                                                                                                                                                                                                                                                              RESULT 13
US-60-324-109-25168
US-60-324-109-25168
Sequence 25168. Application US/60324109
Setuence 25168. Application US/60324109
GENERAL INFORMATION:
APPLICANT: Edgetron, Michael D
APPLICANT: Hinkle, Gregory J.
APPLICANT: Kovalic, David K.
APPLICANT: Liu, Jingdong
APPLICANT: Liu, Jingdong
TITLE OF INVENTION: CDNA SEQUENCES AND USES FOR PLANT IMPROVEMENT
FILE REFERENCE: 38-10(52726)B
CURRENT APPLICATION NUMBER: US/60/324,109
CURRENT FILING DATE: 2001-09-21
NUMBER OF SEQ ID NOS: 33196
SEQ ID NO 25168
LENGTH: 182
                                                                                                     DB 24; Length 177;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 182;
                                                                                                                                           Indels
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Pred. No. 15;
2; Mismatches
                                                                                                 Score 47.5; E
Pred. No. 14;
2; Mismatches
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LOCATION: 1..192

OTHER INFORMATION: Xaa is any amino acid

NAME/KEY: misc_feature

LOCATION: 1..192

OTHER INFORMATION: Ceres Seq. ID 1597431
US-09-689-980-124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 1244, Application US/09689980; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 61.1%;
Matches 11; Conservative
                                                                                                                                                                                                    98 NC-DIPHVNRTEYOLIDI 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   103 NC-DIPHVNRTEYQLIDI 119
                                                                                                                                                                                 3 NCEDIPHVN--EFSAIDL 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 NCEDIPHVN--EFSAIDL 18
                                                                                                 Query Match 47.5
Best Local Similarity 61.1
Matches 11; Conservative
ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Zea mays
                   ; FEATURE:
US-60-324-109-25459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; FEATURE:
US-60-324-109-25168
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47.5%; Score 47.5; DB 20; Length 192;

Query Match

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Gaps

Run on:

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Sequence 49966, Application US/09708427
GENERAL INFORMATION:
APPLICANT: N. ALEXANDROV et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID
TITLE OF INVENTION: THEREBY
FILE REPERENCE: 2750-1243P
CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: Patentin version 3.1
SEQ ID NO 49966
LENGTH: 135
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GENERAL INFORMATION:
APPLICANT: N. ALEXANDROV et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID;
TITLE OF INVENTION: THEREBY
FILE REPRESENCE: 2750-1143P
CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT APPLICATION NUMBER: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SSOFIWARE: Patentin version 3.1
SEQ ID NO 49942
LENGTH: 146
Sequence 3887, Ap Sequence 19776, A Sequence 19776, A Sequence 19775, A Sequence 28967, A Sequence 28967, A Sequence 2965, Ap Sequence 2965, Ap Sequence 515, App Sequence 513, App Sequence 3111, Ap Sequence 28457, A Sequence 2855, A Seq
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                                            US-09-708-427-19777
US-09-708-427-19775
US-09-708-427-28967
US-09-708-427-28967
US-09-708-427-28967
US-09-708-427-2967
US-09-708-427-2967
US-09-708-427-2965
US-09-637-7808-515
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US-09-637-7808-514
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US-09-708-427-3112
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LOCATION: 1..135
OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc_feature
LOCATION: 1..135
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US-09-708-427-49966
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61.1%;
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81 NC-DIPHVNRTEYQLIDI 97
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Matches 11; Conservative
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  1594
1611
22002
22002
22109
2312
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1106
1112
1180
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    RESULT 2
US-09-708-427-49942
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US-09-708-427-49966
       TYPE: PRT
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    Sequence 49966, A Sequence 79313, A Sequence 79313, A Sequence 4961, App Sequence 49964, A Sequence 12548, A Sequence 576, App Sequence 576, App Sequence 576, App Sequence 32250, A Sequence 3229, A Sequence 3268, App Sequence 20568, A Sequence 11605, A Sequence 11604, A Sequence 11
                                                                                                                                                               ; Search time 120.95 Seconds (without alignments) 5.446 Million cell updates/sec
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1: /cgn2_6/ptcdata/2/paa/USO6_NEW_COMB.pep:*

2: /cgn2_6/ptcdata/2/paa/USO6_NEW_COMB.pep:*

3: /cgn2_6/ptcdata/2/paa/USO7_NEW_COMB.pep:*

4: /cgn2_6/ptcdata/2/paa/USO9_NEW_COMB.pep:*

5: /cgn2_6/ptcdata/2/paa/USO9_NEW_COMB.pep:*

5: /cgn2_6/ptcdata/2/paa/USO9_NEW_COMB.pep:*

7: /cgn2_6/ptcdata/2/paa/USO9_NEW_COMB.pep:*
                           GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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US-09-708-427-49942
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US-09-708-427-49964
US-09-708-427-49964
US-09-605-7038-2242
US-09-605-7038-2242
US-09-637-7808-576
US-09-637-7808-576
US-09-637-7808-576
US-09-637-7808-574
US-09-637-7808-574
US-09-637-7808-574
US-09-637-7808-574
US-09-708-427-32250
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US-09-708-427-3256
US-09-708-427-3256
US-09-708-427-20569
US-09-708-427-20569
US-09-708-427-20567
US-09-708-427-11605
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Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match Length
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CURRENT FILING DATE: 2001-12-04
NUMBER OF SEQ ID NOS: 745
                                                                                                                                                            Length 160;
                                                                                                                                                                                                    Indels
                                                                                                                                                              Score 47.5; DB 5;
Pred. No. 0.8;
2; Mismatches 2;
NAME/KEY: misc_feature
LOCATION: 1..160
CTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc_feature
LOCATION: 1..160
CTHER INFORMATION: Ceres Seq. ID 1921936
US-09-708-427-49467
                                                                                                                                                                                                                                                                                                                                                   US-60-337-358-461; Sequence 461, Application US/60337358; GENERAL INFORMATION:
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Madson, Linda L.
Malloy, Kathleen A.
McKiel, Christine L.
Miller, Philip W.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Ball, James A.
Banu, G.
Ball, Erin
Boddupalli, Raghava
Chomet, Paul S.
Daly, MacKenzie
Deikman, Jill
Deng, Jinzhuo
Duff, Stephen M.
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Jung, Vincent
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Lu, Bin
Luethy, Michael M.
                                                                                                                                                                  47.5%;
illarity 61.1%;
Conservative
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Laccetti, Lucille
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Sherman, Paul L.
Start, William G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Shihshieh
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Lee, Gary
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Zeng, Xiaoping
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Vidya, K.R.
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Zhao, Yajuan
Zhou, Li
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Xu, Nanfei
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                                                                                                                                                                     Query Match
Best Local Similarity
Matches 11; Conserv
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APPLICANT:
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Sequence 49467

Sequence 49467

Sequence 49467

Sequence 49467

Sequence 49467

Sequence 49467

APPLICANT: N. ALEXANDROW et al.

TITLE OF INVENTION: THEREBY

TITLE OF INVENTION: THEREBY

CURRENT APPLICATION UNMBER: US/09/708,427

SOFTWARE: Patentin version 3.1

SEQ ID NO 49467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: N. ALEXANDROV et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
FILE REFERENCE: 2750-1243P
CURRENT APPLICATION WUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SEQ ID NO 79333
LENGTH: 149
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Pred. No. 0.73;
2; Mismatches 2;
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LOCATION: 1..149
OTHER INFORMATION: Xaa is any amino acid
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US-09-708-427-79333
                                                              NAME/KET: misc_feature
LOCATION: 1..146
OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc_feature
LOCATION: 1..146
OTHER INFORMATION: Ceres Seq. ID 1923441
US-09-708-427-49942
                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 79333, Application US/09708427 GENERAL INFORMATION:
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ORGANISM: Zea mays subsp. mays
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Zea mays subsp. mays
                                  ORGANISM: Zea mays subsp. mays
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Best Local Similarity 61.1%;
Matches 11; Conservative
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Best Local Similarity 61.1%;
Matches 11; Conservative
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LOCATION: 1..149
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TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID TITLE OF INVENTION: THEREBY PRILE OF INVENTION: THEREBY CURRENT APPLICATION NUMBER: US/09/708,427 CURRENT FILING DATE: 2000-11-09 NUMBER OF SEQ ID NOS: 85364 SEQ ID NOS: 85364 SEQ ID NO 15548 LENGTH: 158
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GENERAL INFORMATION:
APPLICANT: Kroger, Burkhard
APPLICANT: Schroder, Hartwig
APPLICANT: Schroder, Hartwig
APPLICANT: Schroder, Oskar
TITLE OF INVENTION: CORYNBBACTERIUM GLUTAMICUM GENES ENCODING NOVEL
TITLE OF INVENTION: WINDER: US/09/605,703B
FILE REFERENCE: BGI-129CP
CURRENT FILING DATE: 2000-06-27
PRIOR APPLICATION NUMBER: 60/142,764
PRIOR APPLICATION NUMBER: 60/142,764
PRIOR FILING DATE: 1999-07-08
PRIOR FILING DATE: 1999-09-03
SPRIOR FILING DATE: 1999-09-03
SEQ ID NOS: 2934
LENGTH: 283
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                                                                                      Score 47.5; DB Pred. No. 0.87; 2; Mismatches
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Pred. No. 4;
2; Mismatches
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NAME/KEY: misc_feature
| LOCATION: 1.158
| CTHER INFORMATION: Ceres Seq. ID 1829388
| US-09-708-427-15548
; OTHER INFORMATION: Ceres Seq. ID 1923440 US-09-708-427-49941
                                                                                                                                                                                                                                                                                                                     Sequence 2242, Application US/09605703B GENERAL INFORMATION:
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US-09-605-703B-2242
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                                                                                      47.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 63.6%;
Matches 7; Conservative
                                                                                                                                                                                                108 NC-DIPHVNRTEYQLIDI 124
                                                                                                                                                                3 NCEDIPHVN--EFSAIDL 18
                                                                                      Query Match 47.5
Best Local Similarity 61.1
Matches 11; Conservative
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9 DAPHINEFPAL 19
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                                                                                                                                                                                                                                                                                                                                                                         Sequence 4954, Application US/09708427
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: N. ALEXADRON et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: THEREBY
FILE REFERENCE: 2750-1243P
CURRENT FPLILAGION UNDMER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: PALENLIN VERSION 3.1
SEQ ID NO 49964
LENGTH: 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 4991, Application US/09708427
GREERAL INFORMATION:
APPLICAMIT N. ALEXANDEL
APPLICAMIT N. ALEXANDEL
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: THEREBY
FILE REPERENCE: 2750-1243P
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: Patentin version 3.1
SEQ ID NO 49941
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                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 163;
                                                                                                                                                   Length 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                            2; Indels
                                                                                                                                                 Score 47.5; DB 7;
Pred. No. 0.8;
2; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 47.5; DB 5;
Pred. No. 0.81;
2; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc_feature
LOCATION: 1..173
OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc_feature
LOCATION: 1..173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc_feature
CACATION: 1..163
COTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc_feature
CACATION: 1..163
COCATION: 1..163
COTHER INFORMATION: Ceres Seq. ID 1923496
US-09-708-427-49964
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Zea mays subsp. mays
                                                                                                                                                 47.5%;
61.1%;
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61.18;
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                                                                                                                                                                                                                                     3 NCEDIPHVN--EFSAIDL 18
                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 61.1'
Matches 11; Conservative
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Matches 11; Conservative
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                                           TYPE: PRT
; ORGANISM: Zea mays
US-60-337-358-461
                                                                                                                                                                                                                                                                                                                                       RESULT 6
US-09-708-427-49964
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US-09-708-427-49941
    SEQ ID NO 461
LENGTH: 160
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Sequence 3221, Application US/09708427

GENERAL INFORMATION:
APPLICANT: N. ALEXANDROV et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID
TITLE OF INVENTION: THEREBY
FILE REPERENCE: 2750-1243P
CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: Patentin version 3.1
SEQ ID NO 32251
                                                                                                                                                     Sequence 574, Application US/09637780B

Sequence 574, Application US/09637780B

Sequence 574, Application US/09637780B

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai
APPLICANT: BROVER, Vyacheslav
TITLE OF INVENTION: Thereby
TITLE OF INVENTION: Thereby
TITLE OF INVENTION: Thereby
CURRENT APPLICATION NUMBER: US/09/637,780B

CURRENT APPLICATION NUMBER: US/09/637,780B

CURRENT FILING DATE: 2000-08-11

NUMBER OF SEQ ID NOS: 1401

SEQ ID NO 574

LENGTH: 182
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Pred. No. 5.4;
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  3;
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100.0%; Pred. No. 24;
tive 0; Mismatches (
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    Mismatches
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CTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc_feature
LOCATION: 1..679
CTHER INFORMATION: Ceres Seq. ID 1833855
US-09-708-427-32251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc_feature

CATTON: 1.182

COTHER INFORMATION: Ceres Seq. ID 1482445

US-09-637-780B-574
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ORGANISM: Arabidopsis thaliana
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61.5%;
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Best Local Similarity 61.5
Matches 8; Conservative
      Conservative
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LOCATION: 1..182
OTHER INFORMATION: Xaa
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                                            6 DIPHVNEFSAIDL 18
                                                                S ELPHVNILSKIDL 17
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Best Local Similarity
Matches 7; Conserva
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        Matches
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TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
TITLE OF INVENTION: Thereby
FILE REFERENCE: 2750-1096P
CURRENT APPLICATION NUMBER: US/09/637,780B
CURRENT FILING DATE: 2000-08-11
NUMBER OF SEQ ID NOS: 1401
SEQ ID NO 575
LENGTH: 138
                                                                                                                                                                                                                      US-09-637-780B-576
Sequence 576, Application US/09637780B
Sequence 576, Application US/09637780B
GENERAL IRRORMATION:
SEQUENCE STORMATION:
APPLICANT: ALEXANDROV, NICKOLAI
APPLICANT: ALEXANDROV, NICKOLAI
APPLICANT: TITLE OF INVENTION: Thereby
TITLE OF INVENTION: Thereby
FILE REFERENCE: 2750-1096P
CURRENT APPLICATION NUMBER: US/09/637,780B
CURRENT FILING DATE: 2000-08-11
NUMBER OF SEQ ID NOS: 1401
SEQ ID NO 576
LENGTH: 135
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                              Length 158;
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                                                                    2; Indels
                          Score 43.5; DB 5;
Pred. No. 3.8;
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3.8;
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Pred. No. 3.9;
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                                                                    4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COTHER INFORMATION: Xaa is any amino acid NAME/KEY: misc_feature LOCATION: 1.135 CTHER INFORMATION: Ceres Seq. ID 1482447 US-09-637-780B-576
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Pred. No.
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APPLICANT: ALEXANDROV, Nickolai.
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CACATION: 1..138
CTHER INFORMATION: Xaa is any am;
NAME/KEY: misc_feature
CACATION: 1..138
CTHER INFORMATION: Ceres Seq. ID
US-09-637-780B-575
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                              43.5%;
                                                                                                           3 NCEDIPHVN -- EFSAIDL 18
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79 NC-DVPHVNRTDYQLIDI 95
                                Query Match 43.5%
Best Local Similarity 50.0%
Matches 9; Conservative
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Best Local Similarity 61.5
Matches 8; Conservative
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ELPHVNILSKIDL 14
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LOCATION: 1..135
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Best Local Similarity
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US-09-637-780B-575
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Search completed: January 29, 2002, 10:58:15 Job time: 2511 sec
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US-09-70249
US-09-70249
US-09-708427
Sequence 3-2249, Application US/09708427
GENERAL INFORMATION:
APPLICANT: N. ALEXANDROW et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: THEREBY
CURRENT APPLICATION UNMERS: US/09/708,427
CURRENT APPLICATION UNMERS: US/09/708,427
SOUTHAND APPLICATION UNMERS: 2000-11-09
NUMBER OF SEQ ID NOS: 63364
SEQ ID NO 3-2249
LENGTH: 827
                                                                           RESULT 14
US-09-708-427-32250
US-09-708-427-32250
SEGRETAL INFORMATION:
GENERAL INFORMATION:
TILLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES:
TILLE OF INVENTION: THEREBY
FILE REFERENCE: 2750-1243P
CURRENT APPLICATION UNMERS: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SEQ ID NO 32250
LENGTH: 741
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                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc_feature
CCATION: 1..741
COCATION: 1..741
NAME/KEY: misc_feature
LCCATION: 1..741
COTHER INFORMATION: Ceres Seq. ID 1833854
US-09-708-427-32250
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: LOCATION: 1.827
: DTHER INFORMATION: Xaa is any amino acid
: NAME/KEY: misc_feature
: LOCATION: 1.827
: COTER INFORMATION: Ceres Seq. ID 1833853
US-09-708-427-32249
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ORGANISM: Arabidopsis thaliana
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Best Local Similarity 100.
Matches 7; Conservative
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| 160 CEDIPHV 166
12 CEDIPHV 18
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74 CEDIPHV 80
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1: cgn2_6/ptodata/2/paa/PCTUS_COMB.pep:*
2: cgn2_6/ptodata/2/paa/USO0_COMB.pep:*
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4: cgn2_6/ptodata/2/paa/USO0_COMB.pep:*
5: cgn2_6/ptodata/2/paa/USO0_COMB.pep:*
6: cgn2_6/ptodata/2/paa/USO0_COMB.pep:*
7: cgn2_6/ptodata/2/paa/USO0_COMB.pep:*
7: cgn2_6/ptodata/2/paa/USO0_COMB.pep:*
8: cgn2_6/ptodata/2/paa/USO0_COMB.pep:*
10: cgn2_6/ptodata/2/paa/USO0_COMB.pep:*
11: cgn2_6/ptodata/2/paa/USO0_COMB.pep:*
11: cgn2_6/ptodata/2/paa/USO0_COMB.pep:*
13: cgn2_6/ptodata/2/paa/USO0_COMB.pep:*
14: cgn2_6/ptodata/2/paa/USO0_COMB.pep:*
15: cgn2_6/ptodata/2/paa/USO0_COMB.pep:*
16: cgn2_6/ptodata/2/paa/USO0_COMB.pep:*
17: cgn2_6/ptodata/2/paa/USO0_COMB.pep:*
18: cgn2_6/ptodata/2/paa/USO0_COMB.pep:*
19: cgn2_6/ptodata/2/paa/USO0_COMB.pep:*
10: cgn2_6/ptodata/2/paa/USO0_COMB.pep:*
10: cgn2_6/ptodata/2/paa/USO0_COMB.pep:*
10: cgn2_6/ptodata/2/paa/USO0_COMB.pep:*
11: cgn2_6/ptodata/2/paa/USO0_COMB.pep:*
12: cgn2_6/ptodata/2/paa/USO0_COMB.pep:*
13: cgn2_6/ptodata/2/paa/USO0_COMB.pep:*
14: cgn2_6/ptodata/2/paa/USO0_COMB.pep:*
15: cgn2_6/ptodata/2/paa/USO0_COMB.pep:*
16: cgn2_6/ptodata/2/paa/USO0_COMB.pep:*
17: cgn2_6/ptodata/2/paa/USO0_COMB.pep:*
18: cgn2_6/ptodata/2/paa/USO0_COMB.pep:*
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3148936 seqs, 277657034 residues
                                                                                                                                                                                                             January 29, 2002, 10:56:07
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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52
1 GQHGHMHG 8
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Maximum DB seq length: 2000000000
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Result	9	Query	Query	8	í	
2	21000	Marci	The light	9 :		Description
П	52	100.0	89	21	US-09-763-397A-15	Sequence 15, Appl
7	52	100.0	272	-	PCT-US99-26796-59	Sequence 59, Appl
m	52	100.0		71	US-09-763-397A-2	Sequence 2, Appli
4	43	82.7		23	US-09-902-540-15333	Sequence 15333, A
S	41	78.8		23	US-09-902-540-16719	Sequence 16719, A
9	41	78.8		-	PCT-US01-08631-41146	Sequence 41146, A
7	41	78.8		24	US-60-161-932-1547	Sequence 1547, Ap
80	41	78.8		24	US-60-167-217-241	Sequence 241, App
6	41	78.8		24	US-60-173-464-228	Sequence 228, App

1 GOHGHMHG 8

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Sequence 1944, Ap	Sequence 258, App	iO	Sequence 42246, A	Sequence 213, App	2086	Sequence 19849, A	~	2507,	N	18494						Sequence 7880, Ap	6289,		6063,			2573	36, A	φ	e 1082	Sequence 475, App	7042,	Sequence 1015, Ap	$\overline{}$	118	Sequence 14585, A	s 114	Sequence 1632, Ap		Sequence 2041, Ap
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67-324-1944	91-637-258	9-	-637-	÷	-681-	-464-	÷	61-932-2507	-637-	91-681-18494	73-464-30035	91-637-39511	91-681-30544	52-991A-2203	117-507-30578	67-217-7880	73-464-6289	91-637-7785	-98	-637 - 412	-700-114	57	0-207-36	-26524B-6816	89-039A-1082	1-758-442-475	38-352-704	0-584	57-217-14	3-464-1187	11-637-145	11-681-1148	16450-163	.16450A-16	88-725A-2041
US-60-1	US-60-1	US-60-1	US-60-1	US-60-1	US-60-1	US-60-1	US-60-1	US-60-1	US-60-1	US-60-1	US-60-1	US-60-1	Ξ	US-09-2	US-09-41	-09-	Ξ	-60-1	US-60-1	US-60-1	US-60-1	US-60-161	US-08-39	PCT-US00-26524B-	US-09-4	US-09-7	US-09-3	US-60-1	US-60-1	US-60-1	US-60-1	US-60-191	PCT-US01	PCT-US01	US-09-4
24	24	24	24	24	24	24	24	24	24	24	24	24	24	16	18	24	24	24	24	24	24	24		٦	18	21	17	24	24	24	24	24		7	18
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10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

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Sequence 15, Application US/09763397A

GENERAL INFORMATION:
APPLICANT: The Government of the United States of America, as represented by the APPLICANT: Control and Prevention
APPLICANT: Secretary of the Department of Health and Human Services, Centers for APPLICANT: Control and Prevention
APPLICANT: Lal, Altaf A.
APPLICANT: Hasnain. Seyed B.
APPLICANT: Hasnain. Seyed B.
TILE REFERENCE: 6395-57049
FILE REFERENCE: 6395-57049
CURRENT APPLICATION NUMBER: US/09/763,397A
CURRENT FILING DATE: 1998-08-21
PRIOR APPLICATION NUMBER: US 60/097,703
PRIOR FILING DATE: 1999-08-19
PRIOR FILING DATE: 1999-08-19
PRIOR FILING DATE: 1999-08-19
PRIOR FILING DATE: 1999-08-19
CONTWARE: PATON NUMBER: PA
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US-09-902-540-16719

Sequence 16719, Application US/09902540

Sequence 16719, Application US/09902540

GENERAL INFORMATION:
APPLICANT: Goldman, Barry S.
APPLICANT: Blate, Gregory J.
APPLICANT: Blater, Steven C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof;
TITLE OF INVENTION: Myxococcus (S)
CURRENT APPLICATION UNMBER: 05/09/902,540

CURRENT FILING DATE: 2001-07-10

PRIOR PILING DATE: 2001-07-10

PRIOR FILING DATE: 2000-07-10

NUMBER OF SEQ ID NOS: 16825

SEQ ID NO 16719
                     Sequence 1533, Application US/09902540

Sequence 1533, Application US/09902540

GENERAL INFORMATION:
APPLICANT: Goldman, Barry S.
APPLICANT: Glater, Steven C.
APPLICANT: Misgand, Roger C.
APPLICANT: Wisgand, Roger C.
CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
PRIOR FILING DATE: 2000-07-10
PRIOR FILING DATE: 2000-07-10

NUMBER OF SEQ ID NOS: 16825

SEQ ID NO 15333

LENGTH: 198
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PCT-USO1-08631-41146
PCT-USO1.08631
Sequence 41146, Application PC/TUSO108631
GENERAL INFORMATION:
APPLICANT: Hyseq, Inc
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
FILE REPERENCE: 2172-040
CURRENT APPLICATION NUMBER: PCT/USO1/08631
CURRENT FILING DATE: 2001-03-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 41; DB 23;
Pred. No. 1.5e+02;
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PRIOR FILING DATE: 2000-03-31
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75.0%;
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75.0%;
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US-09-902-540-16719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Myxococcus xanthus US-09-902-540-15333
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Best Local Similarity
Matches 6; Conserv
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Best Local Similarity
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142 GEHGHDHG 149
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RESULT 4
JS-09-902-540-15333
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Sequence 2, Application US/09763397A

GENERAL INFORMATION:
APPLICANT: The Government of the United States of America, as represented by the APPLICANT: Control and Prevention
APPLICANT: Control and Prevention
APPLICANT: Lal, Altaf A.
APPLICANT: Hasmain, Seyed E.
APPLICANT: Hasmain, Seyed E.
APPLICANT: Hasmain, Seyed E.
APPLICANT: Bandin, Seyed E.
APPLICANT: Bandin, Seyed E.
APPLICANT: Lal, Altaf A.
APPLICANT: Pain Shi, Ya
APPLICANT: Lal, Altaf A.
APPLICAN
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Sequence 59, Application PC/TUS9926796

GENERAL INFORMATION:
APPLICANT: United States Government as Represented by the APPLICANT: Secretary of the Navy Sequence of Human Malaria Parasite TITLE OF INVENTION: Chromosome 2 Sequence of Human Malaria Parasite TITLE OF INVENTION: Chromosome Useful in Anti-malarial Vaccines and TITLE OF INVENTION: Diagnostic Reagents
FILE REFERENCE:
CURRENT APPLICATION NUMBER: PCT/US99/26796
CURRENT PILING DATE: 1999-11-05
NUMBER OF SEQ ID NOS: 420
SOGTWARE: Patentin Ver. 2.1
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100.0%; Pred. No. 6.9;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; ORGANISM: Plasmodium falciparum PCT-US99-26796-59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT ORGANISM: Artificial Sequence
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Best Local Similarity 100.v
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Best Local Similarity luv...
2.26 8; Conservative
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206 GQHGHMHG 213
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            1 GQHGHMHG 8
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-US99-26796-59
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US-09-763-397A-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
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DESCUIT3-464-228
Sequence 228, Application US/60173464
Sequence 228, Application US/60173464
GENERAL INFORMATION:
TITLE OF INVENTION: ISOLATED G-PROTEIN COUPLED RECEPTORS,
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
FILE REFERENCE: CLOUO173
CURRENT APPLICATION NUMBER: US/60/173,464
CURRENT PILING DATE: 1999-12-29
NUMBER OF SEQ ID NOS: 30269
SOFTWARE: FRASEOF FOR WINGOWS VERSION 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: THEREOF
GURRENT FILING DATE: 1999-11-24
CURRENT FILING DATE: 1999-11-24
NUMBER OF SEQ. ID NOS: 2272
SOFTWARE: FastSEQ for Windows Version 4.0
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Pred. No. 3.3e+02;
0; Mismatches 2; Indels
    Length 363,
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GENERAL INFORMATION:
APPLICANT: Venter, J. Craig
TIPLE OF INVENTION: UNCLEIC ACID DETECTION KITS COMPRISING
    Score 41; DB 24; L Pred. No. 3.3e+02; 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 41; DB 24;
Pred. No. 4.1e+02;
1; Mismatches 1
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75.0%;
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Best Local Similarity 75.0%;
Matches 6; Conservative
  Query Match
Best Local Similarity 75.0%;
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Drosophila
US-60-173-464-228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: Drosophila
US-60-167-324-1944
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Matches 6; Conserv
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195 GEHGHDHG 202
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US-60-167-324-1944
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US-60-191-637-258
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LENGTH: 449
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LENGTH: 363
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GENERAL INCOMATION:
GENERAL INCOMATION:
APPLICANT: Li, Peter W. D.
TITLE OF INVENTION: 1SOLATED DROSOPHILA PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MCLEUCLES ENCODING DROSOPHILA PROTEINS, AND USES;
TITLE OF INVENTION: THEREOF
FILE REFERENCE: CLOODIS
CURRENT APPLICATION NUMBER: US/60/167,217
CURRENT APPLICATION NUMBER: US/60/167,217
NUMBER OF SEQ ID NOS: 23195
SOFTWARE: FastSEQ for Windows Version 4.0
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Pred. No. 2.7e+02;
1; Mismatches 1; Indels
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Pred. No. 2.5e+02;
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: OTHER INFORMATION: Xaa - X or * as defined in Table 2

PCT-US01-08631-41146
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GENERAL INFORMATION:
APPLICANT: Venter, J. Craig
: TITLE OF INVENTION: The Drosophila Genome, Pr.
TITLE OF INVENTION: and Uses Thereof
TITLE FEFRENCE: CL000122
CURRENT APPLICATION NUMBER: US/60/161,932
: CURRENT FILING DATE: 1999-10-28
NUMBER OF SEQ ID NOS: 2626
SEQ ID NO 1547
                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
PRIOR APPLICATION NUMBER: 09/649,167
PRIOR FILING DATE: 2000-08-23
NUMBER OF SEQ ID NOS: 60736
SOFTWARE: Custom
SEQ ID NO 41146
LENGTH: 269
                                                                                                                                                                                                                                                                                                                    78.8%;
85.7%;
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ilarity 75.0%;
Conservative
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Best Local Similarity 85.7
Matches 6; Conservative
                                                                                                                                                                                           NAME/KEY: misc_feature
LOCATION: (1)...(269)
                                                                                                                                                   ORGANISM: Homo sapiens
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US-60-167-217-241
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US-60-161-932-1547
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Best Local Similarity
Matches 6; Conserv
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35 GEHGHDHG 42
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Best Local Similarity 75.0
Matches 6; Conservative
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US-60-191-681-213
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Sequence 42246, Application US/60191637

Sequence 42246, Application US/60191637

GENERAL INFORMATION:

APPLICANT: Venter, J. Craig

TITLE OF INVENTION: GENE SEQUENCES EXPRESSED FROM THE DROSOPHILA GENOME, AND

TITLE OF INVENTION: USES THEREOF

TITLE OF INVENTION: USES THEREOF

FILE REFERENCE: CL000392

CURRENT PILIOR DATE: 2000-03-23

CURRENT PILIOR DATE: 2000-03-23

NUMBER OF SEQ ID NOS: 42660

SOFTWARE: FastSEQ for Windows Version 4.0

FEMALE AA.0.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2621, Application US/60191637
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Venter, J. Craig
APPLICANT: Venter, J. Craig
TITLE OF INVENTION: GENE SEQUENCES EXPRESSED FROM THE DROSOPHILA GENOME, AND
TITLE OF INVENTION: GENE SEQUENCES EXPRESSED FROM THE DROSOPHILA GENOME, AND
TITLE REPERENCE: CL000392
CURRENT APPLICATION NUMBER: US/60/191,637
CURRENT FILIA DAYE: 2000-03-23
TITLE OF INVENTION: GENE SEQUENCES EXPRESSED FROM THE DROSOPHILA GENOME, AND TITLE OF INVENTION: USES THEREOF CLOOMS92
CURRENCE: CLOOMS92
CURRENT APPLICATION NUMBER: US/60/191,637
CURRENT FILING DATE: 2000-03-23
NUMBER OF SEQ ID NOS: 42660
SOCTHARRE: Fastseq for Windows Version 4.0
SEQ ID NO 258
LENGTH: 449
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Pred. No. 4.1e+02;
); Mismatches 2; Indels
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Pred. No. 4.1e+02;
Pred. No. 4.1e+02; Indels
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 26251
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Best Local Similarity 75.0
Matches 6; Conservative
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US-60-191-637-42246
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Best Local Similarity
Matches 6; Conserv
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78.8%; Score 41; DB 24; Length 449;

Query Match

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APPLICANT: Li, Peter, W.D.
TITLE OF INVENTION: ISOLATED DROSOPHILA PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING ISOLATED DROSOPHILA PROTEINS AND
TITLE OF INVENTION: USES THEREOF.
TITLE OF INVENTION: USES THEREOF.
CURRENT APPLICATION NUMBER: US/60/191,681
CURRENT APPLICATION NUMBER: US/60/191,681
SUBRENT FILING DATE: 2000-03-23
NUMBER OF SEQ ID NOS: 30973
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 200860
                                                                                                                                                                                                                             Sequence 213, Application US/60191681

Sequence 213, Application US/60191681

GENERAL INFORMATION:
TYPE OF INVENTION:
TITLE OF INVENTION: USOLATED DROSOPHILA PROTEINS, NUCLEIC
TITLE OF INVENTION: USES THEREOF.
CURRENT APPLICATION UNMER: US/60/191,681
CURRENT FILING DATE: 2000-03-23
NUMBER OF SEQ ID NOS: 30973
SOFTWARE: FastSEQ for Windows Version 4.0
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pred. No. 4.1e+02;
0; Mismatches 2; Indels
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Pred. No. 4.1e+02;
0; Mismatches 2; Indels
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Pred. No. 4.1e+02;
1; Mismatches 1;
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Job time: 2404 sec
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; Sequence 20860, Application US/60191681
; GENERAL INFORMATION:
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Matches 6; Conservative
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US-60-191-681-20860
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: DROSOPHILA
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Best Local Similarity
Matches 6; Conserv
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January 29, 2002, 10:58:14; Search time 120.95 Seconds (without alignments) 2.421 Million cell updates/sec
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(cgn2_6/ptodata/2/paa/USO6_NEW_COMB.pep:*)
(cgn2_6/ptodata/2/paa/USO7_NEW_COMB.pep:*)
(cgn2_6/ptodata/2/paa/USO8_NEW_COMB.pep:*)
(cgn2_6/ptodata/2/paa/USO8_NEW_COMB.pep:*)
(cgn2_6/ptodata/2/paa/USO8_NEW_COMB.pep:*)
(cgn2_6/ptodata/2/paa/USO8_NEW_COMB.pep:*)
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100%
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Gapop 10.0 , Gapext 0.5
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Maximum DB :
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Sequence 2909, Ap Sequence 1474, Ap Sequence 1472, Ap Sequence 1472, Ap Sequence 1472, Ap Sequence 29, Appl Sequence 29, Appl Sequence 3635, Ap Sequence 36335, Ap Sequence 8224, Ap Sequence 6122, Ap Sequence 53064, Ap Sequence 53063, Ap Sequence 3723, Ap Sequence 37 Sequence 27822, A Sequence 27821, A Description US-09-708-427-1474 US-09-708-427-1473 US-09-708-427-1473 US-10-001-137-59 US-10-001-137-59 US-09-708-427-71051 US-09-708-427-71051 US-09-620-394B-8225 US-09-708-427-36335 US-09-708-427-36334 US-09-708-427-36334 US-09-708-427-36345 US-09-708-427-53064 US-09-708-427-53064 US-09-708-427-53065 US-09-708-427-57822 SUMMARIES Query Match Length Score Š

RESULT 2
US-09-708-427-50273
US-09-708-427-50273
Sequence 50273, Application US/09708427
GENERAL INFORMATION:
APPLICANT: N. ALEXANDROV et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID
TITLE OF INVENTION: THEREBY
FILE REFERENCE: 2750-1243P
CURRENT APPLICATION UNDHER: US/09/708, 427
CURRENT APPLICATION UNDHER: 1000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: Patentin version 3.1
SEQ ID NO 50273
TYPE: PRT

1:111 | 11 50 GRHGHRHG 57 1 GQHGHMHG 8

27 35 67.3 325 5 US-09-7 28 35 67.3 344 5 US-09-7 31 35 67.3 356 5 US-09-7 31 35 67.3 360 5 US-09-7 32 35 67.3 360 5 US-09-7 33 35 67.3 360 5 US-09-7 34 35 67.3 360 5 US-09-7 35 67.3 360 5 US-09-7 36 67.3 360 5 US-09-7 37 35 67.3 360 5 US-09-7 38 35 67.3 394 5 US-09-7 39 35 67.3 394 5 US-09-7 39 35 67.3 394 5 US-09-7 40 35 67.3 399 5 US-09-7 41 35 67.3 399 5 US-09-7 42 35 67.3 414 5 US-09-7 43 35 67.3 414 5 US-09-7 44 35 67.3 507 6 US-10-0 45 35 67.3 507 6 US-10-0 45 60.3 50.3 50.3 50.0 0-10-0 45 60.3 50.3 50.0 0-10-0 45 60.3 50.3 50.0 0-10-0 45 60.3 50.3 50.0 0-10-0 45 60.3 50.0 0-10-0 46 60.3 50.0 0-10-0 47 60.3 50.0 0-10-0 48 60.3 50.0 0-10-0 49 60.3 50.0 0-10-0 40 60.3 50.0 0-10-0 40 60.3 50.0 0-10-0 40 60.3 50.0 0-10-0 40 60.3 50.0 0-10-0 40 60.3 50.0 0-10-0 40 60.3 50.0 0-10-0 40 60.3 50.0 0-10-0 40 60.3 50.0 0-10-0 40 60.3 50.0 0-10-0 40 60.3 50.0 0-10-0 40 60.3 50.0 0-10-0 40 60.3 50.0 0-10-0 40 60.3 50.0 0-10-0 40 60.3 50.0 0-10-0 40 60.3 50.0 0-10-0 40 60.3 50.0 0-10-0 40 60.3 60.0 0-10-0 40 60.3 60.0 0-10-0 40 60.3 60.0 0-10-0 40 60.3 60.0 0-10-0 40 60.3 60.0 0-10-0 40 60.3 60.0 0-10-0 40 60.0 0-10 40 60.0 0-10 40 60.0 0-10 40 60.0	S-09-708-427-72922 Sequence 72922, A S-09-708-427-27820 Sequence 27820, A S-09-708-427-72921 Sequence 27820, A S-09-708-427-72921 Sequence 72921, A S-09-708-427-72921 Sequence 72921, A S-09-708-427-73190 Sequence 71922, A S-09-708-427-77939 Sequence 71939, A S-09-708-427-70911 Sequence 71939, A S-09-708-427-70911 Sequence 71938, A S-09-708-427-77938 Sequence 71938, A S-09-708-427-77938 Sequence 71938, A S-09-708-427-77937 Sequence 55, Appl Sequence 71937, A S-09-001-137-55 Sequence 55, Appl Sequence 71937, A S-09-001-137-55 Sequence 56, Appl Sequence 5677, Appl Sequence 5677, Appl Sequence 5677, Appl Sequence 26, App	ALIGNMENTS  action US/09620111B  DROW et al. Sequence-Determined DNA Fragments and Corresponding Polypeptid Thereby 1-1070P NUMBER: US/09/620,111B 2000-07-21 3: 9298 is thaliana ture Xaa is any amino acid Ture Xaa contact of the co	re 42; DB 5; Length 137; d. No. 1.9; Mismatches 1; Indels 0; Gaps 0;
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SEQUENCE 1472. Application US/09708427
SEQUENCE 1472. Application US/09708427
APPLICANT: N. ALEXANDROV et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID TITLE OF INVENTION: THEREBY
FILLE OF INVENTION: THEREBY
FILLE OF INVENTION: UNMBER: US/09/708,427
CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILLING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 1472
FENSION 1472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 6
US-10-015-127-13079
; Sequence 13079, Application US/10015127
; GENERAL INFORMATION:
; APPLICANT: BOWER, Stanley G.
; APPLICANT: Bower, Steven C.
; TITLE OF INVENTION: Sphingomens elodea genome sequences and uses thereof
; FILE REFERENCE: 38-10(15806)B
; CURRENT APPLICATION NUMBER: US/10/015,127
CURRENT FILING DATE: 2001-10-29
; PRIOR PILING DATE: 2000-11-22
; NUMBER OF SEQ ID NOS: 14357
; SEQ ID NO 13079
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                                                                                                                                                          Length 374;
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8.8;
                                                                                                                                                          DB 5;
8;
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Pred. No. 8;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc_feature
LOCATION: 1..408
OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc_feature
LOCATION: 1..408
OTHER INFORMATION: Ceres Seq. ID 1807879
COTHER INFORMATION: Xaa is any amino acid name/KET; name/KET; name/Cetature Location: 1..374; CATION: 1..374; OTHER INFORMATION: Ceres Seq. ID 1807880 US-09-708-427-1473
                                                                                                                                                                                                  0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: PRT; ORGANISM: Sphingomonas elodea
US-10-015-127-13079
                                                                                                                                                            78.8%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                              Query Match 78.8
Best Local Similarity 100.
Matches 6; Conservative
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Best Local Similarity
'.'hos 6; Conserva
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237 HGHMHG 242
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US-09-708-427-1472
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Sequence 1473, Application US/09708427

GENERAL INFORMATION:
THORMATION:
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: THEREBY
FILE REFERENCE: 2750-1243P
CURRENT APPLICATION WUMBER: US/09/708,427

CURRENT APPLICATION WUMBER: US/09/708,427

SOFTWARE: PATELING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: PATELING DATE: 30143
LENGTH: 374
                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-708-427-1474

INCREMENT INFORMATION:
SEQUENCE 1474, Application US/09708427

SEQUENCE 1474, Application US/09708427

SEQUENCE INFORMATION:
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: THEREBY
TITLE OF INVENTION: 2750-1243P

TITLE OF INVENTION: 2750-1243P

CURRENT APPLICATION NUMBER: US/09/708,427

CURRENT FILING DATE: 2000-11-09

NUMBER: PATENTING PATE: 2000-11-09

SOFTWARE: PATENTIN VERSION 3.1

SEQ ID NO 1474
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                                                                                                                                                                                                                               DB 5; Length 406;
                                                                                                                                                                                                                                                                          1; Mismatches
      CRGANISM: Zea mays subsp. mays
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1..406
COTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc_feature
LOCATION: 1..406
COCATION: 1..406
COTHER INFORMATION: Ceres Seq. ID 1924393
US-09-708-427-50273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc_feature
LOCATION: 1..294
OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc_feature
LOCATION: 1..294
OTHER INFORMATION: Ceres Seq. ID 1807881
US-09-708-427-1474
                                                                                                                                                                                                                                  Score 42;
Pred. No.
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ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                  80.8%;
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Best Local Similarity 75.0
Matches 6; Conservative
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Best Local Similarity
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50 GRHGHRHG 57
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162 GGHGHSHG 169
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31 GAHGHGHG 38
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APPLICANT: Meyers, Racinal A.
APPLICANT: Meyers, Racinal A.
APPLICANT: Glucksmann, Maria Alexandra
APPLICANT: Glucksmann, Maria Alexandra
TITLE OF INVENTION: 47476, 67210, 49875, 46842, 33201,
TITLE OF INVENTION: 47476, 67210, 49875, DEAD TYPE HELICASE, CENTAURIN,
TITLE OF INVENTION: DEHYDROGENASE/REDUCTASE, DAD TYPE HELICASE, CENTAURIN,
TITLE OF INVENTION: DEHYDROGENASE/REDUCTASE, AND METAL TRANSPORTER
TITLE OF INVENTION: FAMILY MEMBERS AND USES THEREOF
TITLE OF INVENTION: FAMILY MEMBERS AND USES THEREOF
TITLE OF INVENTION: PAMILY MEMBER: 06/248,332
FILE REFERENCE: 10448-119001
CURRENT FILING DATE: 2000-11-14
PRIOR PELICATION NUMBER: 66/248,331
PRIOR PELICATION NUMBER: 66/248,331
PRIOR FILING DATE: 2000-11-14
PRIOR FILING DATE: 2000-11-14
PRIOR PELICATION NUMBER: 66/250,077
PRIOR APPLICATION NUMBER: 66/250,176
PRIOR PELICATION NUMBER: 66/250,176
PRIOR PELICATION NUMBER: 66/250,176
PRIOR FILING DATE: 2000-11-30
SHORD FILIN
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APPLICANT: CUTLIS, ROYA A. J.
APPLICANT: CUTLIS, ROYA A. J.
APPLICANT: CUTLIS, ROYA A. J.
APPLICANT: CLUCKSMANN, MARÍA ALEXANDRA
TITLE OF INVENTION: 4476, 67210, 49875, 46842, 33201,
TITLE OF INVENTION: 83378, 84233, 64708, 85041, AND 84234,
TITLE OF INVENTION: GLYCOSYLFRANSFERASE, DEAD TYPE HELICASE, CENTAURIN,
TITLE OF INVENTION: DEHYDROGENASE/REDUCTASE, AND METAL TRANSPORTER
TITLE OF INVENTION: FAMILY MEMBERS AND USES THEREOF
FILE REFERENCE: 10448-119001
CURRENT APPLICATION NUMBER: US/10/001,137
CURRENT FILING DATE: 2001-11-14
PRIOR FILING DATE: 2001-11-14
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   DB 6; Length 366;
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                                                                               3; Mismatches
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   Score 39; DB
Pred. No. 17;
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                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 29, Application US/10001137
; GENERAL INFORMATION:
; APPLICANT: Meyers, Rachel A.
   75.0%;
62.5%;
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Best Local Similarity 75.0
Matches 6; Conservative
                                                                               5; Conservative
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                               Best Local Similarity
Matches 5; Conserv
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299 GRHGHLYG 306
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Query Match
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Sequence 71051, Application US/09708427

GENERAL INFORMATION:
APPLICAMY: N. ALEXANDROV et al.
TITLE OF INVENTION: THEREBY
FILE OF INVENTION: THEREBY
FILE REFERENCE: 2750-1243P
CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: Patentin version 3.1
SEQ ID NO 71051
LENGTH: 168
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TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptid
TITLE OF INVENTION: Thereby
FILE REFERENCE: 2750-1067P
CURRENT APPLICATION NUMBER: US/09/620,394B
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17;
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11;
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Pred. No. 17;
0; Mismatches
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Pred. No. 11;
0; Mismatches
PRIOR FILING DATE: 2000-11-14

PRIOR FILING DATE: 2000-11-14

PRIOR FILING DATE: 2000-11-14

PRIOR FILING DATE: 2000-11-14

PRIOR FILING DATE: 2000-11-30

PRIOR FILING DATE: 2000-11-30

PRIOR PHILOR DATE: 2000-11-30

PRIOR APPLICATION NUMBER: 60/250,176

PRIOR APPLICATION NUMBER: 60/250,176

PRIOR FILING DATE: 2000-11-30

NUMBER OF SEQ ID NOS: 62

SOFTWARE: FASTSEQ for Windows Version 4.0

SOFTWARE: FASTSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc_feature
LOCATION: 1..168
OTHER INFORMATION: Xaa is any amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc_feature
CATTON: 1..168
US-09-708-427-71051
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Sequence 8225, Application US/09620394B
; GENERAL INFORMATION:
HAPLICANT: ALEXANDROV, Nickolai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Zea mays subsp. mays
                                                                                                                                                                                                                                                                                                                                                                                            75.0%;
75.0%;
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75.08;
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Best Local Similarity 75.0
Matches 6; Conservative
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Best Local Similarity 75.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                             TYPE: PRT
; ORGANISM: Mus musculus
US-10-001-137-59
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Sequence 36334, Application US/09708427

Sequence 36334, Application US/09708427

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: THEREBY
TITLE OF INVENTION: THEREBY
TITLE OF INVENTION: THEREBY
TITLE OF INVENTION: THEREBY
CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: PatentIn version 3.1
SEQ ID NO 36334

LENGTH: 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: BROVER, Vyacheslav
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptid
TITLE OF INVENTION: Thereby
FILE REFERENCE: 2750-1067P
CURRENT APPLICATION NUMBER: US/09/620,394B
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 9131
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                                                                                                                                                                                                                                                                                   1; Indels
                                                                                                                                                                                                                                               DB 5;
34;
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Pred. No. 39;
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                                                                                                                                                                                                                                                                                   1; Mismatches
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COCATION: 1..389
OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc_feature
COCATION: 1..389
UCATION: 1..389
US-09-620-394B-8224
                                                                                                                                                                                                                                             Score 37;
Pred. No. 3
                                                                      NAME/KEY: misc_feature
LOCATION: 1...34
OTHER INFORMATION: xaa is any amino acid
NAME/KEY: misc_feature
                                                                                                                                                ; LOCATION: 1..344
; OTHER INFORMATION: Ceres Seq. ID 1843031
US-09-708-427-36335
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 8224, Application US/09620394B
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Arabidopsis thaliana
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                                  ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                               71.2%;
71.4%;
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Best Local Similarity (
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Best Local Similarity
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163 EHGHSHG 169
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218 HGHVHG 223
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US-09-620-394B-8224
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LENGTH: 389
LENGTH: 344
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TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: THEREBY
FILE REFERENCE: 2750-1243P
CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: Patentin version 3.1
SEQ ID NO 36335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 36336, Application US/09708427
Sequence 36336, Application US/09708427
GENERAL INFORMATION:
TELE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: THEREBY
TITLE OF INVENTION: THEREBY
FILLE OF INVENTION: 2500-1243P
CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER: OF SEQ ID NOS: 85364
SOUTWARE: PALGHIN VERSION 3.1
SEQ ID NO 36336
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Pred. No. 30;
1; Mismatches 0; Indels
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Mismatches
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LOCATION: 1..330
OTHER INFORMATION: Ceres Seq. ID 1843032
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Pred. No.
                                                                                                                                    NAME/KEY: misc_feature
COCATION: 1.309
OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc_feature
COCATION: 1.309
OTHER INFORMATION: Ceres Seq. ID 1411807
15.09-620-394B-8225
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CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 9131
SEQ ID NO 8225
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71.4%;
                                                                                                  ORGANISM: Arabidopsis thaliana
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ilarity 83.3%;
Conservative 1
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LOCATION: 1..330
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Best Local Similarity
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Matches 5; Conserv
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149 EHGHSHG 155
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| 138 HGHVHG 143
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RESULT 15
US-09-620-394B-8223
US-09-620-394B-8223
Sequence 8223, Application US/09620394B
SEQUENCE 8223, Application US/09620394B
SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE 2750-1067P
TITLE OF INVENTION: Thereby
FILE REFERENCE: 2750-1067P
CURRENT APPLICATION UNMBER: US/09/620,394B
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 9131
SEQ ID NO 8223
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Pred. No. 45;
1; Mismatches 0; Indels
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Pred. No. 40;
1; Mismatches 1; Indels
; FEATURE:

NAME/KEY: misc_feature

LOCATION: 1..398

OTHER INFORMATION: Xaa is any amino acid

NAME/KEY: misc_feature

LOCATION: 1..398

COCATION: 1..398

COTHER INFORMATION: Ceres Seq. ID 1843030

US-09-708-427-36334
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NAME/KEY: misc_feature
LOCATION: 1..453
OTHER INPORMATION: Xaa is any amino acid
NAME/KEY: misc_feature
LOCATION: 1..453
. COTHER INFORMATION: Ceres Seq. ID 1411805
US-09-620-394B-8223
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ORGANISM: Arabidopsis thaliana
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71.2%;
Best Local Similarity 71.4%;
Matches 5; Conservative
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Best Local Similarity 83.3%;
Matches 5; Conservative
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217 EHGHSHG 223
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282 HGHVHG 287
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Search time 1760.55 Seconds (without alignments)
1.262 Million cell updates/sec
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Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                             January 29, 2002, 10:56:06
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Maximum Match 100%
Listing first 45 summaries
                                          OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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1 SNTFINNA 8
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Pred. No. 1s the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

			Description	Sequence 14, Appl	Sequence 59, Appl	Sequence 2, Appli	Sequence 13377, A	Sequence 2046, Ap	Sequence 3944, Ap	Sequence 7203, Ap	Sequence 75, Appl	Sequence 29418, A
SUMMARIES		4		US-09-763-397A-14	PCT-US99-26796-59	US-09-763-397A-2	US-09-489-039A-13377	US-09-757-028-2046	US-08-827-356-3944	US-09-611-529-7203	PCT-US99-26796-75	US-09-417-507-29418
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	æ	Query	Match	100.0	100.0	100.0	87.8	80.5	80.5	80.5	80.5	78.0
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		Result	2	ч	7	e	4	S	9	7	8	6

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Gaps

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Length 8; Indels

Query Match 100.0%; Score 41; DB 21; Best Local Similarity 100.0%; Pred. No. 2.9e+06; Matches 8; Conservative 0; Mismatches 0;

1 SNTFINNA 8

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Sequence 827, App Sequence 4538, Ap	156	1522,	995, A	977,	2852,	966	978,			1597,	1857,	Sequence 623, App	Sequence 1853, Ap	Sequence 7, Appl1	Sequence 55, Appl	Sequence 32055, A	Sequence 7755, Ap	Sequence 1187, Ap	Seguence 30092, A	Sequence 46627, A	1905	415		29473,	5153	27537,		4196,	1205,	1205,				Sequence 1079, Ap
US-60-164-763-827 US-60-169-842-4538	US-60-192-587-1	US-60-194-091-1	US-60-192-587-	US-60-194-091-97	US-60-178-308-	US-60-192-587-	US-60-194-091-97	us-60-178-	US-60-178-308-28	us-60-170-	US-60-170-346-18	US-60-171-480-6	US-60-170-346-18	US-09-747	US-09-747-155-5	US-60-324-109-3	us-09-328-	US-60-229-515-1	663-3	US-09-864-761-4	US-60-236-359-	US-08-827-356-4	US-09-611-529-5	US-60-324-109-2	US-09-328-352-5	US-09-417-507-2	US-09-391-631-1	US-09-391-	US-09-732-	US-60-169-340-1	US-60-19	US-09-252-691	US-09-252-691C-	US-60-192-587
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10	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

Sequence 14, Application US/09763397A

Sequence 14, Application US/09763397A

Sequence 14, Application US/09763397A

APPLICANT: The Government of the United States of America, as represented by the APPLICANT: Control and Prevention

APPLICANT: Lai, Altaf A.

APPLICANT: Lai, Altaf A.

APPLICANT: Ding Shi, Ya

APPLICANT: Hasnain, Seyed E.

TITLE OF INVENTION: Recombinant Multivalent Malarial Vaccine Against Plasmodium Fa FILE REFERENCE: 6395-57049

FILE REFERENCE: 6395-57049

CURRENT APPLICATION NUMBER: US/09/763,397A

CURRENT FILING DATE: 1998-08-21

PRIOR APPLICATION NUMBER: PCT / US99/18869

PRIOR PRILNG DATE: 1999-08-19

NUMBER OF SEQ ID NOS: 26

SOFTWARE: PRETEIN OF APPLICATION NUMBER: PCT / US99/18869

TYPE: PRIOR PLICATION NUMBER: PCT / US99/18869

TYPE: PRIOR PLICATION NUMBER: PCT / US99/18869

ALIGNMENTS

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APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: NUMBER: OS 2004001
CURRENT PEPTICATION NUMBER: US,09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR PELING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 13377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; LOCATION: (62); CTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-09-757-028-2046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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Sequence 2046, Application US/09757028

GENERAL INFORMATION:
TILE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PW01

CURRENT APPLICATION NUMBER: US/09/757,028

CURRENT FILING DATE: 2001-01-09

PRIOR APPLICATION NUMBER: 60/179,065

PRIOR APPLICATION NUMBER: 60/179,065

PRIOR APPLICATION NUMBER: 60/180,628

FRIOR FILING DATE: 2000-01-31

PRIOR APPLICATION NUMBER: 60/180,628

NUMBER OF SEQ ID NOS: 2660

SOFTWARE: PatentIN Ver. 2.0

SEQ ID NO 2046
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Pred. No. 1.1e+02;
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26;
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Pred. No.
                          Sequence 13377, Application US/09489039A GENERAL INFORMATION:
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APPLICANT: George H. Shimer, Jr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: George H. Shimer, Jr. APPLICANT: George H. Miller
                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Klebsiella pneumoniae US-09-489-039A-13377
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Best Local Similarity 75.0
Matches 6; Conservative
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Best Local Similarity 85.7
Matches 6; Conservative
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25 SNTFLNGA 32
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97 NTEVNNA 103
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          US-09-489-039A-13377
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US-08-827-356-3944
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US-09-757-028-2046
                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
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Sequence 2, Application US/09763397A

GENERAL INFORMATION:
APPLICANT: The Government of the United States of America, as represented by the APPLICANT: The Government of the United States of America, as represented by the APPLICANT: Control and Prevention
APPLICANT: Lal, Altaf A.
APPLICANT: Lal, Altaf A.
APPLICANT: Hasnain, Seyed E.
APPLICANT: Hasnain, Seyed E.
TITLE OF INVENTION: Recombinant Multivalent Malarial Vaccine Against Plasmodium Falci
FILE REFERENCE: 6395-57049

CURRENT FILING DATE: 2001-02-16
PRIOR PLICATION NUMBER: US 60/097,703

PRIOR APPLICATION NUMBER: PCT / US99/18869

PRIOR SEQ ID NOS: 26

SEQ ID NO 2.
SEQ ID NO 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                          Sequence 59, Application PC/TUS9926796
Sequence 59, Application PC/TUS9926796
GBMERAL INFORMATION.
APPLICANT: United States Government as Represented by the APPLICANT: United States Government as Represented by the APPLICANT: Secretary of the Navy TITLE OF INVENTION: Chromosome 2 Sequence of Human Malaria Parasite TITLE OF INVENTION: Plasmodium Falciparum and Proteins of Said TITLE OF INVENTION: Chromosome Useful in Anti-malarial Vaccines and TITLE OF INVENTION: Diagnostic Reagents
FILE REPERBURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .;
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Pred. No. 6.2;
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0
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                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: PCT/US99/26796
CURRENT FILING DATE: 1999-11-05
NUMBER OF SEQ ID NOS: 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: Plasmodium falciparum PCT-US99-26796-59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 8; Conservative 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                               PatentIn Ver. 2.1
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1 SNTFINNA
                                                                                                RESULT 2
PCT-US99-26796-59
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LENGTH: 272
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PCT-US99-26796-75

Sequence 75, Application PC/TUS9926796

GENERAL INFORMATION:
APPLICANT: United States Government as Represented by the APPLICANT: Secretary of the Navy
TITLE OF INVENTION: Chromosome 2 Sequence of Human Malaria Parasite
TITLE OF INVENTION: Plasmodium Falciparum and Proteins of Said
TITLE OF INVENTION: Chromosome Useful in Anti-malarial Vaccines and
TITLE OF INVENTION: Diagnostic Reagents
FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 33; DB 20; Length 214;
Pred. No. 2e+02;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: US 09/036,234
PRIOR FILING DATE: 1998-03-06
PRIOR FILING DATE: 1998-03-06
PRIOR PELLING DATE: 1998-03-06
PRIOR PAPLICATION NUMBER: US 09/036,137
PRIOR PAPLICATION NUMBER: US 09/036,082
PRIOR APPLICATION NUMBER: US 09/036,081
PRIOR APPLICATION NUMBER: US 09/036,081
PRIOR APPLICATION NUMBER: US 09/036,091
PRIOR APPLICATION NUMBER: US 09/036,091
PRIOR PILING DATE: 1998-03-06
PRIOR PILING DATE: 1998-04-01
PRIOR PILING DATE: 1997-04-01
PRIOR PILING DATE: 1996-04-01
PRIOR PILING DATE: 1996-06-05-02
PRIOR PILING DATE: 1996-06-01
PRIOR PILING DATE: 1996-06-01
PRIOR PILING DATE: 1996-06-01
                                                PRIOR APPLICATION NUMBER: US 09/266,541
PRIOR FILING DATE: 1999-03-11
PRIOR APPLICATION NUMBER: US 09/037,934
PRIOR PLING DATE: 1998-03-10
PRIOR FILING DATE: 1998-03-06
PRIOR PLICATION NUMBER: US 09/036,720
PRIOR PPLICATION NUMBER: US 09/036,338
PRIOR PLING DATE: 1998-03-06
PRIOR PPLING DATE: 1998-03-06
PRIOR PLING DATE: 1998-03-06
PRIOR PLING DATE: 1998-03-06
PRIOR FILING DATE: 1998-03-06
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CURRENT FILING DATE: 1999-11-05
NUMBER OF SEO ID NOS: 420
SOFTWARE: Patentin Ver. 2.1
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PCT-US99-26796-75
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ilarity 71.4%;
Conservative
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SEQ ID NO 7203
LENGTH: 214
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Best Local Similarity
Matches 5; Conserv
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93 ANTEVNN 99
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LENGTH: 2010
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APPLICANT: ROBERTA S. HATEL
TITLE OF INVENTION: Stabphylococcus aureus Related Compositions and Methods
TITLE OF INVENTION: Stabphylococcus aureus Related Compositions and Methods
FILE REFERENCE: 1034/1C963US1
CURRENT FILING DATE: 2000-06-30
CURRENT FILING DATE: 1999-10-14
PRIOR APPLICATION NUMBER: US 09/417,811
PRIOR APPLICATION NUMBER: US 09/266,557
PRIOR APPLICATION NUMBER: US 09/266,557
PRIOR APPLICATION NUMBER: US 09/266,556
PRIOR FILING DATE: 1999-03-11
PRIOR APPLICATION NUMBER: US 09/266,556
PRIOR APPLICATION NUMBER: US 09/266,555
PRIOR APPLICATION NUMBER: US 09/266,555
PRIOR APPLICATION NUMBER: US 09/266,555
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71.4%; Pred. No. 2e+02;
.ive 2; Mismatches 0; Indels
APPLICANT: Roberta S. Hare
APPLICANT: Karen J. Shaw
TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS RELATED
TITLE OF INVENTION: COMPOSITIONS AND METHODS
NUMBER OF SEQUENCES: 5574
CORRESPONDENCE ADDRESS:
                                                                                                                                                3: Schering-Plough Corporation
2000 Galloping Hill Road
                                                                                                                                                                                                                                                Sequence 7203, Application US/09611529
GENERAL INFORMATION:
APPLICANT: George H. Shimer, Jr.
APPLICANT: George H. Miller
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; LOCATION: 1...214
US-08-827-356-3944
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Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
                                                                                                                                                                                              CITY: Kenilworth
STATE: New Jersey
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93 ANTFVNN 99
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US-09-611-529-7203
                                                                                                                                              ADDRESSEE:
STREET: 20
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FILE REFERENCE: CL000162
CURRENT APPLICATION NUMBER: US/60/169,842
CURRENT FILING DATE: 1999-12-09
NUMBER OF SEQ ID NOS: 5232
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4538
LENGTH: 89
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Best Local, Similarity 85...
6, Conservative
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Best Local Similarity 85.7
Matches 6; Conservative
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73 SDTFINN 79
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13 SDTFINN 19
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ORGANISM: HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: HUMAN
                                                                                                                                                                                                                                                                                                               1 SNTFINN 7
                                                                                                                                        ; TYPE: PRT
; ORGANISM: Human
US-60-169-842-4538
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US-60-194-091-1522
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GENERAL INFORMATION:
APPLICANT: RITH G. WEINSTOCK ET AL.
APPLICANT: RITHG G. WEINSTOCK ET AL.
TITLE OF INVENTION: FUNICATUS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: FUNICATUS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: PATH99-10
CURRENT APPLICATION NUMBER: US/09/417,507
CURRENT FILING DATE: 1999-10-14
NUMBER OF SEQ ID NOS: 44312
SEQ ID NO 29418
LENGTH: 76
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GENERAL INFORMATION:
APPLICARY: BONAZZI, VIVVEN
TITLE OF INVENTION: ISOLATED HUMAN GPCR PROTEIN, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN GPCR PROTEINS AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 827, Application US/60164763
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Bonazzi, Vivien
TITLE OF INVENTION: ISOLATED HUMAN GPCR PROTEIN, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN GPCR PROTEINS AND USES THEREOF FILE REFERENCE: CL000140
CURRENT APPLICATION NUMBER: US/60/164,763
CURRENT FILING DATE: 1999-11-12
NUMBER OF SEQ ID NOS: 1154
SOFTWARE: FastSEQ for Windows Version 4.0
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                                              Length 2010;
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Pred. No. 1.3e+02;
1; Mismatches 0; Indels
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                                              80.5%; Score 33; DB 1; Le
100.0%; Pred. No. 2.1e+03;
ive 0; Mismatches 0;
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Pred. No. 1.1e+02;
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85.7%;
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85.7%;
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Best Local Similarity 85.7
Matches 6; Conservative
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                                                                                        Conservative
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US-09-417-507-29418
                                                                    Best Local Similarity
Matches 6; Conserv
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Best Local Similarity
Matches 6; Conserv
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| 13 SDTFINN 19
                                                                                                                                                    735 NTFINN 740
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US-60-164-763-827
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US-09-417-507-29418
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US-60-169-842-4538
                                                                                                                            2 NTFINN 7
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LENGTH: 89
                                                    Query Match
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Sequence 1522, Application US/60194091
Sequence 1522, Application US/60194091
GBNERAL INFORMATION:
APPLICANT: BORAZZI, VIVIEN
TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED
TITLE OF INVENTION: RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR
TITLE OF INVENTION: RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR
TITLE OF INVENTION: RECEPTORS, NUCLEIC ACID MOLECULES
TITLE OF INVENTION: RECEPTORS, NUCLEIC ACID MOLECULES
CURRENT APPLICATION NUMBER: US/60/194,091
CURRENT FILING DATE: 2000-04-03
NUMBER OF SEQ ID NOS: 1598
SEQ ID NO 1522
LENGTH: 90
LENGTH: 90
                                                                                                                                                                                                                                                                                                                                                APPLICANT: BONDAZI, Vivien
TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED
TITLE OF INVENTION: RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR
TITLE OF INVENTION: PROFINE, AND USES THEREOF
FILE REFERENCE: CL000405
CURRENT APPLICATION NUMBER: US/60/192,587
CURRENT APPLICATION NUMBER: US/60/192,587
NUMBER OF SEQ ID NOS: 1666
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 1563
LENGTH: 90
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Pred. No. 1.3e+02;
1; Mismatches 0; Indels
DB 24; Length 89;
1.3e+02;
ches 0; Indels
                                                        1; Mismatches
     Score 32;
Pred. No.
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CTHER INFORMATION: Xaa = Any Amino Acid
US-60-192-587-1563
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20-60-192-1863 Application US/60192587
GENERAL INFORMATION: .....
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85.7%;
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Search completed: January 29, 2002, 10:56:07 Job time: 2403 sec
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Sequence 977, Application US/60194091

Sequence 977, Application US/60194091

Sequence 977, Application US/60194091

Sequence 977, Application US/60194091

TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED

TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR

TITLE OF INVENTION: PROTEINS, AND USES THEREOF

TITLE OF INVENTION: PROTEINS, AND USES THEREOF

CURRENT APPLICATION NUMBER: US/60/194,091

CURRENT FILLIG DATE: 2000-04-03

NUMBER OF SEQ ID NOS: 1598

SOFTWARE: FastSEQ for Windows Version 4.0

LENGTH: 127

TYPE: PRT
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Sequence 995, Application US/60192587
Sequence 995, Application US/60192587
GENERAL INFORMATION:
TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED
TITLE OF INVENTION: RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR
TITLE OF INVENTION: PROTEINS, AND USES THEREOF
FILE REFERENCE: CL000405
CURRENT APPLICATION NUMBER: US/60/192,587
CURRENT FILING DATE: 2000-03-28
NUMBER OF SEQ ID NOS: 1666
SEQ ID NO 995
LENGTH: 127
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Pred. No. 1.9e+02;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 32; DB 24; Length 127;
Pred. No. 1.9e+02;
1; Mismatches 0; Indels
                                                                                                         Score 32; DB 24; Length 90;
Pred. No. 1.3e+02;
1; Mismatches 0; Indels
: LOCATION: (1)...(90)
; OTHER INFORMATION: Xaa - Any Amino Acid US:60-194-091-1522
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85.7%;
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Best Local Similarity 85.7%;
Matches 6; Conservative
                                                                                                           Query Match 78.0%;
Best Local Similarity 85.7%;
Matches 6; Conservative
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Best Local Similarity 85.77
Matches 6; Conservative
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112 SDTFINN 118
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| 73 SDTFINN 79
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US-60-192-587-995
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DEMONDATION OF THE APPLICANT: N. ALEXANDROV et al.

TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID
TITLE OF INVENTION: THEREBY
FILE REFERENCE: 2750-1243P
CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: Patentin version 3.1
SEQ ID NO 76263
LENGTH: 152
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Sequence 2, Appli
Sequence 424, App
Sequence 424, App
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25, Appl
480, App
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22562, A
68823, A
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                                                                                                                              January 29, 2002, 10:58:14; Search time 120.95 Seconds (without alignments) 2.421 Million cell updates/sec
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Sequence 480
Sequence 790
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1: /cgn2_6/ptodata/2/paa/USO6_NEW_COMB.pep:*

3: /cgn2_6/ptodata/2/paa/USO6_NEW_COMB.pep:*

4: /cgn2_6/ptodata/2/paa/USO8_NEW_COMB.pep:*

5: /cgn2_6/ptodata/2/paa/USO8_NEW_COMB.pep:*

5: /cgn2_6/ptodata/2/paa/USO8_NEW_COMB.pep:*

5: /cgn2_6/ptodata/2/paa/USO8_NEW_COMB.pep:*

7: /cgn2_6/ptodata/2/paa/USO8_NEW_COMB.pep:*
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-09-708-427-76263

US-09-620-394B-4936

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US-09-620-394B-4934

US-09-620-394B-4934

US-09-620-394B-4934

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US-09-620-394B-4934

US-09-708-427-1989B

US-09-708-427-1989B

US-09-708-427-1989B

US-09-801-388-284

PCT-USO1-17103-2

US-09-801-368-22

US-09-801-368-424

US-09-816-028A-19

US-09-816-028A-19

US-09-816-028A-19

US-09-816-028A-19

US-09-816-028A-19

US-09-816-028A-19

US-09-816-028A-19

US-09-708-427-68B23

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US-09-708-427-68B23
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Maximum Match 100%
Listing first 45 summaries
                                                                                          OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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41
1 SNTFINNA 8
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Maximum DB seq length: 200000000
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Match Length
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Perfect score:
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Sequence 68822, A Sequence 22561, A Sequence 68821, A Sequence 17255, A Sequence 13111, A Sequence 2, Appl1 Sequence 2, Appl1 Sequence 2, Appl1 Sequence 23, Appl Sequence 11, Appl	ENTS AND CORRESPONDING POLYPEPTID	Length 143; 1; Indels 0; Gaps 0;
US-09-708-427-68822 US-09-708-427-68821 US-09-708-427-1255 US-09-708-427-12550 US-09-708-427-12550 US-09-815-242-13111 US-09-940-037A-2 US-09-940-037A-2 US-09-940-037A-2 US-09-855-309-2 US-09-855-309-2 US-09-779-679-61 US-09-779-679-61 US-09-779-679-61 US-09-779-679-61 US-09-86-055-11 US-09-800-321A-18 US-09-800-321A-18 US-09-800-321A-10 US-09-800-321A-10 US-09-800-321A-10 US-09-800-321A-10	ALIGNMENTS 15/09708427 al. c-DETERMINED DNA FRACMENTS (05/09/708,427 11-09 3.1 any amino acid any amino acid eq. ID 1959859	Score 31; DB 5; Pred. No. 26; 0; Mismatches 1
28 68.3 208 5 28 68.3 208 5 28 68.3 244 5 28 68.3 244 5 28 68.3 244 5 28 68.3 244 5 28 68.3 292 5 28 68.3 292 5 28 68.3 311 5 28 68.3 314 5	pplication (bxx) EXANDROV et CON: SEQUENCI ON: THEREBY 2070-1143 PP TON NUMBER: ATE: 2000-1 NOS: 85364 In Version in the control of the contr	h Similarity 85.7%; 6; Conservative
7222 7222 7222 7223 7234 7444 7544 7544 7544 7544 7544 7544 75	RESULT 1 17-76264  Sequence 76264, Appl GENERAL INFORMATION: APPLICANT: N. ALEXA: TITLE OF INVENTION: FILE REFERENCE: 275 CURRENT APPLICATION: FILE REFERENCE: 275 CURRENT FILLING DATE: NUMBER OF SEQ ID NO 5264 LENGTH: 143 TYPE: PRT COGATION: 1143 COCATION: 1143 COCATION: 1143 COCATION: 1143 COCATION: 1143 COCATION: 1143 COCATION: 1143	Query Match Best Local Matches

us-09-763-397a-14.rapn

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Sequence 54645. Application US/09708427

GENERAL INFORMATION:
APPLICANT: N. ALEXANDROV et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID
TITLE OF INVENTION: THEREBY
FILE REFERENCE: 2750-1243P
CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SSQ ID NO 54645
LENGTH: 343
                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: N. ALEXANDROV et al.

APPLICANT: N. ALEXANDROV et al.

TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID

TITLE OF INVENTION: THEREBY
FILE REFERENCE: 2750-1243P

CURRENT APPLICATION NUMBER: US/09/708,427

CURRENT FILING DATE: 2000-11-09

NUMBER OF SEQ ID NOS: 85364

SOFTWARE: Patentin version 3.1

SEQ ID NO 54646

LENGTH: 329
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64;
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Pred. No. 53;
0; Mismatches
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Pred. No. 64;
3; Mismatches
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NAME/KEY: misc_feature
LOCATION: 1..343
OTHER INFORMATION: Xaa is any amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 54646, Application US/09708427 GENERAL INFORMATION:
; NAME/KEY: misc_feature
; LOCATION: 1..275
; OTHER INFORMATION: Xaa is any am;
; NAME/KEY: misc_feature
; LOCATION: 1..275
; COTHER INFORMATION: Ceres Seq. II.
US-09-620-394B-4936
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85.7%;
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Best Local Similarity 62.5
Matches 5; Conservative
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Best Local Similarity 85.7
Matches 6; Conservative
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Sequence 4936. Application US/09620394B
Sequence 4936. Application:
Sequence 4936. Application:
Sequence 4936. Application:
APPLICANT: ALEXANDROV, Nickolai
APPLICANT: BROVER, Vyachealav
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
TITLE OF INVENTION: Thereby
FILE REFERENCE: 2750-1067P
CURRENT APPLICATION NUMBER: US/09/620,394B
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 9131
SEQ ID NO 4936
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: N. ALEXANDROV et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: THEREBY
FILE REFERENCE: 2750-1243P
FILE REFERENCE: 2750-1243P
CURRENT APPLICATION WIMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SCOFTWARE: Patentin version 3.1
SEQ ID NO 75262
LENGTH: 190
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Pred. No. 35;
0; Mismatches
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US-09-708-427-76262
                                                                      NAME/KEY: misc_feature
| LOCATION: 1...152
| OTHER INFORMATION: Xaa is any amino acid
| NAME/KEY: misc_feature
| LOCATION: 1...152
| OTHER INFORMATION: Ceres Seq. ID 1959858
| US-09-708-427-76263
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ORGANISM: Arabidopsis thaliana
FEATURE:
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LOCATION: 1..190
OTHER INFORMATION: Xaa is any
                                 ORGANISM: Arabidopsis thaliana
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85.7%;
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Best Local Similarity 85.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                               6; Conservative
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LOCATION: 1..190
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Best Local Similarity
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66 NLFINNA 72
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Sequence 41, Application US/10005368

Sequence 41, Application US/10005368

Sequence 41, Application US/10005368

GENERAL INFORMATION:
TITLE OF INVENTION: SHERMP WHITE SPOT BACILLIFORM VIRUS (WSBV), DISCOVERY
TITLE OF INVENTION: SYSTEMS CONTAINING THIS SEQUENCE AND DETECTION KITS AND
TITLE OF INVENTION: OUTBREAK AND SPREAD
FILLE REPRENCE: CLO000895

FILLE REPRENCE: CLO000895

CURRENT APPLICATION NUMBER: US/10/005,368

CURRENT FILING DATE: 2001-12-07

PRIOR APPLICATION NUMBER: PCT/US00/28888

PRIOR APPLICATION NUMBER: PCT/US00/28888

PRIOR FILING DATE: 2000-11-08
                                                                                                                                                                                                                                                                           Sequence 2, Application US/09881165
GENERAL INFORMATION:
APPLICANT: HOOD, ELIZABETH
APPLICANT: HOWARD, JOHN
APPLICANT: HOWARD, JOHN
APPLICANT: GASTEL, FRANS VAN
APPLICANT: WARD, MICHAEL
CHERENEROR: 1003AR
TITLE OF INVENTION: ENZYMES PRODUCED IN PLANTS
TITLE OF INVENTION: ENZYMES PRODUCED
CURRENT APPLICATION NUMBER: US/09/881,165
CURRENT FILING DATE: 2000-06-15
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PATENT OF ALCHIN VET. 2.1
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Pred. No. 74;
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Pred. No. 1e+02;
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 41
LENGTH: 621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        75.6%;
                                                           Query Match 75.6
Best Local Similarity 85.7
Matches 6; Conservative
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US-09-881-165-2
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Best Local Similarity
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335 TNFFINNA 342
                                                                                                                                                                                171 SNDFINN 177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; ORGANISM: SHRIMP
US-10-005-368-41
                                                                                                                                            1 SNTFINN 7
  US-09-620-394B-4934
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US-09-881-165-2
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                                                                                                                                                                                                                                                                                                                                           Sequence 4935, Application US/09620394B
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai
APPLICANT: BROVER, Vyacheslav
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
TITLE OF INVENTION: Thereby
FILE REPERBNCE: 2750-1067P
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 9131
SEQ ID NO 4935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 4934, Application US/09620394B
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: ALEXANDROW, Nickolai
APPLICANT: ALEXANDROW, Vacheslav
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
TITLE OF INVENTION: Thereby
FILE REFERENCE: 2750-1067P
CURRENT APPLICATION NUMBER: US/09/620,394B
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 9131
SEG OF DO 4934
LENGTH: 374
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                                                                                                                        Length 343;
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Pred. No. 72;
0; Mismatches 1; Indels
                                                                                                                                                                 0; Indels
                                                                                                                      Score 31; DB 5;
Pred. No. 67;
                                                                                                                                                               3; Mismatches
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LOCATION: 1..366
OTHER INFORMATION: Xaa is any amino acid
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CATTON: 1.366
COTHER INFORMATION: Ceres Seq. ID 1393686
US-09-620-3948-4935
; NAME/KEY: misc_feature
; LOCATION: 1..343
; OTHER INFORMATION: Ceres Seq. ID 1933687
US-09-708-427-54645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: Xaa is any amino acid
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ORGANISM: Arabidopsis thallana
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                                                                                                                      75.6%;
62.5%;
                                                                                                 Query Match
Best Local Similarity 62...
Best Conservative
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Best Local Similarity 85.7-
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LOCATION: 1..374
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LOCATION: 1..374
                                                                                                                                                                                                                              325 SSSFVNNA 332
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US-09-620-394B-4935
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US-09-620-394B-4934
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GENERAL 19896

(US-09-708-427-19896

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FILE REFERENCE: 109272.147
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Pred. No. 1.7e+02;
1; Mismatches 0;
           Mismatches
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CURRENT FILING DATE: 2001-03-07
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: LOCATION: 1..518

: OTHER INFORMATION: Ceres Seq. ID 1836874

US-09-708-427-19896
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 284, Application US/09801368 GENERAL INFORMATION:
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ORGANISM: Saccharomyces cerevisiae
           1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Arabidopsis thaliana
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SOFTWARE: PatentIn version 3.0
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APPLICANT: Cali, Brian
APPLICANT: Hecht, Peter
APPLICANT: Hockram, Doug
APPLICANT: Madden, Kevin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
           5; Conservative
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Salama, Sofie
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Silva, Jeff
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Summers, Eric
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Royer, John
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Milne, Todd
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Matches 5; Conserv
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| 308 TFVNNA 313
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292 TFVNNA 297
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                                                                 3 TFINNA 8
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LENGTH: 518
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APPLICANT:
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              Matches
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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: THEREBY
FILE REPERENCE: 2750-1243P
CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: Patentin version 3.1
SEQ ID NO 19897
                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES TITLE OF INVENTION: THEREBY FILE REFERENCE: 2750-1243P CURRENT APPLICATION NUMBER: US/09/708,427 CURRENT FILING DATE: 2000-11-09 NUMBER OF SEQ ID NOS: 85364 SOFTWARE: PALENTIN VERSION 3.1 SEQ ID NO 19898
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                                         Score 31; DB 6; Length 621;
Pred. No. 1.3e+02;
2; Mismatches 0; Indels
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Pred. No. 1.6e+02;
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Pred. No. 1.4e+02;
1; Mismatches 0
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LOCATION: 1..502
OTHER INFORMATION: Xaa is any amino acid
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; OTHER INFORMATION: Ceres Seq. ID 1836876
US-09-708-427-19898
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LOCATION: 1..449
OTHER INFORMATION: Xaa is any amino acid
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LOCATION: 1.502
CTHER INFORMATION: Ceres Seq.
US-09-708-427-19897
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83.38;
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                                               75.68;
71.48;
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                                                     Query Match 75.6
Best Local Similarity 71.4
Matches 5; Conservative
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Matches 5; Conserv
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263 SSTFVNN 269
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239 TFVNNA 244
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US-09-708-427-19898
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US-09-801-368-284

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APPLICANT: Sherman, Amir APPLICANT: Sherman, Amir APPLICANT: Silva, Jeff APPLICANT: Silva, Jeff APPLICANT: Silva, Jeff APPLICANT: Silva, Jeff APPLICANT: Summers, Eric APPLICANT: Summers, Eric APPLICANT: Summers, Eric Silva, Jeff APPLICANT: Summers, Eric Content APPLICANTION: In Fungi TITLE OF INVENTION: In Fungi CURRENT APPLICATION NUMBER: US/09/487,558 CURRENT FILING DATE: 2000-01-19 PRIOR APPLICATION NUMBER: US 09/487,558 PRIOR APPLICATION NUMBER: US 09/487,558 PRIOR APPLICATION NUMBER: US 09/487,558 PRIOR FILING DATE: 2000-01-19 PRIOR FILING DATE: 1999-10-20 SOFTWARE: PARCHING DATE: 1999-10-20 SO
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0
73.2%; Score 30; DB 5; Length 979; 83.3%; Pred. No. 3.4e+02; ive 1; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                 RESULT 15
US-09-487-558-284
Sequence 284, Application US/09487558
GENERAL INFORMATION:
APPLICANT: Busby, Robert
APPLICANT: Call, Brian
APPLICANT: Holtzman, Doug
APPLICANT: Madden, Kevin
Madden, Kevin
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; ORGANISM: Saccharomyces cerevisiae
US-09-487-558-284
Query Match 73.2
Best Local Similarity 83.3
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Salama, Sofie
                                                                                                                                                                                                                         1 SNTFIN 6
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Search completed: January 29, 2002, 10:58:14 Job time: 2510 sec

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January 29, 2002, 10:56:05; Search time 1760.55 Seconds (without alignments) 2.681 Million cell updates/sec
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1: /cgn2_6/ptodata/2/paa/PCTUS_COMB.pep:*
2: /cgn2_6/ptodata/2/paa/PCTUS_COMB.pep:*
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16: /cgn2_6/ptodata/2/paa/USOB_COMB.pep:*
17: /cgn2_6/ptodata/2/paa/USOB_COMB.pep:*
18: /cgn2_6/ptodata/2/paa/USOB_COMB.pep:*
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3148936 seqs, 277657034 residues
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Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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88
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Scoring table:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence:
                                                                                                                                                                                                                                                                       Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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tesult Query No. Score Match Length DB ID Description

No. Score Match Length DB ID Description

1 88 100.0 350 21 US-09-763-397A-13 Sequence 13, Appl 3 US-07-10-000-8 Sequence 2, Appl 3 US-09-710-000-8 Sequence 2, Appl 5 US-09-710-000-8 Sequence 8, Appl 5 US-09-785-768A-2 Sequence 4, Appl 6 US-08 100.0 394 3 US-07-867-768A-4 Sequence 4, Appl 1 US-08-195-705-4 Sequence 2, Appl 1 US-08-195-705-4 Sequence 3, Appl 1 US-09-500-376-2 Sequence 3, Appl 1 US-09-500-376-2 Sequence 3, Appl 1 US-09-500-376-2 Sequence 3, Appl 1 US-08-196-706-3 Sequence 3, Appl 1 US-08-196-106-3 Sequence 3, Appl 1 US-08-196-3 Sequence 3
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Sequence 16, Appl Sequence 37685, A		336,	4	1214	476,	105			Sequence 8267, Ap	Sequence 397, App	Sequence 18213, A	Sequence 13, Appl	Sequence 15, Appl	Sequence 21, Appl	Seguence 21, Appl	m		24041	Sequence 30547, A		7,	Sequence 14, Appl	109			5117,		ഗ	1129	Sequence 5725, Ap		Sequence 53411, A	Sequence 801, App	Sequence 45489, A
9 US-09-500-376-16 8 US-09-417-507-37685	US-09-758-458	US-09-948-933-33	US-60-141-856	US-60-230-445-12	US-60-207			4 US-60-191-637-10565				0 US-09-686-015-13	Д	а				US-60-173-464	US-60-191-637-3054	US-60-191-681			ns-0	0			US-09-758-472-7					1 PCT-US01-08631-53411	US-60-248-505-8	PCT-US01-08631-45489
	189 2																				14 1											308 1		489 1
100.0	51.1	51.1	51.1	51.1	51.1	51.1	51.1	51.1	51.1	50.0	50.0	50.0	50.0	50.0	50.0	48.9	48.9	48.9	48.9	48.9	47.7	47.7	47.7	47.7	47.7	47.7	47.7	47.7	47.7	47.7	47.7	47.7	47.7	47.7
88 48	45	45	45	45	45	45	45	45	45	44	44	44	44	44	44	43	43	43	43	43	42	42	42	42	42	42	42	42	42	42	42	42	42	42
10	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT:
APPLICATION NUMBER:
US/09/763,397A
CURRENT APPLICATION NUMBER:
DEFENSION
FRIOR APPLICATION NUMBER:
PRIOR APPLICANTION NUMBER:
PRIOR APPLICATION NUMBER:
PRIO
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Gaps

; 0

Length 17; Indels

Ouery Match 100.0%; Score 88; DB 21; Best Local Similarity 100.0%; Pred. No. 3.9e-07; Matches 17; Conservative 0; Mismatches 0;

1 GISYYEKVLAKYKDDLE 17

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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:

ZIP: 10111
COMPUTER 10111
COMPUTER FLOPPY disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARB: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
THE DATE: 19920413
                                                                                                                                                                                            APPLICANT: Chang, Sandra
APPLICANT: Chang, Seorge
APPLICANT: Hui, George
APPLICANT: Barr, Philip
TITLE OF INVENTION: BACULOVIRUS PRODUCED PLASMODIUM
TITLE OF INVENTION: FALCIPARUM VACCINE
OWNERS OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 88; DB 3; 100.0%; Pred. No. 1.9e-05; Live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Plasmodium falciparum
STRAIN: falciparum uganda palo alto (FUP)
US-07-867-768A-2
                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Davis Hoxie Faithfull Hapgood
STREET: 45 Rockefeller Pl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11880A3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 5
US-07-867-768A-4
; Sequence 4, Application US/07867768A
; GENERAL INFORMATION:
APPLICANT: Chang, Sandra
appLICANT: Hui, George
                                                                                                                                                  Sequence 2, Application US/07867768A GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-757-2200
TELEFAX: 212-586-1461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        32140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Jacobs, Seth H
REGISTRATION NUMBER: 321
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C-terminal
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Gibson, Helen
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                          119 GISYYEKVLAKYKDDLE 135
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Best Local Similarity 100.
Matches 17; Conservative
    1 GISYYEKVLAKYKDDLE 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
                                                                                                                                                                                                                                                                                                                                                                                                                       New York
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APPLICANT:
                                                                                                                                    US-07-867-768A-2
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STATE:
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                                                                                                                                               APPLICANT: The Government of the United States of America, as represented by the APPLICANT: The Government of the Department of Health and Human Services. Centers for Dis APPLICANT: Secretary of the Department of Health and Human Services. Centers for Dis APPLICANT: Lal, Altaf A.

APPLICANT: Lal, Altaf A.

APPLICANT: Ping Shi, Ya

APPLICANT: Hasnain, Seyed E.

TITLE OF INVENTION Recombinant Multivalent Malarial Vaccine Against Plasmodium Falci

FILE REFERENCE: 6395-57049

CURRENT FILING DATE: 1998-08-19

PRIOR PELICATION NUMBER: DS 60/097,703

PRIOR APPLICATION NUMBER: PCT / US99/18869

PRIOR APPLICATION NUMBER: PCT / US99/18869

NUMBER OF SEQ ID NOS: 26

SOUTHARE: Patentin Version 3.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: amino acid sequence of PfMSP-142 0S\!-\!09\!-\!710\!-\!000\!-\!8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.0%; Pred. No. 1.7e-05;
Matches 17; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 100.0\$; \  \, Score \ 88; \  \, DB \ 21; Best Local Similarity 100.0\$; \  \, Pred. \ No. \ 1.6e-05; Matches 17; \  \, Conservative \  \  \, 0; \  \, Mismatches \  \  \, 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Hui, George, S.N.
APPLICANT: Hoi, Malter K.K.
APPLICANT: Lap-Yin, Pang
TITLE OF INVENTION: Malaria Vaccine
FILE REFERENCE: 23461-2001100
CURRENT APPLICATION NUMBER: US/09/710,000
CURRENT FILING DATE: 2000-11-10
PRIOR PELICATION NUMBER: 60/226,861
PRIOR FILING DATE: 1999-11-12
PRIOR APPLICATION NUMBER: 60/168,327
PRIOR APPLICATION NUMBER: 60/168,327
PRIOR APPLICATION NUMBER: 60/168,327
PRIOR FILING DATE: 1999-11-12
PRIOR FILING DATE: 1999-12-11
NUMBER OF SEQ ID NOS: 11
SOUTHWARE: FASTEEQ for Windows Version 4.0
SEQ ID NO 8
LEWGHH: 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Recombinant DNA/Protein
US-09-763-397A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 8, Application US/09710000
; GENERAL INFORMATION:
; APPLICANT: Hui, George, S.N.
                                                                                                                       Sequence 2, Application US/09763397A GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       334 GISYYEKVLAKYKDDLE 350
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1 GISYYEKVLAKYKDDLE 17
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ORGANISM: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-710-000-8
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 4. Application US/08195705
GENERAL INFORMATION:
APPLICANT: Chang, Sandra
APPLICANT: Hui, George
APPLICANT: Hui, George
APPLICANT: Gibson, Helen
TITLE OF INVENTION: BACULOVIRUS PRODUCED PLASMODIUM
TITLE OF INVENTION: FALCIPARUM VACCINE
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSE: Davis Hoxie Faithfull Hapgood
STREET: 45 Rockefeller Pl.
CITY: New York
STATE: N.Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 14-FEB-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Score 88; DB 5; ; Pred. No. 1.9e-05; 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Plasmodium falciparum
STRAIN: falciparum uganda palo alto (FUP)
                    MBER: US/08/195,705
14-FEB-1994
                                                                               ATTORNET/AGENT INFORMATION:
NAME: Jacobs, Seth H
REGISTRATION NUMBER: 3140
REFERENCE/DOCKET NUMBER: 1188
TELECOMUNICATION INFORMATION:
TELERAN: 212-57-220
TELERAN: 212-56-1461
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 394 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 1186
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-757-2200
TELEFAX: 212-586-1461
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 394 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY AGENT INFORMATION:
NAME: Jacobs, Seth H
REGISTRATION NUMBER: 32140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 17; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                      ANTI-SENSE: NO
FRAGMENT TYPE: C-terminal
ORIGINAL SOURCE:
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MOLECULE TYPE: peptide
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
                      APPLICATION NUMBER:
FILING DATE: 14-FEI
CLASSIFICATION: 439
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US-08-195-705-2
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US-08-195-705-4
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GENERAL INFORMATION:
APPLICANT: Chang, Sandra
APPLICANT: Glang, Sandra
APPLICANT: Glason, Helen
TITLE OF INVENTION: BACULOVIRUS PRODUCED PLASMODIUM
TITLE OF INVENTION: FALCIPARUM VACCINE
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Davis Hoxie Faithfull Hapgood
STREET: 45 Rockefeller Pl.
CITY: New York
STATE: N.Y.
COUNTRY: USA
                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/867,768A
FILING DATE: 199204.3
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Jacobs, Seth H
RECISTRATION NUMBER: 11880A3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-757-2200
TELEPHONE: 212-757-2200
TELEPAX: 212-586-1461
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
TITLE OF INVENTION: BACULOVIRUS PRODUCED PLASMODIUM TITLE OF INVENTION: FALCIPARUM VACCINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                    ADDRESSEE: Davis Hoxie Faithfull Hapgood
STREET: 45 Rockefeller Pl.
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ) ORGANISM: Plasmodium falciparum
; STRAIN: MAD
US-07-867-7688-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 394 amino acids
TYPE: AMINO ACID
STRANDEDNESS: Single
TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HYPOTHETICAL: NO FRAGMENT TYPE: C-terminal ORIGINAL SOURCE:
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Best Local Similarity 100.
Matches 17; Conservative
                                         NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-195-705-2
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RESULT 11
US-09-417-507-37685
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US-09-758-458-380
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US-09-500-376-16
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LENGTH: 402
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Sequence 3, Application US/09500376
GENERAL INFORMATION:
APPLICANT: University of Hawaii
TITLE OF INVENTION: Baculovirus Produced Plasmodium Falciparum Vaccine
FILE REFERENCE: A-67984
CURRENT APPLICATION NUMBER: US/09/500,376
CURRENT FILING DATE: 2000-02-08
PRIOR FILING DATE: 1994-02-14
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Patentin version 3.1
SEQ ID NO 3
LENGIN: 394
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APPLICANT: University of Hawaii
TITLE OF INVENTION: Baculovirus Produced Plasmodium Falciparum Vaccine
FILE REFERENCE: A-67984
CURRENT APPLICATION NUMBER: US/09/500,376
CURRENT FILING DATE: 2000-02-08
PRIOR APPLICATION NUMBER: US 08/195,705
PRIOR APPLICATION NUMBER: US 08/195,705
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Patentin version 3.1
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Pred. No. 1.9e-05;
; Mismatches 0; Indels
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                                                                                                                                                                                                                                             0; Mismatches
                                                                HYPOTHETICAL: NO FRAGMENT TYPE: C-terminal ORIGINAL SOURCE: ORIGINAL SOURCE: ORGANISM: Plasmodium falciparum
                                                                                                                                                                                                                                                                                                                                                                                    US-09-500-376-2; Sequence 2, Application US/09500376; GENERAL INFORMATION:
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; ORGANISM: plasmodium falciparum
US-09-500-376-2
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                                                                                                                                                                                                        100.0%;
ilarity 100.0%;
Conservative 0
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Best Local Similarity 100.
Matches 17; Conservative
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              STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 17; Conserva
amino acid
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Best Local Similarity
Matches 17; Conserv
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US-09-500-376-3
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US-08-195-705-4
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LOCATION: (531)
CTHER INFORMATION: Identity of amino acid sequences at the above locations are un
US-09-417-507-37685
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Sequence 37685, Application US/09417507
GENERAL INFORMATION:
APPLICANT: KEITH G. WEINSTOCK ET AL.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ASPERGILLUS;
TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS
FILE REPERENCE: PATH99-10
CURRENT APPLICATION NUMBER: US/09/417,507
CURRENT FILING DATE: 1999-10-14
SEQ ID NO 37685
LENGTH: 725
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                                                                                                                                                                                                   APPLICANT: University of Hawaii
APPLICANT: University of Hawaii
TITLE OF INVENTION: Baculovirus Produced Plasmodium Falciparum Vaccine
FILE REFERENCE: A-679484
CURRENT APPLICATION UNMBER: US/09/500,376
CURRENT FILING DATE: 2000-02-08
PRIOR PAPLICATION NUMBER: US 08/195,705
PRIOR FILING DATE: 1994-02-14
NUMBER OF SECIED NOS: 16
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GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PM041
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 88; DB.19;
100.0%; Pred. No. 1.9e-05;
tive 0; Mismatches 0;
                                                                                                                                                              ; Sequence 16, Application US/09500376; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: plasmodium falciparum US-09-500-376-16
                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn version 3.1
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Best Local Similarity 75.0
Matches 9; Conservative
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1 GISYYEKVLAKYKDDLE 17
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170 YEEEFAKYKDDL 181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 17; Conserv
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Sequence 469, Application US/60141856
                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Drosophila
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-60-230-445-1214
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Sequence 336, Application US/09948933
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: WITH CARDIOVASCULAR DISEASE AND LIPID DISORDERS, METHODS OF
TITLE OF INVENTION: WITH CARDIOVASCULAR DISEASE AND LIPID DISORDERS, METHODS OF
TITLE OF INVENTION: WITH CARDIOVASCULAR DISEASE AND LIPID DISORDERS, METHODS OF
TITLE OF INVENTION: DETECTION AND USES THEREOF
FILE REFERENCE: CL000787
CURRENT PAPLICATION NUMBER: US/09/948,933
CURRENT PAPLICATION NUMBER: 60/231,399
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 6404
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 336
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                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: SITE
LOCATION: (96)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (113)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                    LOCATION: (28).
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids NAME/KEY: SITE
LOCATION: (60)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: (114)
COTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-09-758-458-380
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Pred. No. 69;
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Pred. No. 1.8e+02;
7; Mismatches 3; Indels
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CURRENT APPLICATION NUMBER: US/09/758,458;
CURRENT FILING DATE: 2001-01-11
SPIGN APPLICATION NUMBER: 60/179,065
PRIOR APPLICATION NUMBER: 60/180,628
PRIOR APPLICATION NUMBER: 60/180,628
NUMBER OF SEQ ID NOS: 520
SOFTWARE: PatentIn Ver: 2.0
SEQ ID NO 380
LENGTH: 189
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41.2%;
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Best Local Similarity 41.2%;
Matches 7; Conservative
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68 GIDYYDRNLALFEEELD 84
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Best Local Similarity 41.2
Matches 7; Conservative
                                                                                                                                                                                                                                                       ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: Human
US-09-948-933-336
                                                                                                                                                                                                                                                                                                    NAME/KEY: SITE
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RESULT 14 US-60-141-856-469

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US-GO-230-445-1214
US-GO-230-445-1214
US-GO-230-445-1214
Sequence 1214, Application US/60230445
Sequence 1214, Application US/60230445
Sequence 1214, Application US/60230445
Sequence 1214, Application US/60230445
TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: AND USES THEREOF
CURRENT APPLICATION NUMBER: US/60/230,445
CURRENT FILING DATE: 2000-09-06
NUMBER OF SEQ ID NOS: 3051
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1214
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APPLICANT: Kerlavage, Anthony
TITLE OF INVENTION: ISOLATED KINASE PROTEINS, NUCLEIC ACID
TITLE OF INVENTION: ISOLATED KINASE PROTEINS, AND USES THEREOF
FILE REFERENCE: CLO00044
CURRENT PAPLICATION NUMBER: US/60/141,856
CURRENT PILING DATE: 1999-07-01
NUMBER OF SEQ ID NOS: 617
SEQ ID NOS 617
SEQ ID NO 469
LENGTH: 498
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Pred. No. 2.3e+02;
1; Mismatches 5; Indels
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COCATION: (1)...(498)
COTHER INFORMATION: Xaa = Any Amino Acid
US-60-141-856-469
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60.0%;
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41.2%;
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58 GIDYYDRNLALFEEELD 74
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Best Local Similarity 41.2
Matches 7; Conservative
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Best Local Similarity 60.0
Matches 9; Conservative
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APPLICANT: Anantharamaiah, Gattadahalli
APPLICANT: Navab, Mohamad
TITLE OF INVENTION: Orally Administered Peptides to Ameliorate Atherosclerosis
FILE REFERENCE: 407T-911200US
CURRENT APPLICATION NUMBER: US/09/645,454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 32, Application US/09645454 GENERAL INFORMATION:
APPLICANT: Fogelman, Alan
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US-09-978-756-3
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LENGTH: 394
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14, Appl
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51279, A
51278, A
51278, A
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5.144 Million cell updates/sec
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                                                                                                                                               Search time 120.95 Seconds
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cgn2_6/ptcdata/2/paa/NSO6_NEW_COMB.pep:*
/cgn2_6/ptcdata/2/paa/USO1_NEW_COMB.pep:*
/cgn2_6/ptcdata/2/paa/USO9_NEW_COMB.pep:*
/cgn2_6/ptcdata/2/paa/USO9_NEW_COMB.pep:*
/cgn2_6/ptcdata/2/paa/USO9_NEW_COMB.pep:*
/cgn2_6/ptcdata/2/paa/USO0_NEW_COMB.pep:*
version 4.5
- 2000 Compugen Ltd.
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US-09-645-454-32

US-09-708-427-51280

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US-09-708-427-51279

US-09-978-427-51279

US-09-978-427-51279

US-09-978-427-51279

US-09-978-427-51279

US-09-9117-4158-22

US-09-117-4158-22

US-09-117-4158-16

US-09-117-4158-16

US-09-117-4158-16

US-09-117-4158-16

US-09-269-874A-7

US-09-269-874A-7

US-09-269-874A-7

US-09-620-3948-2020

US-09-620-3948-2020

US-09-966-521-70

US-09-961-521-20

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US-09-811-242-5459
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US-09-897-516-7123
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Maximum Match 100%
Listing first 45 summaries
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GenCore
(c) 1993
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Maximum DB
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Sequence 5251, Ap Sequence 12141, A Sequence 6164, Ap Sequence 11298, A Sequence 11266, A Sequence 10298, A Sequence 10440, A Sequence 10438, A Sequence 12720, A Sequence 12719, A Sequence 12719, A Sequence 11534, A Sequence 11332, A Sequence 13322, A Sequence 13322, A Sequence 13332, A Sequence 133
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Pred. No. 4e-06;
Mismatches 0;
                       US-09-815-242-12141

US-09-897-516-6564

US-09-815-242-11476

US-09-708-427-10298

US-09-708-427-10298

US-09-708-427-10440

US-09-708-427-10430

US-09-708-427-10430

US-09-708-427-10430

US-09-708-427-10430

US-09-708-427-10430

US-09-708-427-10430

US-09-708-427-12744

US-09-708-427-12744

US-09-708-427-13244

US-09-613-0928-2

US-09-815-242-115340

US-09-815-242-115360
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US-09-815-242-11534
US-09-815-242-13392
US-09-708-427-32718
US-09-815-242-10270
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GENERAL INFORMATION
GENERAL INFORMATION
APPLICANT: Bliddail, Berry
APPLICANT: Bliddail, Berry
APPLICANT: Feeney, James
APPLICANT: Morgan, William
APPLICANT: Syed, Shabih
TITLE OF INVENTION: Malaria Vaccine
FILE REFERENCE: 18396/1005
CURRENT APPLICATION NUMBER: US/09/978,756
CURRENT FILING DATE: 2001-10-16
PRIOR APPLICATION NUMBER: 097/GB00/01558
PRIOR FILING DATE: 2000-4-20
PRIOR FILING DATE: 1999-05-13
PRIOR FILING DATE: 1999-05-25
PRIOR FILING DATE: 1999-05-25
PRIOR FILING DATE: 1999-05-25
PRIOR FILING DATE: 1999-05-25
PRIOR FILING DATE: 1999-04-20
NUMBER OF SEQ ID NOS: 3
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US-09-978-756-3
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Best Local Similarity 100.0%;
Matches 17; Conservative 0,
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Sequence 51278, Application US/09708427

SEQUENCE 51278, Application US/09708427

SEQUENCE 51278, APPLICANT:

APPLICANT:

APPLICANT:

TITLE OF INVENTION:

FILE REFERENCE: 2750-1243P

CURRENT APPLICATION UNMERS: US/09/708,427

CURRENT FILING DATE: 2000-11-09

NUMBER OF SEQ ID NOS: 85364

SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 51279, Application US/09708427
Sequence 51279, Application US/09708427
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID
TITLE OF INVENTION: THEREBY
TITLE OF INVENTION: THEREBY
TITLE REPERENCE: 2750-1249
CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SEQ ID NO 51279
LENGTH: 293
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Pred. No. 33;
1; Mismatches
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COTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc_feature
LOCATION: 1..293
COTHER INFORMATION: Ceres Seq. ID 1926458
US-09-708-427-51279
                                                                                                                                                                                                                     NAME/KEY: misc_feature

// LOCATION: 1..280

// OTHER INFORMATION: Ceres Seq. ID 1926459

08-09-708-427-51280
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2000-11-09
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                NUMBER OF SEQ ID NOS: 85364
SOFTWARE: PatentIn version 3.1
SEQ ID NO 51280
IENGTH: 280
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                        47.78;
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Best Local Similarity 58.3
Matches 7; Conservative
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Best Local Similarity 50...
7; Conservative
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FEATURE:
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278 EQIKAKFKDDLD 289
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LOCATION: 1..280
OTHER INFORMATION: Xaa
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265 EQIKAKFKDDLD 276
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  CURRENT FILING DATE:
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US-09-708-427-51278
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US-09-708-427-51279
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TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: THEREBY
FILE REFERENCE: 2750-1243P
CURRENT APPLICATION NUMBER: US/09/708,427
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Sequence 14, Application US/09645454

Sequence 14, Application US/09645454

Sequence 14, Application US/09645454

GENERAL INFORMATION:
APPLICANT: Anantharamaiah, Gattadahalli
APPLICANT: Navab, Mohamad

TITLE OF INVENTION: Orally Administered Peptides to Ameliorate Atherosclerosis
FILE REFERENCE: 4077-911200US

CURRENT APPLICATION NUMBER: US/09/645,454

CURRENT FILIO DATE: 2000-08-24

NUMBER OF SEQ ID NOS: 39

SOFTWARE: PatentIn version 3.0

SEQ ID NO 14
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                                                                                                                                                                                                                                                                                                                                                                   Length 14;
                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 42; DB 5;
Pred. No. 1.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: synthetic peptide
NAME/KEY: misc_feature
LOCATION: (1)..(1)
OTHER INFORMATION: E is blocked with an acetyl
NAME/KEY: misc_feature
LOCATION: (18)..(18)
OTHER INFORMATION: F is blocked with an amide
US-09-645-454-14
                                                                                                                                                                                                                                                                                                                                                                 Score 42; DB 5;
Pred. No. 1.1;
3; Mismatches
                                                                                                                                                                                                                         CTHER INFORMATION: L is blocked with an acetyl NAME/KEY: misc_feature LOCATION: (14)...(14)
COCATION: (14)...(14)
USCAPION: (14)...(14)
US-09-645-454-32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 51280, Application US/09708427; GENERAL INFORMATION:
                                                                                                                                                                     OTHER INFORMATION: synthetic peptide NAME/KEY: misc_feature LOCATION: (1)...(1)
            2000-08-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               47.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Artificial Sequence
                             NUMBER OF SEQ ID NOS: 39
SOFTWARE: Patentin version 3.0
SEQ ID NO 32
LENGTH: 14
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                       47.7%;
                                                                                                                               ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 63.6
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     :||||| |:|:
6 FYEKVLEKFKE 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 YYEKVLAKYKD 14
                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 7; Conserv
              CURRENT FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-708-427-51280
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                                                                                                                                                  FEATURE:
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Gaps
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Yang, Shutong
TITLE OF INVENTION: Malaria Vaccine Based Upon the Addition
of a MSAl Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Henry D. Coleman, COLEMAN SUDOL SAPONE,
STREET: 714 Colorado Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 41; DB 5; Length 594;
Pred. No. 1.1e+02;
4; Mismatches 5; Indels
                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPad (ASCII)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/117,415B
FILING DATE: 29-Jul-1998
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
RAPLICATION NUMBER: US/09/117,415B
FILING DATE: 29-Jul-1998
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                  NAME: COleman, Henry D.
RECISTRATION NUMBER: 32.559
REFERENCE/DOCKET NUMBER: R12-030
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 679-0090
TELEFA: (212) 679-9121
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Coleman, Henry D.
REGISTRATION NUMBER: 32,559
REFERENCE/DOCKET NUMBER: R12-030
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 679-0090
TELEFAX: (212) 679-9121
INFORMATION FOR SEQ ID NO: 22:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPad (ASCII)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-117-415B-2
    STREET: 714 Colorado Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-117-415B-22; Sequence 22, Application US/09117415B; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 594 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              46.68;
                         CITY: Bridgeport
STATE: Connecticut
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Bridgeport
STATE: Connecticut
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match
Best Local Similarity 43.55
Local 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            338 LGYYKILSEKYKSDLD 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 ISYYEKVLAKYKDDLE 17
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APPLICANT: Davidson, Eugene
TITLE OF INVENTION: Malaria Vaccine Based Upon the Addition
of a MSAl Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: Henry D. Coleman, COLEMAN SUDOL SAPONE, PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 41; DB 5; Length 376;
Pred. No. 66;
4; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                               Score 42; DB 5; Length 306;
Pred. No. 37;
                                                                                                                                                                                                                                                                                                                                                           1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:

APPLICANT: Holder, Anthony
APPLICANT: Birdsall, Berry
APPLICANT: Birdsall, Berry
APPLICANT: Breasy, James
APPLICANT: Morgan, William
APPLICANT: Morgan, William
APPLICANT: Morgan, William
APPLICANT: Syed, Shabih
ITTLE OF INVENTION: Malaria Vaccine
FILE REFERENCE: 18396/1065
CURRENT APPLICATION NUMBER: CUT/CB00/01558
FRIOR FILING DATE: 2001-10-16
PRIOR APPLICATION NUMBER: 097/311,817
PRIOR FILING DATE: 2000-04-20
PRIOR FILING DATE: 1999-05-13
PRIOR FILING DATE: 1999-05-25
PRIOR FILING DATE: 1999-05-25
PRIOR FILING DATE: 1999-05-25
PRIOR FILING DATE: 1999-04-20
NUMBER OF SEQ ID NOS: 3
SOFTWARE: PATENTIN VETSION 3.0
                                                                                                                                                                                                                                                                                                                                                         4; Mismatches
                                                                                                       NAME/KEY: misc_feature
| LOCATION: 1..306
| COTHER INFORMATION: Xaa is any amino acid
| NAME/KEY: misc_feature
| LOCATION: 1..306
| COCATION: 1..306
| OTHER INFORMATION: Ceres Seq. ID 1926457
| US-09-708-427-51278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/09117415B GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Plasmodium falciparum US-09-978-756-2
                                                                ORGANISM: Zea mays subsp. mays
                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 58.3%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 43.8%;
Matches 7; Conservative
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120 LGYYKILSEKYKSDLD 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 ISYYEKVLAKYKDDLE 17
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291 EQIKAKFKDDLD 302
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SEQ ID NO 51278
LENGTH: 306
TYPE: PRT
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US-09-117-4158-2
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US-09-978-756-2
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APPLICANT: Davidson, Eugene
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Davidson, Eugene
TITLE OF INVENTION: Malaria Vaccine Based Upon the Addition
of a MSAl Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
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ADDRESSEE: Henry D. Coleman, COLEMAN SUDOL SAPONE,
STREET: 714 Colorado Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 41; DB 5; Length 631;
pred. No. 1.2e+02;
4; Mismatches 5; Indels
                                                                                                                                                                        Length 613;
                                                                                                                                                                                                           Indels
                                                                                                                                                                      Score 41; DB 5; Le. Pred. No. 1.1e+02; 4; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTECATION NUMBER: US/09/117,415B
FILING DATE: 29-Jul-1998
CLASSIFICATION: 435
ATTORNEY AGENT INFORMATION:
NAME: Coleman, Henry D.
REGISTRATION NUMBER: 32,559
REFERENCE/DOCKET NUMBER: 32,559
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPUTER:
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPad (ASCII)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE DESCRIPTION: SEQ ID NO: 18: US-09-117-415B-18
                                              ; TOPOLOGY: linear ; MOLECULE TYPE: protein ; SEQUENCE DESCRIPTION: SEQ ID NO: 22: US-09-117-415B-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 20, Application US/09117415B GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FELEPHONE: (212) 679-0090 FELEFAX: (212) 679-9121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 631 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 18: SEQUENCE CHARACTERISTICS:
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         SEQUENCE CHARACTERISTICS:
                                                                                                                                                                          46.68;
43.88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 10017
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: Connecticut COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 46.6
Best Local Similarity 43.8
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Bridgeport
                                            TYPE: amino acid
                                                                                                                                                                                                                                                                         375 LGYYKILSEKYKSDLD 390
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                                                                                                                                                                                                             Conservative
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Matches 7; Conserv
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US-09-117-415B-20
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                                                                                                                                                                            Query Match
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Gaps
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APPLICANT: DAILY EUGENE
Yang, Shutong
TITLE OF INVENTION: Malaria Vaccine Based Upon the Addition
of a MSAl Peptide
AFFLECT... Yang, Shutong
TITLE OF INVENTION: Malaria Vaccine Based Upon the Addition
of a MSAl Peptide
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ADDRESSE: Henry D. Coleman, COLEMAN SUDOL SAPONE,
STREET: 714 Colorado Avenue
CITY: Bridgeport
STATE: Connecticut
                                                                                                       Coleman, COLEMAN SUDOL SAPONE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 631;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 41; DB 5; Le
Pred. No. 1.2e+02;
4; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/117,415B
FILING DATE: 29-Jul-1998
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/09/117,415B
FILING DATE: 29-Jul-1998
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: R12-030 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WordPad (ASCII)
                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPad (ASCII)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TOPOLOGY: linear; SEQUENCE TYPE: protein; SEQUENCE DESCRIPTION: SEQ ID NO: 20: US-09-117-4158-20
                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Henry D. Coleman,
STREET: 714 Colorado Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Coleman, Henry D. REGISTRATION NUMBER: 32,559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 12
US-09-117-415B-16
; Sequence 16, Application US/09117415B
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (212) 679-0090
TELEFAX: (212) 679-9121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 631 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 20: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             46.68;
                                                                                                                                                  CITY: Bridgeport STATE: Connecticut
                                                                                                                                                                                                         ZIP: 10017
COMPUTER READABLE FORM:
                                                                     NUMBER OF SEQUENCES: 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 43.5.
..... 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 ISYYEKVLAKYKDDLE 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
                                                                                                                                                                                          COUNTRY: USA
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Score 41; DB 5; Length 1639;
Pred. No. 3.5e+02;
4; Mismatches 5; Indels
                                                                                                                                                         Score 41; DB 5; Length 1621;
Pred. No. 3.5e+02;
4; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Recombinant Process for Preparing a TITLE OF INVENTION: Complete Malaria Antigen, GP190/MSP1. FILE OF INVENTION: Complete Malaria Antigen, GP190/MSP1. FILE OF INVENTION: COMPLETE STORE-003

CURRENT APPLICATION NUMBER: US/09/269,874A

CURRENT FILING DATE: 1999-08-02

PRIOR PILING DATE: 1999-10-02

PRIOR FILING DATE: 1996-10-02

PRIOR FILING DATE: 1996-10-02

NUMBER: OF SEQ ID NOS: 8

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 3

LENGTH: 1639
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                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 3, Application US/09269874A GENERAL INFORMATION:
                                                 ; TYPE: PRT
; ORGANISM: Plasmodium falciparum
US-09-269-874A-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: Plasmodium falciparum
US-09-269-874A-3
                                                                                                                                                              46.6%;
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                                                                                                                                                                                                                                                                                    1383 LGYYKILSEKYKSDLD 1398
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1383 LGYYKILSEKYKSDLD 1398
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Best Local Similarity 43.8
Matches 7; Conservative
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Best Local Similarity 43.8
Matches 7; Conservative
                                                                                                                                                                                                                                                          2 ISYYEKVLAKYKDDLE 17
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US-09-269-874A-3
                            LENGTH: 1621
       SEQ ID NO 5
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GENERAL INFORMATION:
APPLICANT: Bujard, Hermann
TITLE OF INVENTION: Complete Malaria Antigen, GP190/MSP1
FILE REFERENCE: GRUE-003
CURRENT APPLICATION NUMBER: US/09/269,874A
CURRENT FILING DATE: 1999-08-02
PRIOR APPLICATION NUMBER: PCT/EP97/05441
PRIOR FILING DATE: 1997-10-02
PRIOR RELING DATE: 1997-10-02
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NOS: 4
TYPE: PRT
TYPE: PRT
TYPE: PRT
SEQ ID NOS: 8
SOFTWARE: PASTSEQ for Windows Version 4.0
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GENERAL INFORMATION:
APPLICANT: Buljard, Hermann
TITLE OF INVENTION: Recomblinant Process for Preparing a
TITLE OF INVENTION: Complete Malaria Antigen, GP190/MSP1
FILE REFERENCE: GRUE-003
CURRENT APPLICATION NUMBER: US/09/269,874A
CURRENT FILING DATE: 1999-08-02
PRIOR APPLICATION NUMBER: DET/EP97/05441
PRIOR APPLICATION NUMBER: DE 19640817.2
PRIOR FILING DATE: 1997-10-02
PRIOR FILING DATE: 1995-10-02
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 4.0
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Pred. No. 1.2e+02;
4; Mismatches 5; Indels
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Pred. No. 3.4e+02;
4; Mismatches 5; Indels
NAME: COleman, Henry D.
RECISTRATION NUMBER: 32,559
REFERENCE/DOCKET NUMBER: R12-030
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 679-0090
TELEFA: (212) 679-9121
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                        LENGTH: 649 amino acids
TYPE: amino acid
TYPE: amino acid
TYPE: TYPE: TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-09-117-4158-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; ORGANISM: Plasmodium falciparum
US-09-269-874A-7
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Best Local Similarity 43.8%;
Matches 7; Conservative
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Best Local Similarity 43.8%;
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1364 LGYYKILSEKYKSDLD 1379
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2.996 Million cell updates/sec
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                                                                                                                                                                                    January 29, 2002, 10:56:05 ; Search time 1760.55 Seconds
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1: /cgn2_6/ptodata/2/paa/PCTUS_COMB.pep:*
2: /cgn2_6/ptodata/2/paa/USO0_COMB.pep:*
3: /cgn2_6/ptodata/2/paa/USO0_COMB.pep:*
4: /cgn2_6/ptodata/2/paa/USOB_COMB.pep:*
5: /cgn2_6/ptodata/2/paa/USOB_COMB.pep:*
6: /cgn2_6/ptodata/2/paa/USOB_COMB.pep:*
7: /cgn2_6/ptodata/2/paa/USOB_COMB.pep:*
8: /cgn2_6/ptodata/2/paa/USOB_COMB.pep:*
9: /cgn2_6/ptodata/2/paa/USOB_COMB.pep:*
10: /cgn2_6/ptodata/2/paa/USOB_COMB.pep:*
11: /cgn2_6/ptodata/2/paa/USOB_COMB.pep:*
11: /cgn2_6/ptodata/2/paa/USOB_COMB.pep:*
13: /cgn2_6/ptodata/2/paa/USOB_COMB.pep:*
14: /cgn2_6/ptodata/2/paa/USOB_COMB.pep:*
15: /cgn2_6/ptodata/2/paa/USOB_COMB.pep:*
16: /cgn2_6/ptodata/2/paa/USOB_COMB.pep:*
17: /cgn2_6/ptodata/2/paa/USOB_COMB.pep:*
18: /cgn2_6/ptodata/2/paa/USOB_COMB.pep:*
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19: /cgn2_6/ptodata/2/paa/USOB_COMB.pep:*
19: /cgn2_6/ptodata/2/paa/USOB_COMB.pep:*
19: /cgn2_6/ptodata/2/paa/USOB_COMB.pep:*
10: /cgn2_6/ptodata/2/paa/USOB_COMB.pep:*
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/cgn2_6/ptcdata/2/paa/US099_COMB.pep:*
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Compugen Ltd
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US-09-125-031-2
US-09-125-031A-2
US-09-125-031B-2
US-09-134-333-2
US-09-311-817-1
US-09-125-031A-10
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GenCore version (c) 1993 - 2000
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Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

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1 EDSGSNGKKITCECTKPDS 19
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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                           Copyright
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Perfect score:
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APPLICANT: The Government of the United States of America, as represented by the APPLICANT: The Government of the Department of Health and Human Services, Centers for APPLICANT: Secretary of the Department of Health and Human Services, Centers for APPLICANT: Lal, Altaf A. APPLICANT: Lal, Altaf A. APPLICANT: Ping Shi, Ya APPLICANT: Pologo E. TITLE OF INVENTION: Recombinant Multivalent Malarial Vaccine Against Plasmodium Fa FILE REFERENCE: 395-57049
CURRENT APPLICATION NUMBER: US 60/097,703
PRIOR APPLICATION NUMBER: US 60/097,703
PRIOR PLICATION NUMBER: PCT / US99/18869
PRIOR FILING DATE: 1999-08-19
                                                                                                                                              Sequence 2, Appli
Sequence 1, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 16, Appli
Sequence 2, Appli
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Sequence 18, Appl
Sequence 20, Appl
Sequence 18, Appl
Sequence 16, Appl
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Sequence 3, Appli
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Sequence
Sequence
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US-09-134-333-10

US-09-125-0318-5

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US-09-125-0318-8

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US-09-125-0318-8

US-09-125-0318-8

US-09-125-0318-8

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US-09-125-0318-8

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US-09-125-6838-12

US-09-175-6838-12

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US-09-175-683-11

US-09-500-376-2

US-09-501-376-16

US-09-501-376-16

US-09-501-376-16

US-09-501-376-16

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US-09-501-376-16
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Pred. No. 4.3e-08;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                  US-09-269-874-3
US-07-867-768A-3
US-08-195-705-3
US-09-500-376-4
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US-09-117-415-20
US-08-593-006-16
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                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 12, Application US/09763397A GENERAL INFORMATION:
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100.0%; Pr
tive 0;
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SOFTWARE: PatentIn version 3.1
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Best Local Similarity 100.(
Matches 19; Conservative
                             US-09-763-397A-12
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LENGTH: 19
  TYPE: PRT
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1 EDSGSNGKKITCECTKPDS 19

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19 95 95 95 108 108

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Sequence 12, App.

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Mismatches
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ORGANISM: Artificial Sequence
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                                                             EDSGSNGKKITCECTKPDS
  Conservative
                                           1 EDSGSNGKKITCECTKPDS
                                                                                                                                                                                                                                                                           APPLICANT: BARNWELL, JOHN APPLICANT: MENDIS, KAMINI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-134-333-2
  19;
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LENGTH: 95
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    Matches
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APPLICANT: ROTH CHARLES
APPLICANT: ROTH CHARLES
APPLICANT: BARNWELL, JOHN
APPLICANT: BARNWELL, JOHN
APPLICANT: MATO, FARIDABANO
TITLE OF INVENTION: RECOMBLINDIN SPOTIN
FILE REFERENCE: 0660-0139-0XPCT
TITLE OF INVENTION: PLASMODIUM MSP-1
FILE REFERENCE: 0660-0139-0XPCT
CURRENT APPLICATION NUMBER: USO99-02-10
PRIOR PILLING DATE: 1999-03-10
PRIOR PAPLICATION NUMBER: PCT/FR97/00290
PRIOR APPLICATION NUMBER: PCT/FR97/00290
PRIOR FILING DATE: 1999-02-14
PRIOR FILING DATE: 1996-02-14
NUMBER OF SEQ ID NOS: 15
SEQ ID NO 2
LENGTH: 95
                                                                                                           Sequence 2, Application US/09125031

Sequence 2, Application US/09125031

GENERAL INFORMATION:

APPLICANT: LONGACRE-ANDRE, SHIRLEY

APPLICANT: ROTH, CHARLES

APPLICANT: NOTH, CHARLES

APPLICANT: NOTH, CRAINABANO

APPLICANT: BARNWELL, JOHN

APPLICANT: BARNWELL, JOHN

TITLE OF INVENTION: PLASMODIUM MSP-1

FITLE OF INVENTION: PLASMODIUM MSP-1

FILE REFERENCE: 0660-0139-0XPCT

CURRENT APPLICATION NUMBER: US/09/125,031

CURRENT APPLICATION NUMBER: PCT/FR97/00290

EARLIER APPLICATION NUMBER: PCT/FR97/00290

EARLIER APPLICATION NUMBER: FP96/01822

EARLIER FILING DATE: 1996-02-14

NUMBER OF SEQ ID NOS: 14

SOFTWARE: Patentin Ver. 2.1
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; OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC
US-09-125-031-2
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Pred. No. 2.1e-07;
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Best Local Similarity 100.0%; Pred. No. 2.1e-07;
Matches 19; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2, Application US/09125031A GENERAL INFORMATION:
APPLICANT: LONGACRE-ANDRE, SHIRLEY
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100.0%;
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ORGANISM: Artificial Sequence
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             EDSGSNGKKITCECTKPDS 19
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Best Local Similarity
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Sequence 2, Application US/09134333

Sequence 2, Application US/09134333

GENERAL INFORMATION:

APPLICANT: LONGACRE-ANDRE, SHIRLEY

APPLICANT: NOTH, CHARLES

APPLICANT: NOTH, CHARLES

APPLICANT: NATH, CHARLES

APPLICANT: MENDIS, KAMINI

TITLE OF INVENTION: RECOMBINANT PROTEIN CONTAINING A C-TERMINAL FRAGMENT OF

TITLE OF INVENTION: PLASMODIUM MSP-1

FILE REFERENCE: 0660-0135-0XCIP

TITLE OF INVENTION PLASMODIUM MSP-1

FILE REFERENCE: 1999-04-18

CURRENT FILING DATE: 1999-04-18

EARLIER APPLICATION NUMBER: PCT/FR97/00290

EARLIER APPLICATION NUMBER: PC95/02-14

NUMBER OF SEQ ID NOS: 14

SEQ ID NO 2

LENGHA : 95

LENGHA : 95
APPLICANT: MENULO, FARIDAMANO
APPLICANT: NATO, FARIDAMANO
TITLE OF INVENTION: RECOMBINANT PROTEIN CONTAINING A C-TERMINAL FRAGMENT OF
TITLE OF INVENTION: PLASMODIUM MSP-1
FILE REFERENCE: 0660-0139-0XPCT
CURRENT APPLICATION NUMBER: US/09/125,031B
CURRENT FILING DATE: 1999-03-10
PRIOR FILING DATE: 1997-02-14
PRIOR FILING DATE: 1997-02-14
PRIOR FILING DATE: 1996-02-14
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PARCHIN Ver. 2.1
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; OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC
US-09-134-333-2
                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC US-09-125-031B-2
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Best Local Similarity 100.0%; Pred. No. 2.1e-07;
Matches 19; Conservative 0; Mismatches 0;
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Sequence 10, Application US/09125031A

GENERAL INFORMATION:
APPLICANT: LONGACRE-ANDRE, SHIRLEY
APPLICANT: ROTH, CHARLES
APPLICANT: BARWAELL, JOHN
APPLICANT: MATO, FARIDABANO
TITLE OF INVENTION: PLASMODIUM MSP-1
FILE REPRENCE: 0660-0139-OxPCT
CURRENT APPLICATION NUMBER: US/09/125,031A
CURRENT APPLICATION NUMBER: PCT/FR97/00290
PRIOR APPLICATION NUMBER: FF96/01822
PRIOR FILING DATE: 1999-02-14
PRIOR FILING DATE: 1996-02-14
NUMBER OF SEQ ID NOS: 15
SEQ ID NO 10
LENGTH: 108
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Sequence 10, Application US/09125031B
Sequence 10, Application US/09125031B
Sequence 10, Application:
GENERAL INFORMATION:
APPLICANT: CANGACRE-ANDRE, SHIRLEY
APPLICANT: BARNWELL, JOHN
APPLICANT: BARNWELL, JOHN
APPLICANT: MATO, FARIDABANO
TITLE OF INVENTION: PLASMODIUM MSP-1
FILE REFERENCE: 0660-0139-0XPCT
CURRENT FPLIAG DATE: 1999-03-10
FRIOR APPLICATION NUMBER: PCT/FR97/00290
PRIOR FILING DATE: 1999-03-14
PRIOR FILING DATE: 1996-02-14
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 10
LENGTH: 108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
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; ORGANISM: Plasmodium falciparum
US-09-125-031A-10
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ORGANISM: Plasmodium falciparum
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Matches 19; Conservative
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APPLICANT: ROTH, CHARLES
APPLICANT: NATO, FARIDABANO
APPLICANT: NATO, FARIDABANO
APPLICANT: NATO, FARIDABANO
APPLICANT: NATO, FARIDABANO
APPLICANT: MENDIS, KAMINI
TITLE OF INVENTION: RECOMBINANT PROTEIN CONTAINING A C-TERMINAL FRAGMENT OF
TITLE OF INVENTION: PLASMODIUM MSP-1
FILE REFERENCE: 0660-0139-0xPCT
CURRENT FILING DATE: 1999-03-10
EARLIER APPLICATION NUMBER: PCT/FR97/00290
EARLIER PILING DATE: 1997-02-14
EARLIER FILING DATE: 1997-02-14
EARLIER FILING DATE: 1997-02-14
MUMBER OF SEQ ID NOS: 14
SOSTWARE: PALENT NOS: 14
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100.0%; Pred. No. 2.1e-07;
ative 0; Mismatches 0;
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100.0%; Pred. No. 2.4e-07;
iive 0; Mismatches 0;
Score 106; DB 15;
Pred. No. 2.1e-07;
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                                                                                                                                                                                                                                      TITLE OF INVENTION: Malaria Vaccine FILE REFERENCE: May 1396-1210
CURRENT APPLICATION NUMBER: US/09/311,817
CURRENT FILING DATE: 1999-05-13
PRIOR FILING DATE: 1999-04-20
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin version 3.0
SERIOTH: 96
                                     Mismatches
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                                                                                                                                                                                    US-09-311-817-1
; Sequence 1, Application US/09311817
; GENERAL INFORMATION:
Query Match
Best Local Similarity 100.0%; P
Matches 19; Conservative 0;
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                                                                         1 EDSGSNGKKITCECTKPDS 19
                                                                                             67 EDSGSNGKKITCECTKPDS 85
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Best Local Similarity 100.(
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Best Local Similarity 100.0
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Sequence 5, Application US/09125031A GENERAL INFORMATION:
                                                                                LONGACRE-ANDRE, SHIRLEY
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SEQ ID NO 5
LENGTH: 116
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APPLICANT: LONGACRE-ANDRE, SHIRLEY
APPLICANT: ROTH, CHARLES
APPLICANT: NOTH, CHARLES
APPLICANT: NOTH, CHARLES
APPLICANT: MANNELL, JOHN
THE OF INVENTION: RECOMBINANT PROTEIN CONTAINING A C-TERMINAL FRAGMENT OF
TITLE OF INVENTION: RECOMBINANT PROTEIN CONTAINING A C-TERMINAL FRAGMENT OF
TITLE OF INVENTION: RECOMBINANT PROTEIN CONTAINING A C-TERMINAL FRAGMENT OF
CURRENT APPLICATION NUMBER: US/09/125,031
CURRENT FILING DATE: 1999-03.10
EARLIER APPLICATION NUMBER: PTJF/PS/7/00290
EARLIER FILING DATE: 1997-02-14
EARLIER FILING DATE: 1996-02-14
NUMBER OF SEQ ID NOS: 14

SOCTWARE: PATCH OF VERY NOW NUMBER: PROFOLO NUMBER: PATCH OF VERY NUMBER OF SEQ ID NOS: 14
                                                      CHERRAL INFORMATION:
APPLICANT: LONGACRE-ANDRE, SHIRLEY
APPLICANT: ROTH, CHARLES
APPLICANT: NATO, FARIDABANO
APPLICANT: NATO, FARIDABANO
APPLICANT: BARNWELL, JOHN
APPLICANT: BARNWELL, JOHN
TITLE OF INVENTION: RECOMBINANT PROTEIN CONTAINING A C-TERMINAL FRAGMENT OF FILE REFERENCE: 0660-0135-0XCIP
TITLE OF INVENTION: PLASMODIUM MSP-1
FILE REFERENCE: 0660-0135-0XCIP
CURRENT APPLICATION NUMBER: US/09/134,333
CURRENT PILING DATE: 1999-04-14
EARLIER PILING DATE: 1997-02-14
EARLIER FILING DATE: 1997-02-14
EARLIER FILING DATE: 1996-02-14
MUMBER: FILING DATE: 1996-02-14
MUMBER: FILING DATE: 1996-02-14
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. OTHER INFORMATION: Description of Artificial Sequence:SYNTHETIC
US-09-125-031-5
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100.0%; Score 106; DB 15;
Best Local Similarity 100.0%; Pred. No. 2.6e-07;
Matches 19; Conservative 0; Mismatches 0;
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100.0%; Pred. No. 2.4e-07;
tive 0; Mismatches 0;
                    Sequence 10, Application US/09134333 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Plasmodium falciparum US-09-134-333-10
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Best Local Similarity 100.
Matches 19; Conservative
US-09-134-333-10
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Sequence 5. Application US/09125031B
Sequence 5. Application US/09125031B
Sequence 5. Application Sequence 5. Application Sequence 5. Applicant INFORMATION:
APPLICANT: LONGACRE-ANDRE, SHIRLEY
APPLICANT: ROTH, CHARLES
APPLICANT: MATO, FARIDARANO
TITLE OF INVENTION: PLASMODIUM MSP-1
TITLE OF INVENTION: PLASMODIUM MSP-1
FILE REPRENCE: 0660-0139-0XCCT
FILE REPRENCE: 0660-0139-0XCCT
CURRENT APPLICATION NUMBER: PG7/FR97/00290
PRIOR FILING DATE: 1999-03-10
PRIOR APPLICATION NUMBER: PG7/FR97/00290
PRIOR FILING DATE: 1990-02-14
PRIOR FILING DATE: 1990-02-14
PRIOR SEQ ID NOS: L5
NUMBER OF SEQ ID NOS
APPLICANT: BARNWELL, JOHN
APPLICANT: ROTH, CHARLES
APPLICANT: BARNWELL, JOHN
APPLICANT: BARNWELL, JOHN
APPLICANT: MATO, FARLDABANO
APPLICANT: NATO, FARLDABANO
TITLE OF INVENTION: PLESMODIUM MSP-1
TITLE OF INVENTION: PSP-02-14
CURRENT APPLICATION NUMBER: PC99-03-10
PRIOR PRIOR PLING DATE: 1999-02-14
PRIOR PAPLICATION NUMBER: FR96/01822
PRIOR APPLICATION NUMBER: FR96/01822
SOFTWARE: PATENTING DATE: 1990-02-14
NUMBER OF SEQ ID NOS: 15
SEQ ID NO 5
LENGTH: 116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 116;
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100.0%; Pred. No. 2.6e-07;
iye 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.0%; Pred. No. 2.6e-07;
Matches 19; Conservative 0; Mismatches 0;
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ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 19; Conservative
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Sequence 8, Application US/09125031

Sequence 8, Application US/09125031

GENERAL INFORMATION:
APPLICANT: LONGACRE-ANDRE, SHIRLEY
APPLICANT: ROTH, CHARLES
APPLICANT: ROTH, CHARLES
APPLICANT: NATO, FRIDABNO
APPLICANT: MANDIS, KAMINI
TITLE OF INVENTION: RECOMBINANT PROTEIN CONTAINING A C-TERMINAL FRAGMENT OF
TITLE OF INVENTION: PLASMODIUM MSP-1
FILE REFERENCE: 0660-0139-0xPcT
CURRENT FORLICATION NUMBER: US/09/125,031
CURRENT FILING DATE: 1999-03-10
EARLIER APPLICATION NUMBER: FR96/01822
EARLIER PILING DATE: 1999-02-14
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PALENTIN Ver. 2.1
SEQ ID NO 8
HANCE PALENTIN VER. 2.1
SEQ ID NO 8
                                                                                                                                        Sequence's, Application US/09134333

Sequence's, Application US/09134333

GENERAL INFORMATION:
APPLICANT: LONGACRE-ANDRE, SHIRLEY
APPLICANT: ROTH, CHARLES
APPLICANT: NATO, FAIDBANO
APPLICANT: BENDIS, KAMINI
TITLE OF INVENTION: RECOMBINANT PROTEIN CONTAINING A C-TERMINAL FRAGMENT OF
TITLE OF INVENTION: PLASMODIUM MSP-1
FILE REFERENCE: 0660-0135-0XCIP
CURRENT APPLICATION NUMBER: US/09/134,333
CURRENT FILING DATE: 1999-04-18
EARLIER APPLICATION NUMBER: PCT/FR97/00290
EARLIER APPLICATION NUMBER: PCT/FR97/0182
EARLIER RPLING DATE: 1996-02-14
NUMBER OF SEQ ID NOS: 14

SEQ ID NO 5
LENGTH: 116
LENGTH: 116
LENGTH: 116
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100.0%; Score 106; DB 15;
Best Local Similarity 100.0%; Pred. No. 2.6e-07;
Matches 19; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Artificial Sequence
1 EDSGSNGKKITCECTKPDS 19
                      67 EDSGSNGKKITCECTKPDS 85
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Search completed: January 29, 2002, 10:56:05 Job time: 2401 sec

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Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                 OM protein - protein search, using sw model
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1 EDSGSNGKKITCECTKPDS 19
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se : Pending\_Patents\_AA\_New:\*

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2: /cgn2\_6/ptodata/3/paa/US06\_NEW\_COMB.pep:\*

3: /cgn2\_6/ptodata/3/paa/US07\_NEW\_COMB.pep:\*

4: /cgn2\_6/ptodata/3/paa/US09\_NEW\_COMB.pep:\*

5: /cgn2\_6/ptodata/2/paa/US09\_NEW\_COMB.pep:\*

5: /cgn2\_6/ptodata/2/paa/US09\_NEW\_COMB.pep:\*

6: /cgn2\_6/ptodata/3/paa/US10\_NEW\_COMB.pep:\*

7: /cgn2\_6/ptodata/3/paa/US10\_NEW\_COMB.pep:\*

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Minimum DB seq length: 0 Maximum DB seq length: 2000000000 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

18, Appl 20, Appl 16, Appl 7, Appli 3, Appli 3, Appli 3, Appli 5, Appli 5, Appli 5, Appli 5, Appli 5, Appli 5, Appli Appli Appli Appl 1899, A 0, Appl 1898, A Appli 13816, Sequence 10, Sequence 3189 Sequence 8605 Sequence 1, Sequence 2, Sequence 2, Description Sequence 2 Sequence 2 Sequence 1 Sequence US-09-978-756-7 US-09-117-415B-2 US-09-117-415B-18 US-09-117-415B-18 US-09-117-415B-16 US-09-269-874A-7 US-09-269-874A-3 US-09-269-874A-3 US-09-269-874A-3 US-09-978-756-3 US-09-978-756-3 US-09-978-756-3 US-09-708-427-31899 US-09-708-427-31899 US-09-708-427-31898 US-09-708-427-31898 US-09-708-427-31898 US-09-708-427-31898 US-09-708-427-31898 US-09-708-427-31898 US-09-708-427-31898 US-09-708-427-31898 US-09-708-427-13704 US-09-708-427-13703 US-09-708-427-13240 US-09-708-427-13239 US-09-708-427-13238 US-09-708-427-13816 SUMMARIES BB Match Length 100.0 100.0 100.0 40.6 Query Score Result

Sequence 13815, A	Sequence 13814, A	Sequence 68, Appl	Sequence 68, Appl	Sequence 8, Appli	Sequence 72724, A	Sequence 38, Appl		Sequence 57, Appl	Sequence 13, Appl			Sequence 63, Appl	Sequence 31, Appl	Sequence 42719, A	Sequence 42718, A		Sequence 202, App	Sequence 34465, A
US-09-708-427-13815	US-09-708-427-13814	US-09-848-798A-68	US-09-848-798-68	US-09-974-449-8	US-09-708-427-72724	US-09-974-449-38	US-09-708-427-27613	US-10-005-368-57	US-10-005-368-13	US-09-895-298A-70	US-09-848-798A-63	US-09-848-798-63	US-10-006-869-31	US-09-708-427-42719	US-09-708-427-42718	US-09-708-427-42717	US-10-001-857-202	US-09-708-427-34465
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160	263	108	108	114	194	219	321	463	1926	183	110	110	112	137	154	159	221	263
39.5	39.2	38.7	38.7	38.7	38.7	38.7	38.7	38.7	38.7					37.7	37.7	37.7	37.7	37.7
41.5	41.5	41	41	41	41	41	41	41	41	40.5	40	40	40	40	40	40	40	40
27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

US-09-978-756-1

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Sequence 1, Application US/09978756
GENERAL INFORMATION:
APPLICANT: Holder, Anthony
APPLICANT: Birdsall, Berry
APPLICANT: Birdsall, Berry
APPLICANT: Birdsall, Berry
APPLICANT: Syed, Shabih
TITLE OF INVENTION: Malaria Vaccine
FILE REFRENCE: 18396/1005
CURRENT APPLICATION UNMER: US/09/978,756
CURRENT APPLICATION UNMER: PCT/GB00/01558
PRIOR APPLICATION NUMBER: 09/311,817
PRIOR FILING DATE: 1999-05-13
PRIOR APPLICATION NUMBER: 2,211,451
PRIOR APPLICATION NUMBER: 9909072.2
PRIOR FILING DATE: 1999-06-23
PRIOR FILING DATE: 1999-04-20
NUMBER OF SEQ ID NOS: 3
SOFTWARE: Patentin Version 3.0
SEQ ID NO 1
LENGTH: 96
LYPE: PRT
CORGANISM: Plasmodium falciparum
US-09-978-756-1
MAtches 19; Conservative 0; Mismatches 0; Indels
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Gaps

Gaps

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Conservative
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US-09-117-415B-22
  19;
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Sequence 2, Application:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Davidson, Eugene
TITLE OF INVENTION: Malaria Vaccine Based Upon the Addition
of a MSA1 Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
CORRESPONDENCE SAPONE,
STREET: 714 Colorado Avenue
CITY: Bridgeport
STATE: Connecticut
COUNTRY: USA
ZIP: 10017
                                                                                                                                                                                                                                                                                                                                                                                                                             Length 376;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 106; DB 5;
Pred. No. 1.3e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
100.0%; Score 106; DB 5;
Best Local Similarity 100.0%; Pred. No. 8.5e-09;
Matches 19; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPad (ASCII)
CURRENT APPLICATION DATA:
APPLICATION NUABER: US/09/117,415B
FILING DATE: 29-Jul-1998
CLASSIFICATION: 435
ATTORNEY AGENT INFORMATION:
NAME: Coleman, Henry D.
REGISTRATION UNABER: R12-030
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 679-0090
TELEFRAX: (212) 679-9121
INFORMATION FOR SEQ ID NO: 2:
SEGUIENCE CHARACTERISTICS:
          FILE REFERENCE: 18396/1005
CURRENT APPLICATION NUMBER: US/09/978,756
CURRENT FILING DATE: 2001-10-16
PRIOR PPLICATION NUMBER: PCT/GB00/01558
PRIOR FILING DATE: 1000-04-20
PRIOR APPLICATION NUMBER: 09/311,817
PRIOR APPLICATION NUMBER: 2,271,451
PRIOR FILING DATE: 1999-05-15
PRIOR FILING DATE: 1999-05-25
PRIOR FILING DATE: 1999-04-20
NUMBER OF SEQ ID NOS: 3
SOFTWARE: PATENTIN VETSION 3.0
SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO:
US-09-117-415B-2
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Best Local Similarity
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US-09-117-415B-2
                                                                                                                                                                                                                                                                                                               LENGTH: 376
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RESULT 5
US-09-117-415B-18
US-09-117-415B-18
SEQUENCE 18, Application US/09117415B
GENERAL INFORMATION:
APPLICANT: Davidson, Eugene
APPLICANT: Davidson, Eugene
Yang, Shutong
TITLE OF INVENTION: Malaria Vaccine Based Upon the Addition
of a MSAl Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .;
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TITLE OF INVENTION: malaria Vaccine Based Upon the Addition of a MSA1 Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Henry D. Coleman, COLEMAN SUDOL SAPONE, STREET: 714 Colorado Avenue CITY: Bridgeport STATE: Connecticut COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 613;
                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ROBERSE: Henry D. Coleman, COLEMAN SUDOL SAPONE, STREET: 714 Colorado Avenue CITY: Bridgeport
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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100.0%; Pred. No. 1.3e-08;
1ve 0: Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPATER: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPad (ASCII)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/117,415B
FILING DATE: 29-JU1-1998
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION NUMBER: R12-030
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 679-0121
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 22:
US-09-117-415B-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Coleman, Henry D. REGISTRATION NUMBER: 32,559
                                                                                                                                            Sequence 22, Application US/09117415B
GENERAL INFORMATION:
APPLICANT: Davidson, Eugene
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                      NUMBER OF SEQUENCES: 24 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                    STATE: Connecticut
COUNTRY: USA
ZIP: 10017
1 EDSGSNGKKITCECTKPDS 19
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Best Local Similarity 100.
Matches 19; Conservative
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Gaps
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                                                                                                        Length 631;
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ADDRESSEE: Henry D. Coleman, COLEMAN SUDOL SAPONE,
STREET: 714 Colorado Avenue
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Sequence 7. Application US/09269874A
GENERAL INFORMATION:
TITLE OF INVENTION: Recombinant Process for Preparing a
TITLE OF INVENTION: Complete Malaria Antigen, GP190/MSP1
FILE REFERENCE: GRUE-003
                                                                                                        Score 106; DB 5;
Pred. No. 1.4e-08;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 106; DB 5;
100.0%; Pred. No. 1.4e-08;
Live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPad (ASCII)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/117,415B
FILING DATE: 29-Jul-1998
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Coleman, Henry D.
REGISTRATION NUMBER: 32,559
REFERENCE/DOCKET NUMBER: R12-030
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) MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 20:
US-09-117-415B-20
                                                                                                                                                                                                                                                                                                                                Sequence 16, Application US/09117415B GENERAL INFORMATION:
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TELEPHONE: (212) 679-0090
TELEFAX: (212) 679-9121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 649 amino acids TYPE: amino acid
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100.0%;
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STATE: Connecticut
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Best Local Similarity
Matches 19; Conserv
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Best Local Similarity
Matches 19; Conserv
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100.0%; Pred. No. 1.4e-08;
tive 0; Mismatches 0;
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NAME: Coleman, Henry D.
RECISTRATION NUMBER: 32,559
REFERENCE/DOCKET NUMBER: R12-030
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 679-0090
TELEFAX: (212) 679-9121
                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPad (ASCII)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/117,415B
FILING DATE: 29-Jul-1998
CLASSIFICATION: 435
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APPLICATION NUMBER: US/09/117,415B
FILING DATE: 29-Jul-1998
CLASSIFICATION: 435
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 679-0090
TELEPAX: (212) 679-9121
INFORMATION FOR SEQ ID NO: 18:
                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: 11near;

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-09-117-4158-18
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPad (ASCII)
                                                                                                                                                                                                                            NAME: Coleman, Henry D. REGISTRATION NUMBER: 32,559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 714 Colorado Avenue
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APPLICANT: Davidson, Eugene
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LENGTH: 631 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 631 amino acids
TYPE: amino acid
                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
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CORRESPONDENCE ADDRESS:
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STATE: Connecticut
ZIP: 10017
COMPUTER READABLE FORM:
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Best Local Similarity 100.
Matches 19; Conservative
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US-09-117-415B-20
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; LENGTH: 1639
; TYPE: PRT
; ORGANISM: Plasmodium falciparum
US-09-269-874A-3
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NAME/KEY: misc_feature
LOCATION: 1..162
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US_09-708-427-58009
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US-09-978-756-3
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GENERAL INFORMATION:
APPLICANT: Bulyard, Hermann
TITLE OF INVENTION: Recombinant Process for Preparing a
TITLE OF INVENTION: Complete Malaria Antigen, GP190/MSP1
FILE REFREENCE: GRUE-003
CURRENT APPLICATION NUMBER: US/09/269,874A
CURRENT FILING DATE: 1999-08-02
PRIOR APPLICATION NUMBER: DCT/EP97/05441
PRIOR APPLICATION NUMBER: DE 19640817.2
PRIOR FILING DATE: 1997-10-02
PRIOR FILING DATE: 1995-10-02
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FASTESQ for Windows Version 4.0
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GENERAL INFORMATION:
APPLICANT: Bujard, Hermann
TITLE OF INVENTION:
FILE REFERENCE: GRUE-003
CURRENT FILING DATE: 1999-08-02
PRIOR APPLICATION NUMBER: US/09/269,874A
CURRENT APPLICATION NUMBER: US/09/269,874A
PRIOR APPLICATION NUMBER: DET/EP97/05441
PRIOR FILING DATE: 1997-10-02
PRIOR FILING DATE: 1997-10-02
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100.0%; Pred. No. 3.3e-08;
Live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
       CURRENT APPLICATION NUMBER: US/09/269,874A CURRENT FILING DATE: 1999-08-02 PRIOR APPLICATION NUMBER: PCT/EP97/05441 PRIOR FILING DATE: 1997-10-02 PRIOR APPLICATION NUMBER: DE 19640817.2 PRIOR PILING DATE: 1996-10-02
                                                                                                                                                           NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 4.0
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US-09-269-874A-5
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Best Local Similarity 100.
Matches 19; Conservative
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Best Local Similarity
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                                                                                                                                                                                                             SEQ ID NO 7
LENGTH: 1602
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US-09-269-874A-5
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APPLICATI: N. ALEXANDROW et al.
APPLICATI: N. EXANDROW et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID
TITLE OF INVENTION: THEREBY
FILE REFERENCE: 2750-1249
CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT APPLICATION NUMBER: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: Patentin version 3.1
SEQ ID NO 58009
LENGTH: 162
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Length 1639;
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89.5%; Pred. No. 8.4e-07;
tive 1; Mismatches 1; Indels
                                                    Indels
     100.0%; Score 106; DB 5; 100.0%; Pred. No. 3.3e-08;
                                                                                                                                                                                                                                                                                                                             APPLICANT: Birdsall, Berry
APPLICANT: Birdsall, Berry
APPLICANT: Feeney, James
APPLICANT: Seeney, William
APPLICANT: Syed, Shabih
TITLE OF INVENTION: Malaria Vaccine
FILE REFRENCE: 1836/6/1065
CURRENT PELLOATION NUMBER: US/09/978,756
CURRENT FILING DATE: 2001-10-16
PRIOR PELLOATION NUMBER: 09/311,817
PRIOR APPLICATION NUMBER: 09/311,817
PRIOR APLICATION NUMBER: 2,271,451
PRIOR FILING DATE: 1999-05-25
PRIOR APPLICATION NUMBER: 2,271,451
PRIOR FILING DATE: 1999-05-25
PRIOR FILING DATE: 1999-05-25
PRIOR FILING DATE: 1999-05-25
NUMBER OF SEQ ID NOS: 3
SOFTWARE: PATCHIN VETSION 3.0
                                                    Mismatches
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US-09-978-756-3
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ORGANISM: Zea mays subsp. mays
                                                                                                                          DD 1590 EDSGSNGKKITCECTKPDS 1608
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Best Local Similarity 89.5'
Matches 17; Conservative
       Query Match 100.0
Best Local Similarity 100.0
Matches 19; Conservative
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APPLICANT: Birdsall, Berr
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Search completed: January 29, 2002, 10:58:13 Job time: 2509 sec
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Matches 8; Conservative
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LOCATION: 1..230
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TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungi
File REFERENCE: 109272.147
CURRENT APPLICATION NUMBER: US/09/801,368
CURRENT FILING DATE: 2001-03-07
PRIOR APPLICATION NUMBER: US 69/487,558
PRIOR APPLICATION NUMBER: US 60/160,587
PRIOR APPLICATION NUMBER: US 60/160,587
PRIOR FILING DATE: 1999-10-20
NUMBER OF SEQ ID NOS: 440
SOFTWARE: Patentin version 3.0
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                                                                                                             Length 162;
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                                                                                                                                                 5; Indels
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                                                                                                             Score 45; DB 5;
Pred. No. 7.5;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     40.6%; Score 43; DB 5; 57.9%; Pred. No. 51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Mismatches
                : NAME/KEY: misc_feature

: LCCATION: 1..162

:: OTHER INFORMATION: Ceres Seq. ID 1941076

US-09-708-427-58009
   any amino acid
                                                                                                                                                                                                                                                                                         Sequence 50, Application US/09801368 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORCANISM: Saccharomyces cerevisiae US-09-801-368-50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 50, Application US/09487558 GENERAL INFORMATION:
                                                                                                           42.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Busby, Robert
APPLICANT: Call, Brian
APPLICANT: Hecht, Peter
APPLICANT: Hockt, Doug
APPLICANT: Madden, Kevin
                                                                                                                                                                                                                                                                                                                                                           Hecht, Peter
Holtzman, Doug
Madden, Kevin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 57.9
Matches 11; Conservative
                                                                                                                              Best Local Similarity 50.0
Matches 7; Conservative
OTHER INFORMATION: Xaa is
                                                                                                                                                                                                                                                                                                                                                                                                       Maxon, Mary
Milne, Todd
Norman, Thea
Royer, John
Salama, Sofie
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Silva, Jeff
                                                                                                                                                                                                 128 GSRGRRSPCTCTPP 141
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Milne, Todd
Norman, Thea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Royer, John
Salama, Sofie
                                                                                                                                                                               4 GSNGKKITCECTKP 17
                                                                                                                                                                                                                                                                                                                           APPLICANT: Busby, Robert APPLICANT: Call, Brian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Norman,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 14
US-09-487-558-50
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US-09-801-368-50
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APPLICANT:
APPLICANT:
APPLICANT:
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APPLICANT:
APPLICANT:
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APPLICANT:
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APPLICANT:
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                                                                                                             Query Match
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APPLICANT:
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RESULT 15
US-09-708-427-31899
US-09-708-427-31899
Sequence 31899, Application US/09708427
Sequence 31899, Application US/09708427
GENERAL INFORMATION:
APPLICANT: N. ALEXANDROV et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID;
TITLE OF INVENTION: THEREBY
FILE REFERENCE: 2750-1243P
CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SSO ID NO 31899
LENGTH: 230
APPLICANT: Silva, Jeff
APPLICANT: Silva, Jeff
APPLICANT: Summers, Eric
TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production
TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production
TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production
TITLE OF INVENTION: More of Secondary Metabolite Production
FILE REFERENCE: 109272.147
CURRENT APPLICATION NUMBER: US/09/487,558
PRIOR PILING DATE: 2000-01-19
PRIOR PILING DATE: 2000-01-19
PRIOR PILING DATE: 2000-01-19
PRIOR FILING DATE: 1999-10-20
NUMBER OF SEO ID NOS: 440
SOFTWARE: Patentin version 3.0
SEO ID NO SO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match 40.6%; Score 43; DB 5; Length 609; Best Local Similarity 57.9%; Pred. No. 51; Matches 11; Conservative 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       39.6%; Score 42; DB 5; Length 230; 61.5%; Pred. No. 30;
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NAME/KEY: misc_feature
; LCCATION: 1..230
; OTHER INFORMATION: Ceres Seq. ID 1833059
US-09-708-427-31899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-09-487-558-50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 EDSGSNGKKITCECTKPDS 19
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(without alignments)
2.839 Million cell updates/sec
                                                                                                                                                                             January 29, 2002, 10:56:04; Search time 1760.55 Seconds
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/cgn2_6/ptodata/2/paa/US06_COMB.pep:*
/cgn2_6/ptodata/2/paa/US06_COMB.pep:*
/cgn2_6/ptodata/2/paa/US08_COMB.pep:*
/cgn2_6/ptodata/2/paa/US081_COMB.pep:*
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/cgn2_6/ptodata/2/paa/US091_COMB.pep:*
/cgn2_6/ptodata/2/paa/US091_COMB.pep:*
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/cgn2_6/ptodata/2/paa/US092_COMB.pep:*
/cgn2_6/ptodata/2/paa/US093_COMB.pep:*
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/cgn2_6/ptodata/2/paa/US095_COMB.pep:*
/cgn2_6/ptodata/2/paa/US095_COMB.pep:*
/cgn2_6/ptodata/2/paa/US097_COMB.pep:*
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/cgn2_6/ptodata/2/paa/US099_COMB.pep:*
/cgn2_6/ptodata/2/paa/US099_COMB.pep:*
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3148936 seqs, 277657034 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                     OM protein - protein search, using sw model
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                                                                                                                                                                                                                                                                                                                                             105
1 NSGCFRHLDEREECKCLL 18
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                             Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                        Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Searched:
                                                                                                                                                                                                                                                                                                                                                                             Sequence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No. 1 2 3 3 3 4 4 4	Score 105 105 105 105 105	% Query Match 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0	Query Query Match Length DB 100.0 18 215 100.0 95 15 100.0 95 15 100.0 95 15 100.0 95 15	DB 21 15 15 15 15 15 15 15 15 15 15 15 15 15	SUMMARIES  ID  US-09-763-397A-11  US-09-125-031-2  US-09-125-031B-2  US-09-134-333-2  US-09-311-817-1	Description Sequence 11, Appl Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 1, Appli	
7	105	100.0	108	15	US-09-125-031-10	Sequence 10, Appl	
Φ.	105	100.0	108	15	US-09-125-031A-10	Sequence 10, Appl	
ת	COT	100.0	TOR	7	US-09-125-031B-10	Sequence 10, Appl	

Gaps

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Length 18; Indels

Query Match 100.0%; Score 105; DB 21; Best Local Similarity 100.0%; Pred. No. 2.1e-08; Matches 18; Conservative 0; Mismatches 0;

1 NSGCFRHLDEREECKCLL 18

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10,	Sequence 3, Appli	'n	'n	8	ω,	Sequence 8, Appli	æ	Sequence 2, Appli	11	δ	Н	Sequence 10, Appl		Sequence 3, Appl1	Sequence 4, Appli	8, 4	13,	2, 4	11,	8,	2, A	Seguence 4, Appli	Seguence 2, Appl1	4	Sequence 2, Appli	Sequence 3, Appli	Sequence 16, Appl	2, A		22,	Sequence 22, Appl	∢.	Sequence 20, Appl	Sequence 18, Appl
-134-	20-20	US-09-125-	US-09-134-	US-09-12	US-09-12	US-09-1	US-09-134-	92-60-SN	US-09-17	US-09-17	US-09-175-683-	US-09-17	3 US-07-867-768A-3	5 US-08-195-705-3	6	US-09-71	15 US-09-175-683-13	_	2	_ 6	3 US-07-867-768A-2			5 US-08-195-705-4		19 US-09-500-376-3	9 US-09-500-37	9 US-08-593-006-2	5 US-09-117-41	9 US-08-593-006-22	S	93	us-08-593-00	15 US-09-117-415-18
108	116	116	116	127	127	127	127	350	355	355	361	361	375	375	375	375	376	376	379	384	394	394	394	394	394	394	402	594	594	613	613	631	631	631
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105	105	105	105	105	105	105	105	105	105	105	105	105	105	105	105	105	105	105	105	105	105	105	105	105	105	105	105	105	105	105	105	105	105	105
10	11	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29	30	31	32	33	34	32	36	37	38	39	40	41	42	43	44	45

```
RESULT 1

Secuence 11, Application US/09763397A

Sequence 11, Application US/09763397A

GENERAL INFORMATION:
APPLICANT: The Government of the United States of America, as represented by the APPLICANT: Secretary of the Department of Health and Human Services, Centers for APPLICANT: Control and Prevention
APPLICANT: Lal, Altaf A.
APPLICANT: Lal, Altaf A.
APPLICANT: Hasnain, Seyed E.
TITLE OF INVENTION: Recombinant Multivalent Malarial Vaccine Against Plasmodium Fa FILE OF INVENTION WIMBER: US/09/763,397A

CURRENT APPLICATION NUMBER: US 60/097,703
PRIOR FILING DATE: 1999-08-19
PRIOR FILING DATE: 1999-08-19
PRIOR FILING DATE: 1999-08-19
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patentin version 3.1
SEQ ID NO 11
LENGTH: 18
TYPE: PRT

ORGANISM: Plasmodium falciparum
US-09-763-397A-11
```

ALIGNMENTS

Gaps

q

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Sequence 2, Application US/09134333

Sequence 2, Application US/09134333

GENERAL INFORMATION:
APPLICANT: LONGACRE-ANDRE, SHIRLEY
APPLICANT: NATO, FARIDABANO
APPLICANT: NATO, FARIDABANO
APPLICANT: MENDIS, KAMINI
TITLE OF INVENTION: RECOMBINANT PROTEIN CONTAINING A C-TERMINAL FRAGMENT OF
TITLE OF INVENTION: PLASMODIUM MSP-1
FILE REFERENCE: 0660-0135-0XCIP
CURRENT APPLICATION NUMBER: US/09/134,333
CURRENT FILING DATE: 1999-04-14
EARLIER APPLICATION NUMBER: FF866/1822
EARLIER APPLICATION NUMBER: FF866/1822
EARLIER FILING DATE: 1996-02-14
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PATENTIN VOF: 2.1
SEQ ID NO 2
LENGTH: 95
THENCH: 95
THENCH: 95
THENCH: 95
                                                                                                                                                                                                                                                                     APPLICANT: LONGACRE-ANDRE, SHIRLEY
APPLICANT: LONGACRE-ANDRE, SHIRLEY
APPLICANT: LONGACRE-ANDRE, SHIRLEY
APPLICANT: BARNWELL, JOHN
APPLICANT: MENDIS, KAMIN
APPLICANT: MATO, FARIDARANO
TITLE OF INVENTION: RECOMBINANT PROTEIN CONTAINING A C-TERMINAL FRAGMENT OF
TITLE OF INVENTION: RECAMBINANT PROTEIN CONTAINING A C-TERMINAL FRAGMENT OF
TITLE OF INVENTION: RECAMBINANT PROTEIN CONTAINING A C-TERMINAL FRAGMENT OF
TITLE OF INVENTION: RECAMBINANT PROTEIN CONTAINING A C-TERMINAL FRAGMENT OF
TITLE OF INVENTION: RECAMBINANT PROTEIN CONTAINING A C-TERMINAL FRAGMENT OF
FILE REFERENCE: 0660-0139-02RCT
CURRENT FILING DATE: 1997-02-14
PRIOR FILING DATE: 1997-02-14
PRIOR FILING DATE: 1996-02-14
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PATENTIN Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Artificial Sequence
FEATUME:
OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC
US-09-134-333-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC US-09-125-031B-2
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  Indels
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100.0%; Pred. No. 1.1e-07;
Live 0; Mismatches 0;
  ;
0
     Mismatches
                                                                                                                                                                                                 RESULT 4
0S-09-125-031B-2
i Sequence 2, Application US/09125031B
i GENERAL INFORMATION:
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0
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                                                      1 NSGCFRHLDEREECKCLL 18
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Best Local Similarity 100.
Matches 18; Conservative
          Conservative
          18;
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             Matches
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APPLICANT: ROTH, CHARLES
APPLICANT: ROTH, CHARLES
APPLICANT: RENDIS, KAMINI
APPLICANT: MENDIS, KAMINI
APPLICANT: MENDIS, KAMINI
TITLE OF INVENTION: PLASMODIUM MSP-1
FILE REFERENCE: 0660-0139-0XPCT
FILE REFERENCE: 1999-03-10
CURRENT APPLICATION NUMBER: PC7/FR97/00290
PRIOR PLICATION NUMBER: FR96/01822
PRIOR FILING DATE: 1997-02-14
PRIOR APPLICATION NUMBER: FR96/01822
PRIOR FILING DATE: 1997-02-14
PRIOR FILING DATE: 1997-02-14
SPRIOR FILING DATE: 1997-02-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                             APPLICANT: BARNWELL, JOHN
APPLICANT: BARNWELL, JOHN
APPLICANT: BARNWELL, JOHN
TITLE OF INVENTION: RECOMBINANT PROTEIN CONTAINING A C-TERMINAL FRAGMENT OF
TITLE OF INVENTION: PLASMODIUM MSP-1
FILE REFERENCE: 0660-0139-0XRCT
CURRENT FILING DATE: 1999-03-10
EARLIER APPLICATION NUMBER: PCT/FR97/00290
EARLIER PILING DATE: 1997-02-14
EARLIER FILING DATE: 1996-02-14
SOFTWARE: PAPLICATION NUMBER: FR96/01822
EARLIER FILING DATE: 1996-02-14
SOFTWARE: PAPLICATION NUMBER: PCT/FR97/00290
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC
US-09-125-031-2
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Pred. No. 1.1e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 105; DB 15;
Pred. No. 1.1e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/09125031A GENERAL INFORMATION:
APPLICANT: LONGACRE-ANDRE, SHIRLEY
                                                                                                                                                                           Sequence 2, Application US/09125031 GENERAL INFORMATION:
                                                                                                                                                                                                                              APPLICANT: LONGACRE-ANDRE, SHIRLEY APPLICANT: ROTH, CHARLES APPLICANT: NATO, FARIDABANO
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                        1 NSGCFRHLDEREECKCLL 18
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Best Local Similarity 100.
Matches 18; Conservative
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Best Local Similarity
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US-09-125-031A-2
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LENGTH: 95
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APPLICANT: DONGACRE-ANDRE, SHIRLEY
APPLICANT: ROTH, CHARLES
APPLICANT: BARWELL, JOHN
APPLICANT: BARWELL, JOHN
APPLICANT: BARWELL, JOHN
APPLICANT: MENDIS, KAMINI
APPLICANT: NATO, FARIDABANO
TITLE OF INVENTION: RECOMBINANT PROTEIN CONTAINING A C-TERMINAL FRAGMENT OF
TITLE OF INVENTION: PECOMBINANT PROTEIN CONTAINING A C-TERMINAL FRAGMENT OF
TITLE OF INVENTION: PECOMBINANT PROTEIN CONTAINING A C-TERMINAL FRAGMENT OF
TITLE OF INVENTION: PECOMBINANT PROTEIN CONTAINING A C-TERMINAL FRAGMENT OF
TITLE OF INVENTION: DAPPLICATION NUMBER: US/09/125,031A
CURRENT FILING DATE: 1997-02-14
PRIOR FILING DATE: 1997-02-14
PRIOR FILING DATE: 1997-02-14
PRIOR FILING DATE: 1996-02-14
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PATENTIN Ver. 2.1
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APPLICANT: ENTH, CHARLES
APPLICANT: BARNWELL, JOHN
APPLICANT: BARNWELL, JOHN
APPLICANT: BARNWELL, JOHN
APPLICANT: MATO, FARIDABANO
TITLE OF INVENTION: RECOMBINANT PROTEIN CONTAINING A C-TERMINAL FRAGMENT OF
TITLE OF INVENTION: PLASHODIUM MSP-1
FILE REFERENCE: 0660-0139-0XPCT
CURRENT APPLICATION NUMBER: US/09/125,031B
CURRENT PILING DATE: 1999-03-10
PRIOR APPLICATION NUMBER: PCT/FF97/00290
PRIOR APPLICATION NUMBER: FF96/01822
PRIOR FILING DATE: 1997-02-14
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100.0%; Pred. No. 1.3e-07;
tive 0; Mismatches 0;
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100.0%; Pred. No. 1.3e-07;
tive 0; Mismatches 0;
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                                                                  Sequence 10, Application US/09125031A
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; ORGANISM: Plasmodium falciparum
US-09-125-031A-10
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; ORGANISM: Plasmodium falciparum
US-09-125-031B-10
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SOFTWARE: PatentIn Ver. 2.1
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Best Local Similarity 100.
Matches 18; Conservative
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Best Local Similarity 100.
Matches 18; Conservative
                                                                                          GENERAL INFORMATION
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Sequence 10 Application US/09125031
Sequence 10 Application:
Sequence 10 Application:
APPLICANT: LONGACRE-ANDRE, SHIRLEY
APPLICANT: NATO, FARIDABANO
APPLICANT: NATO, FARIDABANO
APPLICANT: BARWELL, JOHN
TITLE OF INVENTION: RECOMBINANT PROTEIN CONTAINING A C-TERMINAL FRAGMENT OF
TITLE OF INVENTION: PLESMODIUM MSP-1
FILE REFERENCE: 0660-0139-0xPCT
CURRENT FILING DATE: 1999-03-10
EARLIER FILING DATE: 1999-03-10
EARLIER FILING DATE: 1997-02-14
EARLIER FILING DATE: 1996-02-14
SOFTWARE: PATCHING DATE: 1996-02-14
SOFTWARE: PATCHING DATE: 1996-02-14
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100.0%; Pred. No. 1.3e-07;
tive 0; Mismatches 0;
100.0%; Score 105; DB 15;
100.0%; Pred. No. 1.1e-07;
iive 0; Mismatches 0;
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GENERAL INFORMATION:
APPLICAMY: Medical Research Council
FILE REFERENCE: 18396-1120
CURRENT FILING DATE: 1999-05-13
FRIOR APPLICATION NUMBER: GB 99099072.2
PRIOR FILING DATE: 1999-04-20
NUMBER OF SEQ ID NOS: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: PRT
; ORGANISM: Plasmodium falciparum
US-09-311-817-1
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                                                                                          1 NSGCFRHLDEREECKCLL 18
                                                                                                                    17 NSGCFRHLDEREECKCLL 34
                  Best Local Similarity 100.
Matches 18; Conservative
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LENGTH: 96
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RESULT 13
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S Application US/09125031
SGUGNEC 5, Application US/09125031
SGUGNEC 5, Application US/09125031
SGUGNEC 5, APPLICANT: LONGACRE-ANDRE, SHIRLEY
APPLICANT: ROTO, FRIDABANO
APPLICANT: BARNWELL, JOHN
APPLICANT: BARNWELL, JOHN
APPLICANT: BRINGEL, JOHN
APPLICANT: BROWENTION: RECOMBINANT PROTEIN CONTAINING A C-TERMINAL FRAGMENT OF
TITLE OF INVENTION: PLASMODIUM MSP-1
FITLE REFERENCE: 0660-0139-0xPCT
CURRENT PAPLICATION NUMBER: PCT/FR97/00290
EARLIER APPLICATION NUMBER: PR96/01822
EARLIER APPLICATION NUMBER: PR96/01822
EARLIER PILING DATE: 1996-02-14
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 5
LENGTH: 116
                                                  GENERAL LICANT: LONGACE-ANDRE, SHIRLEY
APPLICANT: ROTH, CHARLES
APPLICANT: ROTH, CHARLES
APPLICANT: NATO, FARIDABANO
APPLICANT: NATO, FARIDABANO
APPLICANT: BARNWELL, JOHN
APPLICANT: BARNWELL, JOHN
APPLICANT: BARNWELL, JOHN
APPLICANT: BARNWELL, JOHN
TITLE OF INVENTION: PLASMODIUM MSP-1
FILE REFERENCE: 0660-0135-0XCIP
FILE REFERENCE: 0660-0135-0XCIP
FILE REFERENCE: 1999-04-18
EARLIER FILING DATE: 1999-04-18
EARLIER FILING DATE: 1999-04-18
EARLIER FILING DATE: 1996-02-14
NUMBER OF SEQ ID NOS: 14
SEQ ID NO 10
SEQ ID NO 10
LENGTH: 108
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Best Local Similarity 100.0%; Pred. No. 1.4e-07;
Matches 18; Conservative 0; Mismatches 0;
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100.0%; Pred. No. 1.3e-07;
tive 0; Mismatches 0;
                Sequence 10, Application US/09134333 GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 18; Conservative
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US-09-125-031-5
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17 NSGCFRHLDEREECKCLL 34

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APPLICANT: ROTH, CHARLES
APPLICANT: BARWHELL, JOHN
APPLICANT: MENDIS, KAUN
APPLICANT: MENDIS, KALDABANO
TITLE OF INVENTION: RECOMBINANT PROTEIN CONTAINING A C-TERMINAL FRAGMENT OF
TITLE OF INVENTION: PLASMODIUM MSP-1
FILE REPERBACE: 0660-0139-0XPCT
CURRENT APPLICATION NUMBER: US/09/125,031B
CURRENT FILING DATE: 1999-03-10
PRIOR PAPPLICATION NUMBER: PCT-FR97/00290
PRIOR PAPLICATION NUMBER: PCT-FR97/00290
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100.0%; Pred. No. 1.4e-07;
tive 0; Mismatches 0;
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100.0%; Pred. No. 1.4e-07;
ilve 0; Mismatches 0;
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ROTH, CHARLES
BARNWELL, JOHN
MENDIS, KAMINI
NATO, FARIDABANO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 5, Application US/09125031B; GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 18; Conservative
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Best Local Similarity 100.
Matches 18; Conservative
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Search completed: January 29, 2002, 10:56:05 Job time: 2401 sec
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                                                                                                             RESULT 14
US-09-134-333-5
: Sequence 5. Application US/09134333
: GENERAL INFORMATION:
APPLICANT: LONGACRE-ANDRE, SHIRLEY
APPLICANT: ROTH, CHARLES
APPLICANT: NATO, FARIDABAN
APPLICANT: MENDIS, KAMIN
APPLICANT: MENDIS, AMIN
APPLICANT: MENDIS, AMIN
CURREY APPLICATION: PLASMODIUM MSP-1
FILE REFERENCE: 060-0135-0XC10
CURREY APPLICATION NUMBER: US/09/134,333
CURREY FILING DATE: 1999-04-18
EARLIER FILING DATE: 1997-02-14
EARLIER APPLICATION NUMBER: FR96/01822
EARLIER APPLICATION NUMBER: FR96/01822
EARLIER APPLICATION NUMBER: 2.1
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Sequence 8, Application US/09125031

GENERAL INFORMATION:
APPLICANT: LONGARGE-ANDRE, SHIRLEX
APPLICANT: NATO, FARIDABANO
APPLICANT: BARNWALL, JOHN
APPLICANT: BARNWALL, JOHN
TITLE OF INVENTION: RECOMBINANT PROTEIN CONTAINING A C-TERMINAL FRAGMENT OF
TITLE OF INVENTION: PLASMODIUM MSP-1
FILE REFERENCE: 0660-0139-0XPCT
CURRENT APPLICATION NUMBER: US/09/125,031
CURRENT APPLICATION NUMBER: PCJ/FR97/00290
EARLIER APPLICATION NUMBER: PCJ/FR97/00290
EARLIER APPLICATION NUMBER: FR96/01822
EARLIER RELING DATE: 1997-02-14
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; ORGANISM: Plasmodium falciparum
US-09-125-031-8
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                          17 NSGCFRHLDEREECKCLL 34
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US-09-125-031-8
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Sequence 863, App Sequence 862, App Sequence 11, Appl Sequence 49463, A Sequence 936, App Sequence 77213, App Sequence 77213, App Sequence 77212, App Sequence 79660, A Sequence 79660, A Sequence 79660, A Sequence 7496, App 
US-09-708-427-49462 US-09-620-394B-934 US-09-620-394B-7490 US-09-620-394B-7489 US-09-708-427-17436 JS-09-708-427-17435

ALIGNMENTS

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US-09-783-931-13
US-09-708-427-39610
US-09-708-427-862
US-09-708-427-862
US-09-708-427-49464
US-09-708-427-49463
US-09-708-427-49463
US-09-708-427-77213
US-09-708-427-77213
US-09-708-427-77213
US-09-708-427-77213
US-09-708-427-77213
US-09-708-427-77213
US-09-708-427-77213
US-09-708-427-77213
                                                                                                                                                                                                                                                                                                                                                                                           Severate 1. Application US/09978756
GENERAL INFORMATION:
APPLICANT: Holder, Anthony
APPLICANT: Birdsall, Berry
APPLICANT: Feeney, James
APPLICANT: Morgan, William
APPLICANT: Syed, Shabih
TITLE OF INVENTION: Walaria Vaccine
FILE REFERENCE: 18396/1005
CURRENT APPLICATION NUMBER: US/09/978,756
CURRENT FILING DATE: 2001-10-16
PRIOR PILING DATE: 2000-04-20
PRIOR FILING DATE: 1999-05-13
PRIOR FILING DATE: 1999-05-13
PRIOR PRILING DATE: 1999-05-25
PRIOR FILING DATE: 1999-05-25
PRIOR PRILING DATE: 1999-05-25
PRIOR FILING DATE: 1999-06-25
PRIOR PILING DATE: 1999-06-25
PRIOR FILING DATE: 1999-06-25
PRIOR FILING DATE: 1999-06-25
PRIOR FILING DATE: 1999-06-25
SOFTWARR: PALCATION NUMBER: 9909072.2
PRIOR PILING DATE: 1999-06-25
SOFTWARR: PALCATION NUMBER: 9909072.2
PRIOR PILING DATE: 1999-06-25
SOFTWARR: PALCATION NUMBER: 9909072.2
PRIOR PILING DATE: 1999-04-20
SOFTWARR: PALCATION VORS: 3
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APPLICANT: Holder, Anthony; APPLICANT: Birdsall, Berry
APPLICANT: Feeney, James
APPLICANT: Keney, James
APPLICANT: Syed, Shabih
TITLE OF INVENTION: Malaria Vaccine
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US-09-978-756-1
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100.0%;
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Best Local Similarity 100.
Matches 18; Conservative
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                                 US-09-978-756-1
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5022, Ap
63902, A
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Sequence 2,
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Sequence 20
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2: /cgn2_6/ptodata/2/paa/USO6_NEW_COMB.pep:*

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4: /cgn2_6/ptodata/2/paa/USO8_NEW_COMB.pep:*

5: /cgn2_6/ptodata/2/paa/USO8_NEW_COMB.pep:*

5: /cgn2_6/ptodata/2/paa/USO8_NEW_COMB.pep:*

7: /cgn2_6/ptodata/2/paa/USO8_NEW_COMB.pep:*

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Compugen Ltd.
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US-09-978-756-2

US-09-177-4158-3

US-09-117-4158-2

US-09-117-4158-20

US-09-117-4158-20

US-09-117-4158-18

US-09-117-4158-18

US-09-269-874A-7

US-09-269-874A-7

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US-09-269-874A-7

US-09-269-874A-7

US-09-269-874A-7

US-09-269-874A-7

US-09-108-427-32716

US-09-708-427-32714

US-09-708-427-63903

US-09-708-427-63903

US-09-708-427-63902

US-09-708-427-63902

US-09-708-427-63902

US-09-908-193-34

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US-09-908-193-38

US-09-908-193-38
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                 GenCore version
Copyright (c) 1993 - 2000
                                                                                                       January 29, 2002, 10:58:12
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Maximum Match 100%
Listing first 45 summaries
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105
1 NSGCFRHLDEREECKCLL 18
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Perfect score:
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Gaps

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Length 96; Indels

Score 105; DB 5; Pred. No. 5.5e-09; Mismatches 0;

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AFFILENT Yang, Shutong TITLE OF INVENTION: Malaria Vaccine Based Upon the Addition of a MSA1 Peptide
Yang, Shutong
TITLE OF INVENTION: Malaria Vaccine Based Upon the Addition
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ADDRESSEE: Henry D. COLEMAN SUDOL SAPONE,
                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Henry D. Coleman, COLEMAN SUDOL SAPONE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 105; DB 5; 100.0%; Pred. No. 2.6e-08;
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FILING DATE: 29-Jul-1998
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
COMPUTER: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPAG (ASCII)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/117,415B
FILING DATE: 29-Jul-1998
CLASSIFICATION: 435
                                                       of a MSA1 Peptide
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STATE: CONDECTION

ZIP: 10017

COMPUTER READABLE FORM:

COMPUTER: IBM PC COMPATIBLE

COMPUTER: IBM PC COMPATIBLE

SOFTWARE: WOODPOOR

SOFTWARE: WOO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TOPOLOGY: linear MOLECULE TYPE: protein ; SEQUENCE DESCRIPTION: SEQ ID NO: 2: US-09-117-415B-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:

NAME: Coleman, Henry D.

REGISTRATION NUMBER: 32,559

REFERENCE/DOCKET NUMBER: R12-(
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 679-9121
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                        STREET: 714 Colorado Avenue
CITY: Bridgeport
STATE: Connecticut
COUNTRY: USA
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GENERAL INFORMATION:
APPLICANT: Davidson, Eugene
                                                                                                                                                                                                                                                                                                                     ZIP: 10017
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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NAME: Coleman, Henry D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 594 amino acids TYPE: amino acid
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Best Local Similarity 100.0%; P
Matches 18; Conservative 0;
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                                                                                                 NUMBER OF SEQUENCES:
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US-09-117-415B-22
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ilarity 100.0%; Pred. No. 1.8e-08;
Conservative 0; Mismatches n.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 105; DB 5;
ilarity 100.0%; Pred. No. 1.8e-08;
Conservative 0; Mismatches n
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Sequence 3, Application US/09978756
SEGUENEAL INFORMATION:
APPLICANT: Holder, Anthony
APPLICANT: Birdsall, Berry
APPLICANT: Birdsall, Berry
APPLICANT: Feeney, James
APPLICANT: Morgan, William
APPLICANT: Syed, Shabih
TTTLE OF INVENTION: William
APPLICANT: Syed, Shabih
TTLE OF INVENTION: UNDER: US/09/978,756
CURRENT APPLICATION NUMBER: US/09/978,756
CURRENT FILING DATE: 2001-10-16
PRIOR APPLICATION NUMBER: 09/31,817
PRIOR APPLICATION NUMBER: 09/31,817
PRIOR APPLICATION NUMBER: 09/31,817
PRIOR APPLICATION NUMBER: 09/31,451
PRIOR FILING DATE: 1999-05-25
PRIOR FILING DATE: 1999-05-25
PRIOR FILING DATE: 1999-05-25
SPRIOR FILING DATE: 1999-04-20
NUMBER OF SEQ ID NOS: 3
SOFTWARE: PATENTIN VERSION 3.0
                                         CURRENT APPLICATION NUMBER: US/09/978,756
CURRENT APPLICATION NUMBER: US/09/978,756
CURRENT FILING DATE: 2001-10-16
PRIOR APPLICATION NUMBER: OFT/GB00/01558
PRIOR FILING DATE: 1909-04-20
PRIOR FILING DATE: 1999-05-13
PRIOR FILING DATE: 1999-05-13
PRIOR FILING DATE: 1999-05-25
PRIOR FILING DATE: 1999-05-25
PRIOR FILING DATE: 1999-06-25
NUMBER OF SEQ ID NOS: 3
SEQ ID NO 2
SEQ ID NO 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT (CRANISM: Plasmodium falciparum US-09-978-756-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: PRT
; ORGANISM: Plasmodium falciparum
US-09-978-756-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    295 NSGCFRHLDEREECKCLL 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 NSGCFRHLDEREECKCLL 18
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                           REFERENCE: 18396/1005
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Matches 18; Conserv
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Best Local Similarity
Matches 18; Conserv
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US-09-978-756-3
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Pred. No. 2.6 Mismatches

Length 594;

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Yang, Shutong
TITLE OF INVENTION: Malaria Vaccine Based Upon the Addition
of a MSAl Peptide
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                                                                                                                                                                                                                                  ADDRESSEE: Henry D. Coleman, COLEMAN SUDOL SAPONE, STREET: 714 Colorado Avenue
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ADDRESSEE: Henry D. Coleman, COLEMAN SUDOL SAPONE,
STREET: 714 Colorado Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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Pred. No. 2.8e-08;
                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: WOOTGHEN CC-DOS/MS-DOS
SOFTWARE: WOOTGHEN (ASCII)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/117,415B
FILING DATE: 29-U1-1998
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: R12-030
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 679-0090
TELEFAX: (212) 679-9121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 10017
COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Coleman, Henry D. REGISTRATION NUMBER: 32,559
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GENERAL INFORMATION:
APPLICANT: Davidson, Eugene
                                                                           Sequence 20, Application US/09117415B
GENERAL INFORMATION:
APPLICANT: Davidson, Eugene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 631 amino acids TYPE: amino acid
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1larity 100.0%;
Conservative 0;
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INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                      CITY: Bridgeport
STATE: Connecticut
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COUNTRY: USA
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Best Local Similarity
Matches 18; Conserv
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                                                                                                                                                                                                                                                                                             Length 613;
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                                                                                                                                                                                                                                                                                                                                  Indels
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100.0%; Pred. No. 2.7e-08;
Live 0; Mismatches 0;
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Pred. No. 2.8e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/09/117,415B
FILING DATE: 29-Jul-1998
CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: COleman, Henry D.
REGISTARION NUMBER: 32,559
REFERENCE/DOCKET NUMBER: R12-030
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 679-0090
TELEFAX: (212) 679-9121
                  R12-030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPad (ASCII)
CURRENT APPLICATION DATA:
                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 22:
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MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-09-117-4158-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: Henry D. Coleman.
STREET: 714 Colorado Avenue
CITY: Bridgeport
REGISTRATION NUMBER: 32,559
                                TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 679-0090
TELEFAX: (212) 679-9121
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 18, Application US/09117415B
GENERAL INFORMATION:
APPLICANT: Davidson, Eugene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                  LENGTH: 613 amino acids TYPE: amino acid
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100.0%; Pr
tive 0;
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Best Local Similarity 100.
Matches 18; Conservative
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Best Local Similarity
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Sequence 1554, Application US/09605703B
GENERAL INFORMATION
APPLICANT: Pompejus, Markus
APPLICANT: Schroder, Barkhard
APPLICANT: Schroder, Hartwig
APPLICANT: Zelder, Oskar
APPLICANT: Zelder, Oskar
APPLICANT: Haberhauer, Gregor
TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING NOVEL
TITLE OF INVENTION: PROTEINS
FILE REFERENCE: BG1-129CP
CURRENT APPLICATION NUMBER: US/09/605,703B
CURRENT APPLICATION NUMBER: US/09/605,703B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 3, Application US/09269874A
; Sequence 3, Application US/09269874A
; GENERAL INFORMATION:
APPLICANT: Bujard, Hermann
; TITLE OF INVENTION: Recombinant Process for Preparing a
TITLE OF INVENTION: Recombinant Antigen, GP190/MSP1
TITLE OF INVENTION: Complete Malaria Antigen, GP190/MSP1
TITLE OF INVENTION: Complete Malaria Antigen, GP190/MSP1
FILE REPERENCE: GRUE-003
CURRENT APPLICATION NUMBER: US/09/269,874A
CURRENT FILING DATE: 1999-08-02
PRIOR FILING DATE: 1997-10-02
PRIOR FILING DATE: 1996-10-02
PRIOR FILING DATE: 1996-10-02
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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100.0%; Pred. No. 6.3e-08;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                   ; Score 105; DB 5;
; Pred. No. 6.2e-08;
0; Mismatches 0;
PRIOR APPLICATION NUMBER: PCT/EP97/05441
PRIOR FILING DATE: 1997-10-02
PRIOR APPLICATION NUMBER: DE 19640817.2
PRIOR FILING DATE: 1996-10-02
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FASLSEQ for Windows Version 4.0
SEQ ID NO 5
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PRIOR FILING DATE: 1999-07-08
PRIOR APPLICATION NUMBER: 60/152,318
PRIOR FILING DATE: 1999-09-09-09
NUMBER OF SEQ ID NOS: 2934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: PRT ORGANISM: Plasmodium falciparum US-09-269-874A-3
                                                                                                                                                                                                                                                      TYPE: PRT ORGANISM: Plasmodium falciparum; US-09-269-874A-5
                                                                                                                                                                                                                                                                                                                                                                                                            100.0%;
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Best Local Similarity 100.
Matches 18; Conservative
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Best Local Similarity 100.7
Matches 18; Conservative
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US-09-605-703B-1594
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US-09-269-874A-3
                                                                                                                                                                                                                                   LENGTH: 1621
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; Sequence 7, Application US/09269874A
; GENERAL INFORMATION:
    GENERAL INFORMATION:
    TITLE OF INVENTION: Complete Malaria Antigen, GP190/MSP1
    TITLE OF INVENTION: Complete Malaria Antigen, GP190/MSP1
; TITLE REFERENCE: GGUE-003
    CURRENT FILIAG DATE: 1999-08-02
    CURRENT FILIAG DATE: 1999-08-02
    PRIOR APPLICATION NUMBER: DCT/EP97/05441
    PRIOR APPLICATION NUMBER: DCT/E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 649;
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Sequence 5. Application US/09269874A.
GENERAL INFORMATION:
APPLICANT: Bujard, Hermann
TITLE OF INVENTION: Recombinant Process for Preparing a
TITLE OF INVENTION: Complete Malaria Antigen, GP190/MSP1
FILE REFERENCE: GRUE-003
CURRENT APPLICATION NUMBER: US/09/269,874A
; CURRENT FILING DATE: 1999-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 105; DB 5;
Pred. No. 6.1e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.0%; Pred. No. 2.8e-08;
Matches 18; Conservative 0; Mismatches 0;
                                      SOFTWARE: WOLDPAD (ASCII)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/117,415B
FILING DATE: 29-U11-1998
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: COLEMAN, HENRY D.
REGISTRATION NUMBER: 32,559
TELECOMMUNICATION INFORMATION:
TELECHONE: (212) 679-0900
TELECHONE: (212) 679-0900
TELECHONE: (212) 679-0121
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
TYPE: maino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear

MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-09-117-415B-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%;
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Best Local Similarity 100."
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 NSGCFRHLDEREECKCLL 18
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US-09-269-874A-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 1602
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APPLICANT: N. ALEXANDROV et al.

TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID
TITLE OF INVENTION: THEREBY
FILE REFERENCE: 2750-1243P
CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTHARE: PATENTIN VEFSION 3.1
SEQ ID NO 32214
LENGTH: 1444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ä
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                                                                                                                                                                                              Score 44; DB 5;
Pred, No. 65;
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Pred. No. 69;
                                                                                                                                                                                                                                                                                           1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COTHER INFORMATION: Xaa is any amino acid:
NAME/KEY: misc_feature
LOCATION: 1..1444
COTHER INFORMATION: Ceres Seq. ID 1834858
US-09-708-427-32714
; OTHER INFORMATION: Ceres Seq. ID 1834859
US-09-708-427-32715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Search completed: January 29, 2002, 10:58:12 Job time: 2508 sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 32714, Application US/09708427; GENERAL INFORMATION:
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                                                                                                                                                                                              41.9%;
52.9%;
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52.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  955 GCFSHLKTVFQELEECR 971
                                                                                                                                             Ouery Match
Best Local Similarity 52.30
المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المال
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Best Local Similarity 52.>>
المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المالية المال
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc_feature
LOCATION: 1..1444
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US-09-708-427-32714
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US-09-708-427-32716
US-09-708-427-32716
Sequence 32716.
GENERAL INFORMATION:
TITLE OF INVENTION: THEREBY
TITLE OF INVENTION: THEREBY
FILE REFERENCE: 2750-1243P
CURRENT APPLICATION NUMBER: US-09/708,427
CURRENT APPLICATION NUMBER: US-09/708,427
SOFTWARE: Patentin version 3.1
SEQ ID NO 32716
LENGTH: 1315
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US-09-708-427-32715
US-09-708-427-32715
SEQUENCE 32715. Application US/09708427
SEQUENCE 32715. Application US/09708427
GENERAL INFORMATION:
APPLICANT: N. ALEXANDROV et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: THERENE
FILE REFERENCE: 2750-1243P
CURRENT APPLICATION UNDER: US/09/708,427
CURRENT APPLICATION UNDER: US/09/708,427
SOFTWARE: PATENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: PATENT NOS: 85364
SOFTWARE: PATENT NOS: 85364
SOFTWARE: PATENT NOS: 85364
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Pred. No. 64;
1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                       Length 85;
                                                                                                                                                                                                                                                                                                                                                                                                                                    5; Indels
                                                                                                                                                                                                                                                                                                                                  Score 45; DB 5;
Pred. No. 4.3;
4; Mismatches
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COTHER INFORMATION: Ceres Seq. ID 1834860 US-09-708-427-32716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc_feature
LOCATION: 1..1342
UNTER INFORMATION: Xaa is any amino acid
NAME/KEY: misc_feature
LOCATION: 1..1342
                                                                                                                                        ; ORGANISM: Corynebacterium glutamicum US-09-605-703B-1594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Arabidopsis thaliana
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52.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23 TGVIRMLDEGEDCKAVV 39
                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 47.1
Matches 8; Conservative
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Matches 9; Conservative
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LOCATION: 1..1315
    ; SEQ ID NO 1594
; LENGTH: 85
                                                                                                                                                                                                                                                                                                                                       Query Match
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us-09-763-397a-11.rapn

Sequence:

Run on:

Searched:

Database

**64500000** 

Result è

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Sequence 332, App
Sequence 6362, Ap
Sequence 6281, Ap
Sequence 6281, Ap
Sequence 1026, Ap
Sequence 1026, Ap
Sequence 1026, Ap
Sequence 1200, Ap
Sequence 5168, Ap
Sequence 5168, Ap
Sequence 1269, Ap
Sequence 1269, Ap
Sequence 1269, Ap
Sequence 2246, Ap
Sequence 435, App
Sequence 2246, Ap
Sequence 2777, Ap
Sequence 2777, Ap
Sequence 2777, Ap
Sequence 2777, Ap
                     Sequence 318, App
Sequence 3037, Ap
Sequence 19706, A
Sequence 19706, A
Sequence 332, App
Sequence 330, App
Sequence 22032, A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING TITLE OF INVENTION: CTL IMMUNITY NUMBER OF SEQUENCES: 153
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew STREET: Steuart Street Tower, One Market Plaza CITY: San Francisco STATE: California COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 94105-1493
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPOTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOGTWARE: Patentin Release #1.0, version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/197,484
FILING DATE: 16-FEB-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/935,811
FILING DATE: 26-AUG 1992
PRIOR APPLICATION DATA:
         PCT-US01-03782A-314

US-09-758-441-318

US-09-758-441-318

US-09-733-089-19706

US-09-173-089-19706

US-09-617-681A-332

US-09-617-681A-332

US-09-617-681A-332

US-09-617-681A-332

US-09-617-681A-332

US-09-617-632-1027

US-09-252-691-6281

US-09-252-691-6281

US-09-107-532-5168

US-09-107-637-435

US-09-208-538-2245

PCT-US99-228538-2245

PCT-US99-228538-2245

PCT-US99-228538-2245

US-09-107-637-438-0

US-09-248-796-6574

US-09-248-796-6574

US-09-108-114197

US-09-108-114197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 19, Application US/08197484 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: VITIELLO, Maria A.
APPLICANT: CHESTNUT, Robert W.
APPLICANT: STTF, Alessandro D.
APPLICANT: CELIS, Esteban
APPLICANT: GRAY, HOWARD
                                                                                                                                                                                                                                418
7618
7676
290
290
296
313
366
399
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US-08-197-484-19
 Sequence 19, Appl
Sequence 2, Appli
Sequence 10, Appl
Sequence 41, Appl
Sequence 2, Appli
Sequence 22032, A
Sequence 7128, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 19, Appli
Sequence 2, Appli
                                                                                                     (without alignments)
1.262 Million cell updates/sec
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                                                                                      Search time 1760.55 Seconds
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                                                                                                                                                                                                                                                                                                                                                                                     GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-197-484-19
US-08-318-856-2
US-08-820-360-19
8 US-09-454-204A-2
1 US-09-763-397A-10
8 US-09-454-204A-41
US-09-763-397A-2
1 US-09-834-366-22032
4 US-09-844-366-22032
                                                                                                                                                                                                                                                         hits satisfying chosen parameters:
                                                                                                                                                                                                                                3148936 segs, 277657034 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUMMARIES
                                                                                      January 29, 2002, 10:56:03
                                                                                                                                                                                                                                                                                                                        Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                               OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                              Pending_Patents_AA_Main:*
                                                                                                                                                                                           BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                        US-09-763-397A-10
                                                                                                                                                                                                                                                                                  Minimum DB seq length: 0
Maximum DB seq length: 200000000
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                                                                                                                                                                 1 KPNDKSLY 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score
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us-09-763-397a-10.rapm

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APPLICANT: CHESTNUT, Robert W.
APPLICANT: SETTE, Alessandro D.
APPLICANT: CELIS, Esteban
APPLICANT: GRAY, Howard
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING
TITLE OF INVENTION: CTL IMMUNITY
NUMBER OF SEQUENCES: 154
                                                                                                                                                                                                                                                                                                                           Length 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC compatible
COMPUTER: ISM PC compatible
COMPUTER: ISM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/820,360
FILING DATE: 12-MAR-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: US 60/013,366
FILING DATE: 13-MAR-1996
PRIOR APPLICATION NUMBER: US 60/013,466
FILING DATE: 16-FEB-1994
                                                                                                                                                                                                                                                                                                                         100.0%; Score 44; DB 7; I
100.0%; Pred. No. 2.9e+06;
Live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 16 FEB-1994

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/935,811
FILING DATE: 26 AUG-1992

PRIOR APPLICATION NUMBER: US 07/874,491
FILING DATE: 27-APR-1992

PROPER APPLICATION DATA:
APPLICATION NUMBER: US 07/827,682

PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
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APPLICATION DATA:
APPLICATION DATA:
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REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 14137-26-4
                                                                                                                                                                                                                                 ), ORGANISM: Plasmodium falciparum
US-08-318-856-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 19, Application US/08820360 GENERAL INFORMATION:
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ATTORNEY/AGENT INFORMATION:
TELETAX: (202) 371-8856
TELEX:
                                         INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 8; Conserv
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100.0%; Pred. No. 2.9e+06;
Live 0; Mismatches 0;
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805 Fifteenth Street, N.W., #700
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                                    PRILING JUSTE: 2.7-AFW-1992
PRILING JUSTE: 2.7-AFW-1992
PRILOR JUSTE: 29-JAN-1992
PRILOR JUSTE: 29-JAN-1992
PRILOR JUSTE: 29-JAN-1992
PRILOR APPLICATION DATA: 30-JAN-1992
PRILOR JUSTE: 26-MCG-1991
ATTORNEY, 26-MCG-1991
ATTORNEY, 26-MCG-1991
REGISTRATION NUMBER: 31,990
REFERENCE, DOCKET NUMBER: 31,990
REFERENCE, DOCKET NUMBER: 14137-26-4
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION SEQ 10 NO: 19:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PAPLICATION NUMBER: US/08/318,856
PILING DATE: October 3, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 92 08 068.8
FILING DATE: APPLI 3, 1992
PRIOR APPLICATION NUMBER: GB 92 17 704.7
FILING DATE: August 20, 1992
PRIOR APPLICATION NUMBER: WO PCT/GB93/00711
APPLICATION NUMBER: WO PCT/GB93/00711
FILING DATE: APPLICATION NUMBER: APPLICATION NUMBER: WO PCT/GB93/00711
FILING DATE: APPLICATION NUMBER: WO PCT/GB93/00711
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO PCT/GB93/00711
  APPLICATION NUMBER: US 07/874,491
FILING DATE: 27-APR-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WordPerfect 5.1+ CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/08318856 GENERAL INFORMATION:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)-371-8850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25,154
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Best Local Similarity 100.
Matches 8; Conservative
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TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: PEP
TITLE OF INVENTION: REC
TITLE OF INVENTION: MEL
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 8 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-197-484-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Matthew Jacob REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                             amino acid
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20005
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ION: Recombinant Multivalent Malarial Vaccine Against Plasmodium Fa
6395-57049
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GENERAL INFORMATION:
APPLICANT: The Government of the United States of America, as represented by the
APPLICANT: The Government of the Department of Health and Human Services, Centers for
                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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APPLICANT: Hill, Adrian V.S.
APPLICANT: Hill, Adrian V.S.
APPLICANT: Gilbert, Sarah C.
APPLICANT: Schneider, Jorg
APPLICANT: Schneider, Jorg
APPLICANT: Plebanski, Magdalena
APPLICANT: Blanchard, Tomas
APPLICANT: Blanchard, Tom
TITLE OF INVENTION: Which Generate A CD8 T Cell Immune Response
FILE REPERENCE: 2907.1000-0006.
CURRENT APPLICATION NUMBER: US/09/454,204A
CURRENT FILING DATE: 1999-12-09
PRIOR PRILING DATE: 1999-12-09
PRIOR PILING DATE: 1998-06-09
PRIOR FILING DATE: 1997-06-09
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                                                                                                                                                                                                                                                                                                                                                                                           Length 8;
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                                                                                                                                                                                                                                                                                                                                                                                    Score 44; DB 21;
Pred. No. 2.9e+06;
Mismatches 0;
      TITLE OF INVENTION: Recombinant Multivalent ME FILE REFERENCE: 6395-57049
CURRENT APPLICATION NUMBER: US/09/763,397A
CURRENT FILING DATE: 2001-02-16
PRIOR APPLICATION NUMBER: US 60/097,703
PRIOR FILING DATE: 1998-08-21
PRIOR FILING DATE: 1999-08-19
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patentin version 3.1
SECTION NO 10
LENGTH: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 41
LENGTH: 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 41, Application US/09454204A GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Solitarity 100.0%; Processive 0;
                                                                                                                                                                                                                                                                                                ORGANISM: Plasmodium falciparum US-09-763-397A-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 100.
Matches 8; Conservative
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Best Local Similarity
Matches 8; Conserv
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29 KPNDKSLY 36
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US-09-763-397A-2
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GENERAL INFORMATION:
APPLICANT: The Government of the United States of America, as represented by the
APPLICANT: Secretary of the Department of Health and Human Services, Centers for
APPLICANT: Lal, Altaf A.
APPLICANT: Lal, Altaf A.
APPLICANT: Hasnain, Seyed E.
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SERIEMATION:
APPLICANT: Hill, Adrian V.S.
APPLICANT: Hill, Adrian V.S.
APPLICANT: Glibert, Sarah C.
APPLICANT: Schneider, Jorg
APPLICANT: Schneider, Jorg
APPLICANT: Plebanski, Magdalena
APPLICANT: Blanchard, Tomas
APPLICANT: Blanchard, Tom
TITLE OF INVENTION: Methods and Reagents for Vaccination
TITLE OF INVENTION: Mhich Generate A CD8 T Cell Immune Response
FILE REFERENCE: 2907.1000-000
CURRENT APPLICATION NUMBER: US/09/454,204A
CURRENT FILING DATE: 1999-12-09
PRIOR PAPLICATION NUMBER: CT/GB98/01681
PRIOR FILING DATE: 1998-06-09
PRIOR FILING DATE: 1998-06-09
PRIOR FILING DATE: 1997-06-09
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                                                                                                                                                                                                                                                                                                                                               Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 44; DB 18;
100.0%; Pred. No. 2.9e+06;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                              100.0%; Score 44; DB 12;
100.0%; Pred. No. 2.9e+06;
1ve 0; Mismatches 0;
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 2, Application US/09454204A; GENERAL INFORMATION:
           TELECOMMUNICATION INFORMATION:
                           TELEPHONE: (206) 467-9600
TELEFAX: (206) 623-6793
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
                                                                                                                                                                                                                                                                                            Query Match 100.
Best Local Similarity 100.
Matches 8; Conservative
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Best Local Similarity 100.

Matches 8; Conservative
                                                                                                                                                                 STRANDEDNESS: unknown
TOPOLOGY: unknown
                                                                                                                                                                                                         ; MOLECULE TYPE: peptide US-08-820-360-19
                                                                                                                                          TYPE: amino acid
STRANDEDNESS: unk
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                                                                                                                                                                                                                                                                                                                                                                                      1 KPNDKSLY 8
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APPLICANT: Ford, John E et al
TITLE OF INVENTION: Novel Bone Marrow Nucleic Acids and Polypeptides
TITLE OF INVENTION: Novel Bone Marrow Nucleic Acids and Polypeptides
FILE REFERENCE: 21272-040
CURRENT PRILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: 09/496,914
PRIOR APPLICATION NUMBER: 09/496,914
PRIOR APPLICATION NUMBER: 09/598,075
PRIOR APPLICATION NUMBER: 09/598,075
PRIOR PILING DATE: 2000-06-20
PRIOR PILING DATE: 2000-07-19
PRIOR PILING DATE: 2000-07-19
PRIOR PILING DATE: 2000-07-19
PRIOR PILING DATE: 2000-07-19
PRIOR PILING DATE: 2000-11-30
NUMBER OF SEC ID NOS: 386
SOFTWARE: Custom
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ed. No. 18;
Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Tanaka, Hiroaki
APPLICANT: Tanaka, Hiroaki
APPLICANT: Dumas Milne Edwards, Jean Baptiste
APPLICANT: Jobert, Severin
APPLICANT: Giordano, Jean-Yves
TITLE OF INVENTION: ESTS and Encoded Human Proteins.
FILE REFERENCE: 81.US1.PRO
CURRENT APPLICATION UNDER: US/60/197,873
UUMBER OF SEQ ID NOS: 52153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Mismatches
FILE REFERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/60/147,499
CURRENT FILING DATE: 1999-08-05
NUMBER OF SEQ ID NOS: 19935
SOFTWARE: Patent.pm
SEQ ID NO 7128
LENGTH: 67
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PCT-10301-03782A-314
PCT-10501-03782A-314
Sequence 314, Application PC/TUS0103782A
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 22032, Application US/60197873; GENERAL INFORMATION:
APPLICANT: Bejanin, Stephane
APPLICANT: Tanaka, Hiroaki
APPLICANT: Dumas Milne Edwards, Jean E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               81.8%;
75.0%;
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75.0%;
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Best Local Similarity 75.0
Matches 6; Conservative
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Best Local Similarity 75.0
Matches 6; Conservative
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US-60-197-873-22032
                                                                                                                                                                                      ; ORGANISM: Homo sapiens
US-60-147-499-7128
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58 KPNDKLIY 65
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58 KPNDKLIY 65
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SOFTWARE: Pater
SEQ ID NO 22032
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                        APPLICANT: Lal, Altaf A.

APPLICANT: Ping Shi, Ya

APPLICANT: Ping Shi, Ya

APPLICANT: Banafu, Seyed E.

TITLE OF INVENTION: Recombinant Multivalent Malarial Vaccine Against Plasmodium Falci
FILE REFERENCE: 6395-57049

CURRENT APPLICATION NUMBER: US/09/763,397A

CURRENT APPLICATION NUMBER: US 60/097,703

PRIOR FILING DATE: 1998-08-21

PRIOR FILING DATE: 1999-08-19

NUMBER OF SEQ ID NOS: 26

SOFTWARE: Patentin version 3.1
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Best Local Similarity 100.0%; Pred. No. 3;
Matches 8; Conservative 0; Mismatches 0; Indels
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Pred. No. 18;
1; Mismatches 1; Indels
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Sequence 22032, Application US/09834366
GENERAL INFORMATION:
APPLICANT: Bejanin, Stephane
APPLICANT: Tanaka, Hiroaki
APPLICANT: Dumas Milne Edwards, Jean Baptiste
APPLICANT: Jobert, Severin
APPLICANT: Jobert, Severin
FILE OF INVENTION: ESTS and Encoded Human Proteins.
FILE REFERENCE: 81.USZ.REG
CURRENT APPLICATION NUMBER: US/09/834,366
CURRENT APPLICATION NUMBER: US/09/834,366
CURRENT FILING DATE: 2001-04-13
PRIOR FILING DATE: 2000-04-18
NUMBER OF SEQ ID NOS: 52153
SOFTWARE: Patent.Pm
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APPLICANT: Jobert, S.
APPLICANT: Glocato, J.Y.
TITLE OF INVENTION: ESTS and Encoded Human Proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: Recombinant DNA/Protein US-09-763-397A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-60-147-499-7128; Sequence 7128, Application US/60147499; GENERAL INFORMATION:
       Control and Prevention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           81.8%;
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US-09-834-366-22032
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Best Local Similarity
Matches 6; Conserv
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58 KPNDKLIY 65
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Haley-Vicente, Dana

Ma, Yunqing Asundi, Vinod Wang, Zhiwei Weng, Gezhi

Zhou, Ping Ghosh, Malabika Wang, Dunrui

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APPLICANT: Drmanac, Radoje T
TITLE OF INVENTION: Novel Nucleic Acids and
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 810
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION: (9)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-09-758-441-318
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TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PM040
CURRENT APPLICATION NUMBER: US/09/758,441
CURRENT FILING DATE: 2001-01-11
PRIOR APPLICATION NUMBER: 60/179,065
PRIOR FILING DATE: 2000-01-31
PRIOR APPLICATION NUMBER: 60/180,628
PRIOR FILING DATE: 2000-02-04
NUMBER OF SEQ ID NOS: 328
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 36; DB 21; Length 586;
Pred. No. 2.5e+02;
1; Mismatches 0; Indels
                                                                                                                                                                                                           81.8%; Score 36; DB 1; Length 514;
85.7%; Pred. No. 2.2e+02;
ive 1; Mismatches 0; Indels
                                                                             ; NAME/KEY: misc_feature
; LCCATION: (1)...(514)
; OTHER INFORMATION: Xaa = any amino acid or nothing
PCT-USO1-03782A-314
                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 318, Application US/09758441 GENERAL INFORMATION:
                                                                                                                                                                                       Query Match
Best Local Similarity 85.77
S. Conservative
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Best Local Similarity 85.7
Matches 6; Conservative
                                     ORGANISM: Homo sapiens
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29 PNDRSLY 35
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US-09-758-441-318
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LENGTH: 514
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Gaps
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Pred. No. 2.9e+02;
1; Mismatches 0; Indels
CURRENT APPLICATION NUMBER: US/60/324,631
CURRENT FILING DATE: 2001-09-24
PRIOR FILING DATE: 2000-01-21
PRIOR FILING DATE: 2000-01-21
PRIOR FILING DATE: 2000-01-21
PRIOR FILING DATE: 2000-01-25
PRIOR FILING DATE: 2000-12-25
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-25
PRIOR FILING DATE: 2000-12-25
PRIOR APPLICATION NUMBER: PCT/WS01/02623
PRIOR APPLICATION NUMBER: PCT/WS01/02623
PRIOR APPLICATION NUMBER: PCT/WS01/02623
PRIOR APPLICATION NUMBER: PCT/WS01/02623
PRIOR APPLICATION NUMBER: US 09/496,914
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: US 09/300,873
PRIOR PELING DATE: 2000-04-27
PRIOR PLING DATE: 2001-02-05
PRIOR PELING DATE: 2001-02-05
PRIOR PELING DATE: 2000-02-28
PRIOR PELING DATE: 2000-02-28
PRIOR PELING DATE: 2000-05-18
PRIOR FILING DATE: 2000-05-18
PRIOR PELING DATE: 2000-05-18
PRIOR PELING DATE: 2001-02-26
PRIOR APPLICATION NUMBER: US 09/519,705
PRIOR APPLICATION NUMBER: US 09/519,705
PRIOR PELING DATE: 2000-03-07
PRIOR PELING DATE: 2000-03-07
PRIOR PELING DATE: 2000-03-19
PRIOR PELING DATE: 2000-03-19
PRIOR PELING DATE: 2000-03-19
PRIOR PELING DATE: 2000-03-19
PRIOR PELING DATE: 2000-03-11
PRIOR FILING DATE: 2000-03-31
PRIOR FILING DATE: 2000-03-31
PRIOR PELING DATE: 2000-03-31
PRIOR FILING DATE: 2000-03-31
PRIOR FILING DATE: 2000-03-31
PRIOR PELING DATE: 2000-03-31
PRIOR PELING DATE: 2000-03-31
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PRIOR PLING DATE: 2000-05-19
PRIOR PLING DATE: 2001-03-05
PRIOR PELING DATE: 2001-03-05
PRIOR PELICATION NUMBER: PCT/USO1/04941
PRIOR PELING DATE: 2000-03-31
PRIOR PELING DATE: 2000-03-31
PRIOR FILING DATE: 2000-03-30
PRIOR FILING DATE: 2001-03-30
PRIOR FILING DATE: 2001-03-30
PRIOR PELING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: US 09/770,160
PRIOR APPLICATION NUMBER: PCT/USO1/08656
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PRIOR APPLICATION NUMBER: PCT/US01/14827
PRIOR FILING DATE: 2001-05-16
                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 2000-02-03
APPLICATION NUMBER: US 09/560,875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR FILING DATE: 2001-04-18
PRIOR APPLICATION NUMBER: US 09/577,408
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Best Local Similarity 85./*
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US-60-324-631-3037
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RESULT 13
US-60-324-631-3037
Sequence 3037, Application US/60324631
GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom

Zhang, Jie Ren, Feiyan Xue, Aidong J. Zhao, Qing A. Wang, Jian-Rui

APPLICANT: APPLICANT: APPLICANT: APPLICANT:

APPLICANT:

111:111 93 PNDRSLY 99

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HESULT 14

OUS 08-7-19-19-10-6

SEQUENCE TO SECURATE DELICATION US/09733089

SEQUENCE TO SECURATE DELICATION US/09733089

SEQUENCE TO SECURITY DELICATION US/09733089

TITLE OF INVENTION TATE ATTACKED TO SECURE AND OTHER MOLECULES ASSOCIATED WITH TATE OF INVENTION TATE ATTACKED TO SECURE TO SECUR
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Ouery Match
Best Local Similarity 75.0%; Pred. No. 8.7e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Oy 1 KPNDKSLY 8
Search completed: January 29, 2002, 10:56:04
Job time: 2400 sec
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

January 29, 2002, 10:58:11 ; Search time 120.95 Seconds (Without alignments) 2.421 Million cell updates/sec

US-09-763-397A-10

44 1 KPNDKSLY 8 Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

173191 seqs, 36597120 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Maximum Match 100% Listing first 45 summaries Post-processing: Minimum Match 0%

Database :

Pending\_Patents\_AA\_New:\*

1: /cgn2\_6/ptcdata/2/paa/USO6\_NEW\_COMB.pep:\*

2: /cgn2\_6/ptcdata/2/paa/USO6\_NEW\_COMB.pep:\*

3: /cgn2\_6/ptcdata/2/paa/USO8\_NEW\_COMB.pep:\*

4: /cgn2\_6/ptcdata/2/paa/USO8\_NEW\_COMB.pep:\*

5: /cgn2\_6/ptcdata/2/paa/USO8\_NEW\_COMB.pep:\*

5: /cgn2\_6/ptcdata/2/paa/USO8\_NEW\_COMB.pep:\*

7: /cgn2\_6/ptcdata/2/paa/USO8\_NEW\_COMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Sequence 6362, Ap				Sequence 21871, A	٠.	Sequence 122, App	4, 1	27	196,	7269	Sequence 195, App	•		• -		26,	5683	Sequence 5330, Ap		4611,		11445,	Sequence 16149, A	Sequence 16148, A	Sequence 16147, A
QI	US-09-897-516-6362	US-09-815-242-11291	US-09-708-427-21872	US-09-897-516-5176	US-09-708-427-21871	US-09-708-427-21870	US-09-981-353-122	US-60-337-444-4	US-60-337-444-27	US-09-637-780B-196	US-09-708-427-72696	US-09-637-780B-195	US-09-708-427-72695	US-09-637-780B-194	US-09-708-427-72694	US-09-605-703B-54	US-09-605-703B-56	US-09-897-516-5682	US-09-815-242-5330	US-09-815-242-12189	US-09-897-516-4611	. US-09-897-516-6876	US-09-815-242-11445	US-09-708-427-16149	US-09-708-427-16148	US-09-708-427-16147
DB	Ŋ	S	2	'n	2	Ŋ	s	7	7	Ŋ	S	S	ഗ	ഗ	വ	'n	ഗ	Ŋ	2	ഹ	S	'n,	S	Ŋ	S	S
% Query Match Length DB	219	380	290	300	334	341	696	2115	2150	220	220	236	236	291	292	293	319	365	801	1055	4099	94	166	377	381	467
% Query Match	77.3	77.3	72.7	72.7	72.7	72.7	72.7	72.7	72.7	70.5	70.5	70.5	70.5	70.5	70.5	70.5	70.5	70.5	70.5	70.5	70.5	68.2	68.2	68.2	68.2	68.2
Score	34	34	32	32	32	32	32	32	32	31	31	31	31	31	31	31	31	31	31	31	31	30	30	30	30	30
Result No.	-	7	m	4	S	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56

APPLICANT: Haselbeck, Robert
APPLICANT: Haselbeck, Rari L.
APPLICANT: Dissen, Kari L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Tawaick, John D.
APPLICANT: Tamamoto, Robert T.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in

Sequence 11291, Application US/09815242 GENERAL INFORMATION:

RESULT 2 US-09-815-242-11291

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27	30	68.2	484	n	US-09-611-526-2907	Seguence 2907, Ap
28	30	68.2	929	ഹ	US-09-991-496-6	Sequence 6, Appli
29	30	68.2	718		US-09-815-242-12915	
30	30	68.2	803		US-09-801-368-394	Sequence 394, App
31	30		803		US-09-487-558-394	Sequence 394, App
32	30		904		US-10-015-127-12469	Sequence 12469, A
33	30		1427		US-09-991-496-97	Sequence 97, Appl
34	30	68.2	1641	5	US-09-991-496-96	Sequence 96, Appl
35	29		10		US-09-392-941A-69	Sequence 69, Appl
36	29		10		US-09-392-941A-84	Sequence 84, Appl
37	29		10		US-09-392-941A-90	Sequence 90, Appl
38	29		10		US-09-392-941A-91	Sequence 91, Appl
39	29		222		US-09-574-735C-4	Sequence 4, Appli
40	29		278		US-09-708-427-27528	Sequence 27528, A
41	29		318		US-09-935-720-1	Sequence 1, Appli
42	29		341		US-09-708-427-27527	
43	29		402		US-09-989-723-367	Sequence 367, App
44	29		402		US-09-989-724-367	Sequence 367, App
45	29	62.9	402		US-09-989-730-367	Sequence 367, App
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			٠		ALIGNMENTS	
E TITOGG	-					

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APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hueshig, Joseph E.
APPLICANT: Kasomil-Osterfeld, Karina C.
APPLICANT: State Steven C.
APPLICANT: Spater, Spater, Steven C.
APPLICANT: Spater, Spater, Steven C.
APPLICANT: Spater, S
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Pred. No. 16; .
0; Mismatches 2; Indels
Sequence 6362, Application US/09897516
GENERAL INFORMATION:
APPLICANT: Corbin, David R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        77.3%;
75.0%;
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Best Local Similarity 75.0
Matches 6; Conservative
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Sequence 21871, Application US/09708427
Sequence 21871, Application US/09708427
Sequence 21871, Application US/09708427
GENERAL INFORMATION:
APPLICANT: N. ALEXANDROV et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID
TITLE OF INVENTION: THEREBY
FILE REFERENCE: 2750-1243P
CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SSEQ ID NOS: 85364
SSEQ ID NO 21871
LENGTH: 334
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APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Huesing Joseph E.
APPLICANT: Rasomil-Osterfeld, Karina C.
APPLICANT: Slater, Steven C.
APPLICANT: Spiridonov, Sergei
TITLE OF INVENTION: Xenorhabdus sp. Genome Sequences And Uses Thereof
FILE REFERENCE: 38-21(51847)8
CURRENT APPLICATION NUMBER: US/09/897,516
CURRENT APPLICATION NUMBER: US 60/215, 161
PRIOR APPLICATION NUMBER: US 60/215, 161
PRIOR FILING DATE: 2000-06-30
NUMBER OF SEQ ID NOS: 8409
SEQ ID NO 5176
LENGTH: 300
TYPE: Pr.
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55;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Mismatches
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NAME/KEY: misc_feature
CATATON: 1.334
US-09-708-427-21871
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Best Local Similarity 71.4
Matches 5; Conservative
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Best Local Similarity 100.
Matches 6; Conservative
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COCCANISM: Xenorhabdus sp.
US-09-897-516-5176
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307 PHDKSIY 313
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US-09-708-427-21870
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US-09-708-427-21871
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GENERAL INFORMATION:
APPLICANT: N. ALEXANDROW et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: THEREBY
FILE REFERENCE: 2750-1243F
CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT APPLICATION NUMBER: US/09/708,427
SOFTWARE: PATENTIANG DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: PATENTIANG PATENTIANG ADDITION OF SEQ ID NOS: 85364
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71.4%; Pred. No. 53;
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Pred. No. 28;
1; Mismatches
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LOCATION: 1..290
CTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc_feature
LOCATION: 1..290
CTHER INFORMATION: Ceres Seq. ID 1840164
US-09-708-427-21872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                        US/09/815,242
                                                                                                                            CURRENT APPLICATION NUMBER: US/09/815,2.
CURRENT APPLICATION NUMBER: US/09/815,2.
CURRENT FILING DATE: 2010.03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000.03-21
PRIOR FILING DATE: 2000.03-21
PRIOR FILING DATE: 2000.05-23
PRIOR FILING DATE: 2000.05-26
PRIOR FILING DATE: 2000.05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/245,578
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR PELLING DATE: 2000-12-22
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75.0%;
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Best Local Similarity 75.0
Matches 6; Conservative
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Best Local Similarity
Matches 5; Conserv
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132 KPNTKALY 139
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263 PHDKSIY 269
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LENGTH: 290
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"" TITLE OF INVENTION: Sequence—Determined DNA Fragments and Corresponding Polypeptid TITLE OF INVENTION: Sequence—Determined DNA Fragments and Corresponding Polypeptid; TITLE OF INVENTION: Thereby; FILE REFERENCE: 2750-1096P; CURRENT APPLICATION NUMBER: US/09/637,780B; CURRENT FILING DATE: 2000-08-11

NUMBER OF SEQ ID NOS: 1401

SEQ ID NO 196

LENGTH: 220
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pred. No. 4.6e+02;
2; Mismatches 0; Indels
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APPLICANT Tarcaynski, Mitchell C.
APPLICANT Shan, Bo.
APPLICANT Lid, Stein E.
APPLICANT Lid, Stein E.
APPLICANT Lid, Stein E.
APPLICANT Gruis, Darren B.
APPLICANT Gruis, Darren B.
APPLICANT Manalev, Evgueni
APPLICANT Manalev, Evgueni
TITLE OF INVENTION: Methods for Improving Seed and Grain
TITLE OF INVENTION: Characteristics
FILE REFERENCE: 1390p2
CURRENT APPLICATION NUMBER: US/60/337,444
CURRENT FILING DATE: 2001-10-25
NUMBER OF SEQ IO NOS: 28
SOCTWARE: FastSEQ for Windows Version 3.0
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Pred. No. 4.7e+02;
2; Mismatches 0; Indels
               TITLE OF INVENTION: Methods for Improving Seed and Grain TITLE OF INVENTION: Characteristics FILE REFERENCE: 1390P2
CURRENT APPLICATION UNMBER: US/60/337,444
CURRENT FILING DATE: 2001-10-25
SOFTWARE: FastSEO for Windows Version 3.0
SEO ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-60-337-444-27; Sequence 27, Application US/60337444; GENERAL INFORMATION:
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; OKGANISM: Arabidopsis thaliana
US-60-337-444-27
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Best Local Similarity 71.4%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                       Query Match 72.7%;
Best Local Similarity 71.4%;
Matches 5; Conservative
                                                                                                                                                                                                                                   ; ORGANISM: arabidopsis
US-60-337-444-4
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| Db | 1703 PNDRSLF 1709
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SEQ ID NO 27
                                                                                                                                                                                             LENGTH: 2115
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63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
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GENERAL INFORMATION:
APPLICANT: Lasek, Amy W.
APPLICANT: Lasek, Amy W.
TITLE OF INVENTION: GENES EXPRESSED IN COLON CANCER FILE REFERENCE: PA-0038 US
CURRENT APPLICATION NUMBER: US/09/981,353
CURRENT FILING DATE: 2001-10-11
NUMBER OF SEQ ID NOS: 194
SOFTWARE: PERL Program
FILE REFERENCE: 2750-1243P; FILE REFERENCE: 2750-1243P; CURRENT APPLICATION NUMBER: US/09/708,427; CURRENT FILING DATE: 2000-11-09; NUMBER OF SEQ ID NOS: 85364; SOFTWARE: PatentIn version 3.1; SEQ ID NO 21870
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 32; DB
Pred. No. 63;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: 1344279CD1
US-09-981-353-122
                                                                                                                                                                                                                                                                                        OTHER INFORMATION: Xaa is any amino acid:
NAME/KEY: misc_feature
LOCATION: 1.341
OTHER INFORMATION: Ceres Seq. ID 1840162
US-09-708-427-21870
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 4, Application US/60337444
GENERAL INFORMATION:
APPLICANT: Tarczynski, Mitchell C.
APPLICANT: Olsen, Odd-Arne
APPLICANT: Shen, Bo
APPLICANT: Lid, Stein E.
APPLICANT: Lid, Stein E.
APPLICANT: Lid, Stein E.
APPLICANT: Li, Chiangjiang
APPLICANT: Gruis, Natoolf
APPLICANT: Gruis, Darren B.
                                                                                                                                                                                                               ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                  72.78;
71.48;
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Nichols, Scott E
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 72.7
Best Local Similarity 71.4
Matches 5; Conservative
                                                                                                                                                                                                                                                       NAME/KEY: misc_feature
LOCATION: 1..341
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314 PHDKSIY 320
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95 PNDRGLY 101
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US-09-981-353-122
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LENGTH: 969
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APPLICANT:
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Sequence 194, Application US/09637780B
Sequence 194, Application US/09637780B
GENERAL INFORMATION:
APPLICANT: ALEXANDROW, Nickolai
APPLICANT: BROVER, Vyacheslav
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptid
TITLE OF INVENTION: Thereby
TITLE OF INVENTION: Thereby
TITLE OF INVENTION: Thereby
CURRENT APPLICATION NUMBER: US/09/637,780B
CURRENT FILING DATE: 2000-08-11
NUMBER OF SEQ ID NOS: 1401
SEQ ID NO 194
LENGTH: 291
                                                                                                                                                                                                                                                                                                                                                        APPLICANT: N. ALEXANDROV et al.

APPLICANT: N. ALEXANDROV et al.

ITILE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID

TITLE OF INVENTION: THEREBY

FILE REFERENCE: 2750-1243P

CURRENT PELLING NUMBER: US/09/708,427

CURRENT FILING DATE: 2000-11-09

NUMBER OF SEQ ID NOS: 85364

SOFTWARE: Patentin version 3.1

SEQ ID NO 72695

LENGTH: 236
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67;
                                                                                                                                           Score 31; DB 5;
Pred. No. 67;
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Pred. No. 67;
2; Mismatches
                                                                                                                                                                               2; Mismatches
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LOCATION: 1..236
OTHER INFORMATION: Xaa is any amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: 1..291
OTHER INFORMATION: Xaa is any amino acid
                                              NAME/KEY: misc_feature
CCATION: 1..236
COTHER INFORMATION: Ceres Seq. ID 1481829
0S-09-637-780B-195
                                amino acid
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ORGANISM: Zea mays subsp. mays
NAME/KEY: misc_feature
LOCATION: 1..236
OTHER INFORMATION: Xaa is any
                                                                                                                                             70.5%;
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62.5%;
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Best Local Similarity 62.5
Matches 5; Conservative
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Best Local Similarity 62.5
Matches 5; Conservative
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40 KPADKAIY 47
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US-09-637-780B-194
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GENERAL INFORMATION:
APPLICANT: N. ALEXANDROV et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE REPERENCE: 2750-1243P
CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 8534
SOFTWARE: PATENTIN version 3.1
SEQ ID NO 72696
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62;
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Pred. No. 62;
2; Mismatches
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NAME/KEY: misc_feature
COCATION: 1..220
US-09-708-427-72696
                                               NAME/KEY: misc_feature
LOCATION: 1..220
CTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc_feature
LOCATION: 1..220
COTHER INFORMATION: Ceres Seq. ID 1481830
US-09-637-7808-196
                                                                                                                                                                                                    70.5%; Score 31; 62.5%; Pred. No.
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                    ORGANISM: Arabidopsis thaliana
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Best Local Similarity
Than 5; Conserve
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Best Local Similarity
Matches 5; Conserv
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24 KPADKAIY 31
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24 KPADKAIY 31
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US-09-708-427:72696
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RESULT 15
US-09-708427-72694
US-09-708427-72694, Application US/09708427
GENERAL INFORMATION:
APPLICANT: N. ALEXANDROW et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES:
TITLE OF INVENTION: THEREBY
FILE REFERENCE: 2750-1143P
CURRENT APPLICATION UNMER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SEQ ID NO 72694
LENGTH: 292
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70.5%; Score 31; DB 5; Length 291;
Best Local Similarity 62.5%; Pred. No. 84;
Matches 5; Conservative 2; Mismatches 1; Indels
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1..292
COCATION: 1..292
NAME/KEY: misc_feature
1..292
LOCATION: 1..292
COTHER INFORMATION: Ceres Seq. ID 1942389
US-09-708-427-72694
; NAME/KEY: misc_feature
; LOCATION: 1..291
; OTHER INFORMATION: Ceres Seq. ID 1481828
US-09-637-7808-194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Zea mays subsp. mays
FEATURE:
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96 KPADKAIY 103
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95 KPADKAIY 102
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Search completed: January 29, 2002, 10:58:12 Job time: 2508 sec

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Perfect score: Sequence: Scoring table:

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Minimum DB Maximum DB

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Sequence 41, Appli
Sequence 2, Appli
Sequence 15255, A
Sequence 4701, Ap
Sequence 1784, A
Sequence 1784, A
Sequence 11, Appli
Sequence 11, Appli
Sequence 17817, A
Sequence 23065, A
Sequence 2447, A
Sequence 2440, A
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Sequence 213, App
Sequence 1555, A
Sequence 1653, Ap
Sequence 26696, A
Sequence 27139, Ap
Sequence 27139, Ap
Sequence 27131, Ap
Sequence 2, App11
Sequence 28, App1
Sequence 28, App1
Sequence 28, App1
Sequence 28, App1
Sequence 29958, App1
Sequence 28605, App1
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Sequence 39361, A
Sequence 26, Appl
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: TITLELO, Maria A.
APPLICANT: SETTE, Alessandro D.
APPLICANT: GRAY, Howard
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING
TITLE OF INVENTION: CAPOSITIONS AND METHODS FOR ELICITING
TITLE OF INVENTION: TAKE IS A CORRESPONDENCES:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: Stead Francisco
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: ISM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/197,484
FILING DATE: 16-FEB-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/935,811
FILING DATE: 26-AUG-1992
PRIOR APPLICATION DATA:
1 US-09-763-397A-9
1 US-09-763-397A-9
1 US-09-763-397A-9
1 US-09-763-397A-1
2 US-09-763-397A-1
2 US-09-248-796-15255
2 US-09-248-796-17364
1 US-09-248-796-17364
1 US-09-248-796-17364
1 US-09-248-796-17317
1 US-09-248-796-17317
2 US-09-173-3301-2317
3 US-09-173-3301-2317
3 US-09-173-3558
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COUNTRY:
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    Sequence 21, Appl
Sequence 15, Appl
Sequence 10, Appl
Sequence 40, Appl
Sequence 21, Appl
Sequence 21, Appl
Sequence 21, Appl
                                                                                                                             January 29, 2002, 10:56:02 ; Search time 1760.55 Seconds (without alignments) 1.419 Million cell updates/sec
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13: /cgn2_6/ptodata/2/paa/US092_COMB.pep:*
14: /cgn2_6/ptodata/2/paa/US092_COMB.pep:*
15: /cgn2_6/ptodata/2/paa/US092_COMB.pep:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /cgn2_6/ptodata/2/paa/US097_COMB.pep:*
/cgn2_6/ptodata/2/paa/US098_COMB.pep:*
/cgn2_6/ptodata/2/paa/US099_COMB.pep:*
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                       GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-08-278-634-35
US-08-38-856-1
US-08-344-84-40
US-08-344-824A-40
US-08-714-175-21
US-08-714-175-21
US-08-14-1754-21
US-08-820-360-21
US-08-820-360-21
                                                                                                                                                                                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                  3148936 seqs, 277657034 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                               seq length: 0
seq length: 200000000
                                                                                                                                                                                                                         US-09-763-397A-9
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Match 1
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100.0
100.0
100.0
100.0
100.0
100.0
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Sequence 6,

26450786

Result

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Peptides of an Antigen, Capable of Recognition by or Induction of Cytotoxic T Lymphocytes, and Method of Identification
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                                                   Length 9;
                                                                                              Indels
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100.0%; Pred. No. 2.9e+06;
Live 0; Mismatches 0;
                                                     100.0%; Score 50; DB 6; 100.0%; Pred. No. 2.9e+06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.14
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/318,856
FILING DATE: October 3, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 92 08 068.8
FILING DATE: APril 3, 1992
PRIOR APPLICATION NUMBER: GB 92 17 704.7
FILING DATE: August 20, 1992
PRIOR APPLICATION NUMBER: WO PCT/GB93/00711
FILING DATE: APRIL 5, 1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER: 25,154
REFERRNCE/DOCKET NUMBER: 263-PPIR1577US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)-371-8850
                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Plasmodium falciparum
                                                                                                                                                                                                                                                                                Sequence 1, Application US/08318856 GENERAL INFORMATION: APPLICANT:
                                                                                              ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (202) 371-8856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 100.
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Flore:
COMPUTER
                                                         Query Match 100.
Best Local Similarity 100.
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: peptide ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Matthew Jacob REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     amino acid
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                                                                                                                                                              1 KPIVQYDNF
US-08-278-634-35
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US-08-318-856-1
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GENERAL INFORMATION:
APPLICANT: SETTE, Alessandro
APPLICANT: SIDNEY, John
TITLE OF INVENTION: HLA BINDING PEPTIDES AND THEIR USES
NUMBER OF SEQUENCES: 288
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: One Market Plaza, Steuart Street Tower, 20th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM: DEPOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
SOFTWARE: PATENTIN Release #1.0, Version #1.30
SURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/278,634
FILING DATE: 21-UTL-1994
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: BASTIAN, REVIN L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 14137-80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 50; DB 5; I
100.0%; Pred. No. 2.9e+06;
iive 0; Mismatches 0;
                                                                                                PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/749,568
FILING DATE: 26-MG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Parmelee, Steven W.
REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 14137-26-4
TELEPHONE: (206) 467-9600
TELEPHONE: (206) 623-6793
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
  APPLICATION NUMBER: US 07/874,491
FILING DATE: 27-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/827,682
FILING DATE: 29-JAN-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/543-9600
TELEFAX: 415/543-5043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 415/543-5043
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 100.
Best Local Similarity 100.
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                 unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                        9 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                   ; MOLECULE TYPE: peptide US-08-197-484-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                  unknown
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STRANDEDNESS: unk
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PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 100.0%; Score 50; DB 7; L
Best Local Similarity 100.0%; Pred. No. 2.9e+06;
Matches 9; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
APPLICANT:
APPLICANT:
TITLE OF INVENTION: MALARIA PEPTIDES
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
STREET: 805 Fifeenth St., Suite 799,
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/344,824A
ELLING DATE: 23-NOV-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/278,634
FILING DATE: 21-JUN 1994
FILING DATE: 21-JUN 1994
PRIOR APPLICATION DATA:
FILING DATE: 06-AUG-1993
PRIOR APPLICATION DATA:
FILING DATE: 05-MAR-1993
PRIOR APPLICATION DATA:
FILING DATE: 05-MAR-1993
PRIOR APPLICATION DATA:
FILING DATE: 07-AUG-1992
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: MS-DOS 7
SOFTWARE: Wordbad for Windows 95
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/714,175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 21, Application US/08714175 GENERAL INFORMATION: APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Alicea, Hector A.
REGISTRATION NUMBER: 40,891
REFERENCE/DOCKET NUMBER: 0118
TELECOMMUNICATION INFORMATION:
TELEFAX: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 40:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS
LENGTH: 9 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 KPIVQYDNF 9
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APPLICANT:
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                                     Sequence 40, Application US/08344824
GENERAL INFORMATION:
APPLICANT: SETTE, Alessandro
APPLICANT: SIDNEY, John
TITLE OF INVENTION: HLA BINDING PEPTIDES AND THEIR USES
NUMBER OF SEQUENCES: 399
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: One Market Plaza, Steuart Street Tower, 20th
STREET: Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match

100.0%; Score 50; DB 7; Length 9; Best Local Similarity 100.0%; Pred. No. 2.9e+06; Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 40, Application US/08344824A
GENERAL INFORMATION:
APPLICANT: Sette, Alessandro
APPLICANT: Sidney, John
TITLE OF INVENTION: HLA Binding Peptides and Their Uses;
NUMBER OF SEQUENCES: 308
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IDAPPY disk
COMPUTER: IDAPPY disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
CORFWATING SYSTEM: PC-DGS/MS-DGS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/344,824
FILING DATE: 23-NOV-1994
ATTOREX/AGENT INFORMATION:
APPLICATION NUMBER: US/08/278,634
FILING DATE: 21-JUL-1994
ATTOREX/AGENT INFORMATION:
NAME: Bastian, Kevin 1.1.
REGISTRATION NUMBER: 34,774
REGISTRATION NUMBER: 34,774
RECECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION OF 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
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ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: Two Embarcac
CITY: San Francisco
STATE: California
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US-08-344-824A-40
RESULT 4
US-08-344-824-40
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APPLICANT: VITELLO, Maria A.
APPLICANT: VITELLO, Maria A.
APPLICANT: SETTE, Alessandro D.
APPLICANT: SETTE, Alessandro D.
APPLICANT: SETTE, Alessandro D.
APPLICANT: CHESTNUT: SETEBAN
APPLICANT: CHESTNUT: COMPOSITIONS AND METHODS FOR ELICITING
TITLE OF INVENTION: CTL IMMUNITY
NUMBER OF SEQUENCES: 154
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTY: US
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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OPERATING SYSTEM:
OPERATING SYSTEM:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/020,360
FILING DATE: 12-MAR-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: US 60/013,366
FILING DATE: 13-MAR-1996
PRIOR APPLICATION NUMBER: US 60/013,366
FILING DATE: 13-MAR-1996
PRIOR APPLICATION NUMBER: US 60/197,484
PRIOR APPLICATION NUMBER: US 08/197,484
FILING DATE: 16-FEB-1994
PRIOR APPLICATION NUMBER: US 07/935,811
FILING DATE: 26-AUG-1992
PRIOR APPLICATION NUMBER: US 07/935,811
FILING DATE: 27-APR-1992
PRIOR APPLICATION NUMBER: US 07/874,491
FILING DATE: 27-APR-1992
PRIOR APPLICATION NUMBER: US 07/827,682
FILING DATE: 29-JAN-1992
PRIOR APPLICATION NUMBER: US 07/749,568
FILING APPLICATION NUMBER: US 07/749,568
                                                                                                                                                                                                                                                                                                                                            100.0%; Score 50; DB 11;
100.0%; Pred. No. 2.9e+06;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 14137-26-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 21, Application US/08820360 GENERAL INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Parmelee, Steven W
                              TELEPHONE: (202)-371-8850
TELEFAX: (202)-371-8856
                                                                                                                                                                                                                                                                                                                               TELEX:
INFORMATION FOR SEQ ID NO:
                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
                                                                                                                                                                                                                           ; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-714-175A-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                1 KPIVQYDNF 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS
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US-08-820-360-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 50; DB 11; Length 9; 100.0%; Pred. No. 2.9e+06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/GB95/26982
FILING DATE: 30 -MAR-1995
PRIOR APPLICATION NUMBER: GB 9406492.0
FILING DATE: 31 -MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: WATEN CHECK, JT.
RECISTATION NUMBER: 263/KPIR2867US
RECISTATION NUMBER: 263/KPIR2867US
                    FILING DATE:
CLASSIETCATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/GB95/26982
FILING DATE: 30-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9406492.0
FILING DATE: 31-MAR-1994
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: MALARIA PEPTIDES
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: WENDEROTH, LIND & PONACK
STREET: Washington
STATE: D.C.
                                                                                                                                                                                                                                           NAME: Warren M Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER: 263/KPIR2867US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)-371-8850
TELEFAX: (202)-371-8856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS-DOS 7
SOFTWARE: WordPad for Windows 95
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/714,175A
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 21. Application US/08714175A GENERAL INFORMATION:
APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      , MOLECULE TYPE: peptide US-08-714-175-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
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TITLE OF INVENTION: Recombinant Multivalent Malarial Vaccine Against Plasmodium Fa
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GENERAL INFORMATION:
APPLICANT: The Government of the United States of America, as represented by the
APPLICANT: Secretary of the Department of Health and Human Services, Centers for
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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TITLE OF INVENTION: Which Generate A CD8 T Cell Immune Response
FILE REFERENCE: 2907.1000-000
CURRENT APPLICATION NUMBER: US/09/454,204A
CURRENT FILING DATE: 1999-12-09
PRIOR FILING DATE: 1998-06-09
PRIOR FILING DATE: 1998-06-09
PRIOR FILING DATE: 1998-06-09
PRIOR FILING DATE: 1997-06-09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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                                                                                                                                                                                                                                                                                                                                                                                                ; Score 50; DB 21;
; Pred. No. 2.9e+06;
0; Mismatches 0;
                                                                                     PRIOR PELICATION NUMBER: US 6/097,703
PRIOR FILING DATE: 1998-08-21
PRIOR APPLICATION NUMBER: PCT / US99/18869
PRIOR FILING DATE: 1999-08-19
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PatentIn version 3.1
                        FILE REFERENCE: 6395-57049
CURRENT APPLICATION NUMBER: US/09/763,397A
CURRENT FILING DATE: 2001-02-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 78
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 41, Application US/09454204A GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Schneider, Jorg
APPLICANT: Plebanski, Magdalena
APPLICANT: Hanke, Tomas
APPLICANT: Smith, Geoffrey L.
APPLICANT: Blanchard, Tom
                                                                                                                                                                                                                                                                                                 ; ORGANISM: Plasmodium falciparum
US-09-763-397A-9
                                                                                                                                                                                                                                                                                                                                                                                                Query Match
100.0%;
Best Local Similarity 100.0%;
Matches 9; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: McMichael, Andrew
APPLICANT: Hill, Adrian V.S.
APPLICANT: Gilbert, Sarah C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 KPIVQYDNF 9
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                                                                                                                                                                                                           SOFTWARE: PE
SEQ ID NO 9
LENGTH: 9
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: The Government of the United States of America, as represented by the APPLICANT: The Government of the Department of Health and Human Services, Centers for Dis APPLICANT: Control and Prevention
APPLICANT: Land Altaf A.
APPLICANT: Hasnain, Xa
APPLICANT: Hasnain, Seyed E.
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APPLICANT: Plebanski, Magdalena
APPLICANT: Plebanski, Magdalena
APPLICANT: Hanke, Tomas
APPLICANT: Blanchard, Tom
TITLE OF INVENTION: Methods and Reagents for Vaccination
TITLE OF INVENTION: Mich Generate A CD8 T Cell Immune Response
FILE REFERENCE: 2907.1000-000
CURRENT PILLOR DATE: 1999-12-09
PRIOR APPLICATION NUMBER: PCT/GB98/01681
PRIOR FILING DATE: 1999-12-09
PRIOR FILING DATE: 1997-06-09
PRIOR FILING DATE: 1997-06-09
NUMBER OF SEQ ID NOS: 78
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 6
LENGTH: 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: CTL Epitope of the Malaria String US-09-454-204A-6
                                                                                                                                                                                                                                                                                                   100.0%; Score 50; DB 12;
100.0%; Pred. No. 2.9e+06;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 50; DB 18; 100.0%; Pred. No. 2.9e+06;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 6, Application US/09454204A GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: MCMichael, Andrew
APPLICANT: Hill, Adrian V.S.
APPLICANT: Gilbert, Sarah C.
APPLICANT: Schneider, Jorg
APPLICANT: Plebanski, Magdalena
APPLICANT: Hanke, Tomas
APPLICANT: Smith, Geoffrey L.
TELECOMMUNICATION INFORMATION:
                   TELEPANE: (206) 467-9600
TELEFAX: (206) 623-6793
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.
Matches 9; Conservative
                                                                                                                                    TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                      Query Match 100.

Best Local Similarity 100.

Matches 9; Conservative
                                                                                                                                                                                     ; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-820-360-21
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ORGANISM: Unknown
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RESULT 15
US-09-450-969-6185
US-09-450-969-6185
Sequence 6185. Application US/09450969
Sequence 6185. Application US/09450969
SITLE OF INFORMATION:
TITLE OF INVENTION: EPIDEMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: EPIDEMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: PATH99-09A
CURRENT APPLICATION NUMBER: US/09/450,969
UNMBER OF SEQ ID NOS: 7544
SEQ ID NO 6185
LENGTH: 464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 38; DB 18; Length 464;
Pred. No. 81;
1; Mismatches 1; Indels
                                                                                                                                                                     DB 15; Length 464;
81;
                                                                                                                                                                     Score 38; DB
Pred. No. 81;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Search completed: January 29, 2002, 10:56:03 Job time: 2399 sec
                                                                    TYPE: PRT ; ORGANISM: Staphylococcus epidermidis US-09-134-001C-4701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                76.0%;
75.0%;
                                                                                                                                                                        76.0%;
75.0%;
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Best Local Similarity 75.0.
                                                                                                                                                                          Query Match 76.0
Best Local Similarity 75.0
Matches 6; Conservative
          NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 4701
LENGTH: 464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; ORGANISM: S.epidermidis US-09-450-969-6185
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APPLICANT: LYON DOUGETE-Stamm et al
TITLE OF INVENTION: BETDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: BETDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: BETDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-10-08
APPLICANT: Control and Prevention
APPLICANT: Lal, Altaf A.
APPLICANT: Lal, Altaf A.
APPLICANT: High Shi, Ya
APPLICANT: Handle Shi, Ya
APPLICANT: Hashain, Seyed E.
TITLE OF INVENTION: Recombinant Multivalent Malarial Vaccine Against Plasmodium Falci
FILE REFRENCE: 6395-57049
CURRENT FILING DATE: 1909-08-16
PRIOR FILING DATE: 1998-08-21
PRIOR APPLICATION NUMBER: US 60/097,703
PRIOR FILING DATE: 1999-08-19
PRIOR FILING DATE: 1999-08-19
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patentin Version 3.1
SEQ ID NO 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS TITLE OF INVENTION: POR DIAGNOSTICS AND THERAPEUTICS CURRENT APPLICATION NUMBER: US/09/248,796

CURRENT APPLICATION NUMBER: US/09/248,796

CURRENT FILING DATE: 1999-02-12

NUMBER OF SEQ ID NOS: 28206

LENGTH: 329
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Pred. No. 35;
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                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Recombinant DNA/Protein US-09-763-397A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 15255, Application US/09248796
GENERAL INFORMATION:
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75.0%;
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Best Local Similarity 75.v.
6; Conservative
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US-09-248-796-15255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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Best Local Similarity
The 9; Conserve
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118 PLAQYDNF 125
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US-09-134-001C-4701
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ORGANISM:
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2.723 Million cell updates/sec
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                                                                                                                                                                                                                January 29, 2002, 10:58:11; Search time 120.95 Seconds
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1. /cgn2_6/ptodata/2/paa/USO6_NEW_COMB.pep:*

2. /cgn2_6/ptodata/2/paa/USO6_NEW_COMB.pep:*

3. /cgn2_6/ptodata/2/paa/USO3_NEW_COMB.pep:*

4. /cgn2_6/ptodata/2/paa/USO8_NEW_COMB.pep:*

5. /cgn2_6/ptodata/2/paa/USO9_NEW_COMB.pep:*

5. /cgn2_6/ptodata/2/paa/USO9_NEW_COMB.pep:*

5. /cgn2_6/ptodata/2/paa/USO0_NEW_COMB.pep:*
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-09-708-427-51401
US-09-708-427-51400
US-09-708-427-49343
US-09-708-427-49343
US-09-708-427-49343
US-60-333-726-1355
US-60-333-726-1355
US-60-333-726-1345
US-09-509-234A-41
US-09-509-234A-
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US-09-708-427-65942
US-09-897-516-5513
US-09-976-800-83
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          173191 seqs, 36597120 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUMMARIES
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                 protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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50
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Match Length
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Maximum DB s
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                                                                                                                                                                                                                        Run on:
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Sequence 51402, Application US/09708427
GENERAL INFORMATION:
APPLICANT: N. ALEXANDROV et al.
TITLE OF INVENTION: THEREBY
FILLE REFERENCE: 2750-1243P
CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILLING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SEQ ID NO 51402
LENGTH: 215
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US-09-708-427-51401

US-09-708-427-51401

Sequence 51401, Application US/09708427

GENERAL INFORMATION:
APPLICANT: N. ALEXANDROV et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID
TITLE OF INVENTION: THEREBY
FILE REFERENCE: 2750-1243P

CURRENT APPLICATION NUMBER: US/09/708,427

CURRENT PILING DATE: 2000-11-09

NUMBER OF SEQ ID NOS: 85364

SOFTWARE: Patentin version 3.1

SEQ ID NO 51401

LENGTH: 239
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           Sequence 117, App
Sequence 118, App
Sequence 14, Appl
Sequence 16, Appl
Sequence 31790, A
Sequence 3139, Ap
Sequence 15, Appl
Sequence 31789, A
                                                                                                                      Sequence 36, Appl
Sequence 2171, Ap
Sequence 2170, Ap
Sequence 2170, Ap
Sequence 625, App
Sequence 51, Appl
Sequence 51, Appl
Sequence 51, Appl
Sequence 51, Appl
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          US-09-976-800-117
US-09-976-800-118
US-09-635-949-14
US-09-635-949-16
US-09-708-427-31790
US-09-708-427-31790
US-09-708-427-31789
US-09-708-427-31789
US-09-708-427-31789
US-09-626-585C-36
US-09-620-3948-2171
US-09-620-3948-2170
                                                                                                                                                                       PCT-US01-27760-625
PCT-US01-27760A-625
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US-09-509-234C-51
US-09-708-427-7448
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc_feature
LOCATION: 1..215
OTHER INFORMATION: Xaa is any amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc_feature

CATATON: 1..215

US-09-70BR INFORMATION: Ceres Seq. ID 1926741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 75.0
Matches 6; Conservative
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82 KPLVKYDN 89
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US-09-708-427-51402
  Query Match
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US-09-708-427-54153
US-09-708-427-54153
Sequence 54153, Application US/09708427
Sequence 54153, Application US/09708427
GENERAL INFORMATION:
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID
TITLE OF INVENTION: THEREBY
TITLE OF INVENTION: THEREBY
CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT PILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: Patentin version 3.1
SEQ ID NO 54153
LENGTH: 355
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                                                                                                                                           Length 115;
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Pred. No. 9.6;
3; Mismatches
                                                                                                                                             DB 5;
                                                                                                                                           Score 34; DB 5
Pred. No. 7.7;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: 1..355
OTHER INFORMATION: Xaa is any amino acid
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CATTON: 1.139
US-09-708-427-49343
NAME/KEY: misc_feature
COGATION: 1..115
OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc_feature
COGATION: 1..115
USCATION: 1..115
US-09-708-427-49931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: Xaa is any amino acid
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55.6%;
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55.6%;
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Best Local Similarity 55.0
المالية 55.0
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Best Local Similarity 55.6
Matches 5; Conservative
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LOCATION: 1..355
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LOCATION: 1..139
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94 KPVLGYDDF 102
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US-09-708-427-49343
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GRNERAL INFORMATION:
GRNERAL INFORMATION:
GRNERAL INFORMATION:
TITLE OF INVENTION: THEREBY
FILE FERENCE: 2750-1243P
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                    Sequence 1400, Application US/09708427
GENERAL INFORMATION:
APPLICANT: N ALEXANDROV et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES TITLE OF INVENTION: THEREBY FILE REFERENCE: 2750-1243P
CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOGTWARE: PETCHIN VERSION 3.1
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Pred. No. 3.2;
2; Mismatches
                                                                                                                                                                                                   DB 5;
                                                                                                                                                                                                  Score 38; DB Pred. No. 2.8; 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTHER INFORMATION: Xaa is any amino acid NAME/KEY: misc_feature COCATION: 1..267
COCATION: 1..267
US-09-708-427-51400
                                                                    LOCATION: 1..239
COTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc_feature
LOCATION: 1..239
COTHER INFORMATION: Ceres Seq. ID 1926740
US-09-708-427-51401
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ORGANISM: Zea mays subsp. mays
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ORGANISM: Zea mays subsp. mays
                       ORGANISM: Zea mays subsp. mays
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75.0%;
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75.0%;
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Best Local Similarity 75.0
Matches 6; Conservative
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Best Local Similarity 75...
6; Conservative
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LOCATION: 1..267
                                                        NAME/KEY: misc_feature
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| 134 | KPLVKYDN 141
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LENGTH: 115
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LENGTH: 267
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Length 1328;
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                                                                                                                                                                                                                 Score 33; DB 7; Length 132
Pred. No. 2.1e+02;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Gala, Jean-Luc
TITLE OF INVENTION: GENETIC SEOS.,...METHODS & DEVICES FOR
TITLE OF INVENTION: TD. OF STAPHYLOCOCCI STRAINS
FILE REFERENCE: DECLEZ7.001APC
CURRENT APPLICATION NUMBER: US/09/509,234A
CURRENT FILING DATE: 2000-09-25
PRIOR PILLOR DATE: 1997-09-26
NUMBER OF SEQ ID NOS: 64
SOFTWARE: FASTSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Qiandong Zeng et al.
TITLE OF INVENTION: Systemic Discovery of New Genes FILE REFERENCE: 032796-090
CURRENT APPLICATION WOMBER: US/60/333,726
CURRENT APPLICATION WOMBER: US/60/333,726
NUMBER OF SEQ ID NOS: 1346
SEQ ID NO 1345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 33; DB 7; I
Pred. No. 2.1e+02;
1; Mismatches 1;
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Pred. No. 85;
2; Mismatches
FILE REFERENCE: 032796-090
CURRENT APPLICATION NUMBER: US/60/333,726
CURRENT FILING DATE: 2001-11-29
NUMBER OF SEQ ID NOS: 1346
SEQ ID NO 1323
LENGTH: 1328
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; GENERAL INFORMATION:
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                                                                                                                      TYPE: PRT; ORGANISM: Saccharomyces cerevisiae US-60-333-726-1323
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75.0%;
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ilarity 75.0%;
Conservative
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Best Local Similarity 57.1%;
Matches 4; Conservative
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Best Local Similarity
'-hea 6; Conserve
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Best Local Similarity
Matches 6; Conserv
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129 PIVQYGDF 136
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|129 PIVQYGDF 136
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US-60-333-726-1345
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US-09-509-234A-47
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LENGTH: 411
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                                                                                                                      Length 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 33; DB 7; Length 13; Pred. No. 2.1e+02; 1; Mismatches 1; Indels
                                                                                                                                                            1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1306, Application US/60333726
GENERAL INFORMATION:
APPLICANT: Qlandong Zeng et al.
TITLE OF INVENTION: Systemic Discovery of New Genes; File Reference: 032796-090
CURRENT APPLICATION NUMBER: US/60/333,726
CURRENT FILING DATE: 2001-11-29
NUMBER OF SEQ ID NOS: 1346
SEQ ID VO 1306
LENGTH: 1328
                                                                                                                                                                                                                                                                                                                             Sequence 1295, Application US/60333726
GENERAL INFORMATION:
APPLICANT: Qiandong Zeng et al.
TITLE OF INVENTION: Systemic Discovery of New Genes
FILE REFERENCE: 032796-090
CURRENT APPLICATION NUMBER: US/60/333,726
CURRENT FILING DATE: 2001-11-29
NUMBER OF SEQ ID NOS: 1346
SEQ ID NO 1295
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; GSMRRAL INFORMATION:
APPLICANT: Qiandon:
TITLE OF INVENTION: Systemic Discovery of New Genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   66.0%; Score 33; DB 7; Ilarity 75.0%; Pred. No. 2.1e+02; Conservative 1; Mismatches 1,
                                                                                                                      ď.
                                                                                                                    Score 33; DB E
Pred. No. 45;
2; Mismatches
    ; NAME/KEY: misc_feature
; LOCATION: 1..355
; OTHER INFORMATION: Ceres Seq. ID 1932726
US-09-708-427-54153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-60-333-726-1295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Saccharomyces cerevisiae US-60-333-726-1306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             66.0%;
75.0%;
                                                                                                                      66.0%;
62.5%;
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Matches 6; Conservative
                                                                                                                    Query Match 66.0
Best Local Similarity 62.5
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                         101 KPLLYYDN 108
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129 PIVQYGDF 136
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129 PIVQYGDF 136
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US-60-333-726-1295
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Trawick, Joh
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Best Local Similarity
Matches 4; Conserv
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Best Local Similarity
Matches 4; Conserv
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76 PVIDYDN 82
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                                                                                                                                                                                                                                                                                                                           2 PIVQYDN 8
                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 15
US-09-815-242-13515
                                                                                                                                                 LENGTH: 420
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                                                                                      Sequence 47, Application US/09509234C

Sequence 47, Application US/09509234C

Sequence 47, Application US/09509234C

APPLICANT: Vannuffel, Pascal

APPLICANT: Gala, Jean-Luc

TITLE OF INVENTION: ID. OF STAPHYLOCCCCI STRAINS

TITLE OF INVENTION: ID. OF STAPHYLOCCCCI STRAINS

TITLE OF INVENTION: UD. OF STAPHYLOCCCCI STRAINS

TITLE OF INVENTION: US/09/509,234C

CURRENT APPLICATION NUMBER: US/09/509,234C

CURRENT FILING DATE: 1997-09-26

NUMBER OF SEQ ID NOS: 64

SEQ ID NO 47

LENGTH: 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 420;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 5; Length 411;
85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Gala, Jean-Luc
TITLE OF INVENTION: GENETIC SEGS.,...METHODS & DEVICES FOR
TITLE OF INVENTION: ID. OF STAPHYLOCOCCI STRAINS
TITLE REFERENCE: DECLEZZ. 001APC
CURRENT APPLICATION NUMBER: US/09/509,234A
CURRENT FILING DATE: 2000-09-25
PRIOR APPLICATION UNBER: EP 97870146.4
PRIOR FILING DATE: 1997-09-26
NUMBER OS SEQ ID NOS: 64
SOFTWARE: FASTERQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Vannuffel, Pascal
APPLICANT: Gala, Jean-Luc
TITLE OF INVENTION: GENETIC SEQS.,...METHODS & DEVICES FOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT ORGANISM: Staphylococcus haemolyticus femA
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 32;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Staphylococcus capitis fema
US-09-509-234C-47
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US-09-509-234C-41
Sequence 41, Application US/09509234C;
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 41, Application US/09509234A GENERAL INFORMATION:
APPLICANT: Vannuffel, Pascal
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57.1%;
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57.1%;
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Best Local Similarity 57.12
Character 4; Conservative
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Best Local Similarity
Matches 4; Conserv
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76 PVIDYDN 82
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70 PVIDYDN 76
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70 PVIDYDN 76
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US-09-509-234A-41
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                                                                                      US-09-509-234C-47
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LENGTH: 420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Xu, Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: PROKARYOTES
FILE REPERRACE: ELITAR.011A
CURRENT APPLICATION NUMBER: 60/19,078
PRIOR PILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR PALICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-10-22
PRIOR PILING DATE: 2000-10-22
PRIOR PILING DATE: 2000-10-22
PRIOR PILING DATE: 2000-10-22
PRIOR PILING DATE: 2001-22-16
NUMBER OF SEQ IO NOS: 14110
SEQ ID NO 13515
                                                                                                                                                                                                                                                                                                                                                          Length 420;
                                                                                                                                                                                                                                                                                                                                                                                                            1; Indels
TITLE OF INVENTION: ID. OF STAPHYLOCOCCI STRAINS FILE REFERENCE: DECLE27.001APC CURRENT APPLICATION NUMBER: US/09/509,234C CURRENT FILING DATE: 2000-09-25 PRIOR PAPLICATION NUMBER: EP 97870146.4 PRIOR FILING DATE: 1997-09-26 SOFTWARE: PASSEQ for Windows Version 4.0 SEQ ID NOS: 64
                                                                                                                                                                                                                                                                                                                                                               5;
                                                                                                                                                                                                                                                                                                                                                               DB
87;
                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                TYPE: PRT; ORGANISM: Staphylococcus haemolyticus femA
US-09-509-234C-41
                                                                                                                                                                                                                                                                                                                                                               Score 32;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 13515, Application US/09815242; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Trawick, John D.
Carr, Grant J.
Yamamoto, Robert T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ohlsen, Kari L.
Zyskind, Judith W.
                                                                                                                                                                                                                                                                                                                                                               64.0%;
57.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Haselbeck, Robert
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Search completed: January 29, 2002, 10:58:11 Job time: 2507 sec

us-09-763-397a-9.rapn

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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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Perfect score:
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                                                                                                                                                                        NO.
                                        4001
                                                                                                                                                                                                                                                          and is derived
                                                                                                                                                                                                                                                      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                      Score
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Gapop 10.0 , Gapext 0.5
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59
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                                                                                                                                                                                                                                                                                                                                                                                    : /cgn2_6/ptodata/2/paa/US085_COMB.pep:*
    /cgn2_6/ptodata/2/paa/US086_COMB.pep:*
    /cgn2_6/ptodata/2/paa/US086_COMB.pep:*
    /cgn2_6/ptodata/2/paa/US087_COMB.pep:*
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/cgn2_6/ptodata/2/paa/US06_COMB.pep:*
/cgn2_6/ptodata/2/paa/US07_COMB.pep:*
/cgn2_6/ptodata/2/paa/US080_COMB.pep:*
/cgn2_6/ptodata/2/paa/US081_COMB.pep:*
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/cgn2_6/ptodata/2/paa/US083_COMB.pep:*
/cgn2_6/ptodata/2/paa/US084_COMB.pep:*
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/cgn2_6/ptodata/2/paa/US098_COMB.pep:*
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11 US-09-763-397A-8

US-07-947-033-1

US-07-947-033-9

US-07-947-033-9

US-07-947-033-9

US-07-947-033-10

US-07-947-033-10

US-08-119-694-7
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1.419 Million cell updates/sec
                          Sequence 2, Appli
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Sequence 8, Appli
Sequence 9, Appli
Sequence 10, Appli
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09-454-204A-41 09-763-397A-2	8- 2-	-119-694	-119-694B-	8-119-	8-119-694-	08-119-694-	07-947-033-	US-07-947-033-4	07-947-033-	-60-297-863-	60-258	952-	4	PCT-US99-31025-46	34	-60-138-684-	-602-2	PCT-US98-25922-33	US98-25922-9	US-60-143-992-856	-09-454-204A-2	08-395-	08-119-694B-	8-119-694B-	US-08-119-694B-8	US-08-119-694B-7	-08-119-694B	-08-119-694-	-08-119-694-	US-08-119-694-8
	5, Ap e 1057	Sequence 4, Appli	'n	Sequence 5, Appli	٠ س	ν,	ۍ . د	Sequence 4. Appli	'n	6,	6	5, -	e 46,	46,	34, App	e 10	2, A	33	9, Apr	856,	e 28	1, 1	10,	9	ω,	7,	1, A	10,	9	Sequence 8, Appli

## ALIGNMENTS

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CURRENT APPLICATION NUMBER: US/09/197,770A
CURRENT FILING DATE: 1998-11-23
NUMBER OF SEQ ID NOS: 38
SOFTWARE: PATENTIN VEr. 2.0
SEQ ID NO 2
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                        ; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: fragment/ analog of thrombospondin
US-09-197-770-2
                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application US/09197770A
GENERAL INFORMATION:
APPLICANT: TUSZYNSKI GEOTGE
APPLICANT: Williams, Taffy
APPLICANT: Actor, Paul
В
                               Q
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                                                                     Matches
                                                                                    Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: RETROINVERSO POLYPEPTIDES THAT MIMIC OR INHIBIT TITLE OF INVENTION: THROMBOSPONDIN ACTIVITY FILE REFERENCE: 07206-0021
                                                                   Local Similarity
hes 9; Conserv
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                               1 WSPCSVTCG
WSPCSVTCG
                                                                     Conservative
                                  9
                                                                                    100.0%;
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                                                                                    Score 59; DB 15;
Pred. No. 2.9e+06;
                                                                     Mismatches
                                                                     0
                                                                                                  Length 9;
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RESULT 3
US-07-947-033-1
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LENGTH: 9
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT FILING DATE: 2001-02-16
PRIOR APPLICATION NUMBER: US 60/097,703
PRIOR FILING DATE: 1998-08-21
PRIOR APPLICATION NUMBER: PCT / US99/18869
PRIOR FILING DATE: 1999-08-19
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILE REFERENCE: 6395-57049
CURRENT APPLICATION NUMBER: US/09/763,397A
CURRENT FILING DATE: 2001-02-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Ping Shi, Ya
APPLICANT: Hasnain, Seyed E.
TITLE OF INVENTION: Recombinant Multivalent Malarial Vaccine Against Plasmodium Falc.
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Plasmodium falciparum
                                      ATTORNEY AGENT INFORMATION:
NAME: Adda C. Gogoris, Esq.
REGISTRATION NUMBER: 29,714
REFERENCE/DOCKET NUMBER: 5986/07607
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 527-7700
TELEFAX: (212) 753-6237
                                                                                                                                                                                                                                                 SOFTWARE: Word Perfect 5.1 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Sinnis, Photini
APPLICANT: Nussenzweig, Victor
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR INHIBITING
TITLE OF INVENTION: HEPATOCYTE INVASION BY MALARIAL SPOROZOITES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Cerami, Carla
        TELEFAX: (2.7 TELEFAX: 236687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
nes 9; Conserv
                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Diskette, 5, inch, 1.2 MB storage COMPUTER: AST Premium II 386/33 OPERATING SYSTEM: DOS 3.3
                                                                                                                                                                                                        APPLICATION NUMBER: US/07/947,033 FILING DATE: 19920917
                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
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                                                                                                                                                                                     CLASSIFICATION:
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nilarity 100.0%;
Conservative (
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Sinnis, Photini
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Pred. No. 2.9e+06;
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; TOPOLOGY: unknown US-07-947-033-1
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The 9; Conserve
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US-07-947-033-8
; Sequence 8, Application US/07947033
; GENERAL INFORMATION:
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                                           RESULT
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Best Local
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LENGTH: 18 amino acids
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/9
                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER: 29,714
REFERENCE/DOCKET NUMBER: 5986/07607
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 527-7700
TELEPAX: (212) 753-6237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 19920917
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Adda C. Gogoris, E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Nussenzweig, Victor
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR INHIBITING
TITLE OF INVENTION: HEPATOCYTE INVASION BY MALARIAL SPOROZOITES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
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                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                               TYPE: AMII
TOPOLOGY:
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TENGTH: IS u....

TYPE: AMINO ACID

"YPE: AMINO ACID
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                                                                                     2 WSPCSVTCG 10
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                                                                                                                                            Similarity 9; Conserv
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Sinnis, Photini
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Pred. No. 0.16;
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Pred. No. 0.16;
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APPLICANT: Cerami, Carla

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Query Match
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TELEX: 236687
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
OF WIGHT: 18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 9, Application:
                                                                                                                                                                                                                                                    APPLICANT: Cerami, Carla
APPLICANT: Frevert, Ute
APPLICANT: Sinnis, Photini
APPLICANT: Nussenzweig, Victor
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR INHIBITING
TITLE OF INVENTION: HEPATOCYTE INVASION BY MALARIAL SPOROZOITES
RUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
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COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5, inch, 1.2 MB storage
COMPUTER: AST Premium II 386/33
COMPUTER: AST Premium II 386/33
                       MEDIUM TYPE: Diskette, 5, inch, 1.2 MB storage COMPUTER: AST Premium II 386/33
OPERATING SYSTEM: DOS 3.3
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/947,033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Adda C. Gogoris, Esq.
REGISTRATION NUMBER: 29,714
REFERENCE/DOCKET NUMBER: 5986/07607
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 527-7700
TELLERAX: (212) 753-6237
                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/947,033
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CORRESPONDENCE ADDRESS:
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR INHIBITING
TITLE OF INVENTION: HEPATOCYTE INVASION BY MALARIAL SPOROZOITES
NUMBER OF SEQUENCES: 27
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APPLICANT: Sinnis, Photini
APPLICANT: Nussenzweig, Vi
                                                                                                                                                                                  STATE: New York
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                                                                                                                                                                                          New York
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805 Third Avenue
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19920917 US/07/947,033
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                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Adda C. Gogoris, Esq.
REGISTRATION NUMBER: 29,714
REFERENCE/DOCKET NUMBER: 5986
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 527-7700
TELEPAX: (212) 53-6237
TELEEX: 236887
INFORMATION FOR SEQ ID NO: 10:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 10, Application US/07947033 GENERAL INFORMATION:
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Best Local Similarity
Matches 9; Conserv
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SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: AST Premium 11 300
OPERATING SYSTEM: DOS 3.3
SOFTWARE: WOR'D PERFECT 5.1
CURRENT APPLICATION DATA:
TOTAL MINUSER: US/07/9
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NAME: Adda C. Gogoris, Esq.
REGISTRATION NUMBER: 29,714
REFERENCE/DOCKET NUMBER: 5986/07607
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 527-7700
TELEPHONE: (212) 753-6237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Cerami, Carla
APPLICANT: Frevert, Ute
APPLICANT: Sinnis, Photini
APPLICANT: Nussenzweig, Victor
                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: AMINO ACID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR INHIBITING TITLE OF INVENTION: HEPATOCYTE INVASION BY MALARIAL SPOROZOITES NUMBER OF SEQUENCES: 27
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                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: UFILING DATE: 19920917 CLASSIFICATION: 530
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ZIP: 10022
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                                                                                                                                COPOLOGY:
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         100.0%; Score 59; DB 3; Length 18; ilarity 100.0%; Pred. No. 0.16; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                PE: Diskette, 5, inch,
AST Premium II 386/33
SYSTEM: DOS 3.3
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Pred. No. 0.16;
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Query Match
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US-08-119-694-1
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GENERAL INFORMATION:
                                                                                                                                                                                                                             Sequence 7, Applications GENERAL INFORMATION:
APPLICANT: Cerami
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER: 29,714
REFERENCE/DOCKET NUMBER: 5986/17607-US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 527-7700
TELEFAX: (212) 753-6237
TELEFAX: (212) 753-6237
TELEX: 236687
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Frevert, Ute
APPLICANT: Sinnis, Photini
APPLICANT: Nussenzweig, Victor
APPLICANT: Sinnis, Photini
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/119,694
FILING DATE: 10-Sept-1993
ATTORNEY/AGENT INFORMATION:
NAME: Adda C. Gogoris, Esq.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                            APPLICANT: Frevert, Ute
APPLICANT: Sinnis, Photini
APPLICANT: Nussenzweig, Victor
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR INHIBITING
TITLE OF INVENTION: HEPATOCYTE INVASION BY MALARIAL
TITLE OF INVENTION: SPOROZOITES
NUMBER OF SEQUENCES: 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                           CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM: DOS 3.3 SOFTWARE: Word Perfect 5.1
  STREET:
CITY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: New York
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
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                                         ADDRESSEE:
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SEE: Darby & Darby, P.C
: 805 Third Avenue
New York
                                                                                                                                                                                                                                                                         Application US/08119694
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cerami, Carla
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                                                                                                                                                                                                                                  Cerami, Carla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E: Diskette, 5, inch, 1.2 MB storage AST Premium II 386/33
SYSTEM: DOS 3.3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 59; DB 5; Length 18; Pred. No. 0.16;
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US-08-119-694-7
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TELEEX: 236687
TELEX: 236687
INFORMATION FOR SEO ID NO: 7:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
APPLICATE
APPLICATE
FILING DATE: 10-Sepularion:
ATTORNEY/AGENT INFORMATION:
NAME: Adda C. Gogoris, Esq.
REGISTRATION NUMBER: 29,714
REFERENCE/DOCKET NUMBER: 5986/17607-US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 527-7700
TELEFAX: (212) 753-6237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 8, Application US/08119694 GENERAL INFORMATION:
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FILING DATE: 10-Sept-1993
ATTORNEY/AGENT INFORMATION:
NAME: Adda C. Gogoris, Esq.
REGISTRATION NUMBER: 29,714
REFERENCE/DOCKET NUMBER: 5986/17607-US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 527-7700
TELEPAX: (212) 753-6237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIIM TYPE: Diskette, 5, inch, 1.2 MB storage
COMPUTER: AST Premium II 386/33
OPERATING SYSTEM: DOS 3.3
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/119,694
FILING DATE: 10-Sept-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Darby & Darby, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR INTITLE OF INVENTION: HEPATOCYTE INVASION BY MALARIAL TITLE OF INVENTION: SPOROZOITES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: . United States of America
                                                                                                                                                                                                                                                                                                                                                                                     STREET: 805 Thi:
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 WSPCSVTCG 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Frevert, Ute
Sinnis, Photini
Nussenzweig, Victor
                                                                                                                                                                                                                                                                                                                                                                United States of America
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 59; DB 5
100.0%; Pred. No. 0.16;
Live 0; Mismatches
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US-08-119-694-10; Sequence 10, Application US/08119694; GENERAL INFORMATION: APPLICANT: Cerami, Carla; APPLICANT: Frevert, Ute
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                                                                                            RESULT 12
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GENERAL INFORMATION:
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Best Local Similarity
                                                                                                                                                                                                                                    Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: U5/08/119,694
FILING DATE: 10-Sept-1993
ATTORNEY/AGENT INFORMATION:
NAME: Adda C. Gogoris, Esq.
REGISTRATION NUMBER: 29,714
REFERENCE/DOCKET NUMBER: 5986/17607-US1
TELECOMMUNICATION INFORMATION:
TELEPAN: (212) 753-6237
TELEFAN: (212) 753-6237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                     Matches
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                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Frevert, Ute
APPLICANT: Sinnis, Photini
APPLICANT: Nussenzweig, Victor
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR INHIBITING
TITLE OF INVENTION: HEPATOCYTE INVASION BY MALARIAL
TITLE OF INVENTION: SPOROZOITES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: AST Premium II 386/33

OPERATING SYSTEM: DOS 3.3

SOFTWARE: Word Perfect 5.1
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CITY: New York
STATE: New York
                                                                                                                                                                                                             Match 100.0%; Score 59; DI Local Similarity 100.0%; Pred. No. 0; Mismatches 9; Conservative 0; Mismatches
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805 Third Avenue
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                                                                                                                                                                                                                                                                                                                           unknown
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Applicati
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/119,694
FILING DATE: 10-Sept-1993
ATTORNEY/AGENT INFORMATION:
NAME: Adda C. Gogoris, Esq.
REGISTRATION NUMBER: 29,714
REFERENCE/DOCKET NUMBER: 5986/17607-US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 527-7700
TELEPHO: (212) 53-6237
TELEX: 236687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 18 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: OF TITLE OF INVENTION: FOR THE TITLE OF INVENTION: SOURCES:
             COMPUTER READABLE FORM:
MEDIUM TYPE: DISKELLE, 5, inch, 360 KB storage
COMPUTER: COMPAQ PROLINEA MT 4/66
OPERATING SYSTEM: DOS 3.3
SOFTWARE: Word Perfect 5.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/119,694B
                                                                                                                                                                                                                                                                              APPLICANT: NUSSENZWEIG, VICTOR
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: INHIBITING HEPATOCYTE INVASI
TITLE OF INVENTION: BY MALARIAL SPOROZOITES
NUMBER OF SEQUENCES: 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: AST Premium II 38
OPERATING SYSTEM: DOS 3.3
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
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STATE: New Yor
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STATE: New York
                                                                                                                                                                    COUNTRY:
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amino acid
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                                                                                                                                                                                      New York
                                                                                                                                                                                                                       E: Darby & Darby, P.C.
805 Third Avenue
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Sinnis, Photini
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 59; DB 5 ilarity 100.0%; Pred. No. 0.16; Conservative 0; Mismatches
                                                                                                                                                                  United States
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Nussenzweig, Victor
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10-Sept-1993
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II 386/33
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ATTORNEY/AGENT INFORMATION:

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Matches 9; Conserv
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                                                                  Query Match
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                    TELEX: 236687
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
APPLICATION NUMBER: U5/08/119,694B
FILING DATE: 10-Sept-1993
ATTORNEY/AGENT INFORMATION:
NAME: Adda C. Gogoris, Esq.
REGISTRATION NUMBER: 29,714
REGISTRATION NUMBER: 29,714
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                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 5986/17607-US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 527-7700
TELEPAX: (212) 753-6237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Cerami, Carla APPLICANT: Frevert, Ute APPLICANT: Sinnis, Photir
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CORRESPONDENCE ADDRESS:
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OPERATING SYSTEM: DOS 3.3
SOFTWARE: WORD Perfect 5.2
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                                                                                                                                                     : 18 amino acids amino acid
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Sinnis, Photini
Nussenzweig, Victor
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                                                    Score 59; DB 5
Pred. No. 0.16;
                                    Mismatches
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Search completed: January 29, 2002, 10:56:02 Job time: 2398 sec

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Best Local Similarity
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MEDIUM TYPE: Diskette, 5, inch, 360 KB storage
COMPUTER: COMPAO PROLINEA MT 4/66
OPERATING SYSTEM: DOS 3.3
SOFTWARE: WOR'D PEFfect 5.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/119,694B
FILING DATE: 10-Sept-1993
ATTORNEY/AGENT INFORMATION:
NAME: Adda C. Gogoris, Esq.
REGISTRATION NUMBER: 29,714
REGISTRATION NUMBER: 29,714
                                                                                                                                                                                                                                     TELEFAX: (212) 753-62:
TELEX: 236687
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: CÓMPOSITIONS AND METHODS FOR TITLE OF INVENTION: INHIBITING HEPATOCYTE INVASION TITLE OF INVENTION: BY MALARIAL SPOROZOITES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 59
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 527-7700
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TOPOLOGY:
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805 Third Avenue
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Sinnis, Photini
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                                                                   Conservative
                                                                                                                                                                     unknown
                                                                                   100.0%;
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                                                                   Score 59; DB 5. Pred. No. 0.16; Mismatches
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Result
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Maximum Match 100%
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cgn2_6/ptodata/2/paa/US06_NEW_COMB.pep:*

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Gapop 10.0 , Gapext 0.5
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1 WSPCSVTCG 9
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US-09-978-627-301
US-09-978-627-301
US-09-970-966-286
US-09-617-770B-15
US-09-197-770B-9
US-09-197-770B-15
US-09-197-770B-15
US-09-197-770B-15
US-09-197-770B-15
US-09-197-770B-12
US-09-197-094-6
US-09-198-687-7
US-09-989-687-10
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US-09-462-999B-2

US-09-980-564-13

US-09-858-068-6

US-09-858-068-6

US-09-858-070-9
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50	51	51	51	51	51	51	51	51	51	51	51	51	51	51	51	51	51
84.7	86.4	86.4	86.4	86.4	86.4	86.4	86.4	86.4	86.4	86.4	86.4	86.4	86.4	86.4	86.4	86.4	86.4
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Sequence 12, App	, <u>1</u>	4 , P	12	S.	N	1, 1	•	Sequence 12, App	Sequence 4, Appl	Sequence 8, Appl	Sequence 2, Appl	Sequence 6, Appli	Sequence 14, App	Sequence 16, App	Sequence 28, App	Sequence 50, App	Sequence 7, Appl

ALIGNMENTS

#### Sequence 2, Application US/09462909B GENERAL INFORMATION: APPLICANT: MEINIEL, Annie APPLICANT: MONNERIE, Hubert APPLICATI GOBRON, Stephane TITLE OF INVENTION: NOVEL PEPTIDES AND POLYPE TITLE OF INVENTION: SYSTEM FILE REFERENCE: 065691/0179 CURRENT APPLICATION NUMBER: US/09/462,909B CURRENT FILING DATE: 2000-02-14 PRIOR APPLICATION NUMBER: FR 97/09016 RESULT 2 US-09-462-909B-2 FEATURE: OTHER INFORMATION: Description of Artificial Sequence: OTHER INFORMATION: fragment/ analog of thrombospondin US-09-197-770B-2 멍 20 RESULT 1 US-09-197-770B-2 Sequence 2, Application US/09197770B GENERAL INFORMATION: SEQ ID NO 2 LENGTH: 9 TYPE: PRT ORGANISM: Artificial Sequence Query Match Best Local : Matches APPLICANT: Tuszyński, George APPLICANT: Williams, Taffy APPLICANT: Williams, Taffy APPLICANT: Williams, Taffy APPLICANT: Actor, Paul TITLE OF INVENTION: RETROINVERSO POLYPEPTIDES THAT MIMIC OR INHIBIT TITLE OF INVENTION: THROMBOSPONDIN ACTIVITY FILE REPERENCE: 07206-0021 CURRENT APPLICATION NUMBER: US/09/197,770B CURRENT FILING DATE: 1998-11-23 NUMBER OF SEQ ID NOS: 38 SOFTWARE: Patentin Ver. 2.0 Local Similarity nes 9; Conserv 1 WSPCSVTCG 1 WSPCSVTCG 9 100.0%; Score 59; DB 5; ilarity 100.0%; Pred. No. 1.6e+05; Conservative 0; Mismatches 0; 9 AND POLYPEPTIDES Length USEFUL FOR REGENERATING synthetic 0; Gaps

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SEQ ID NOS: 24

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Best Local Similarity
---hes 9; Conserv
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; DATE: 1995
US-09-980-564-13
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GENERAL INFORMATION:
APPLICANT: University of Washington
APPLICANT: University of Washington
TITLE OF INVENTION: RECOMBINANT ADENOVIRAL VECTORS FOR CELL SPECIFIC
TITLE OF INVENTION: INFECTION AND GENOME INTEGRATION AND EXPRESSING
TITLE OF INVENTION: CHIMERIC FIBER PROTEINS
FILE REFERENCE: 30429.2WOO1
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Best Local Similarity
Matches 9; Conserv
Sequence 6, Application US/09858068
GENERAL INFORMATION:
APPLICANT: Kapeller-Liebermann, Rosana
APPLICANT: Cook, William James
APPLICANT: Silos-Santiago, Inmaculada
TITLE OF INVENTION: 33428, A NOVEL HUMAN METALLOPROTEASE
TITLE OF INVENTION: FAMILY MEMBER AND USES THEREOF
FILE REFERENCE: 10448-057001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 13
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SOFTWARE:
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CURRENT FILING DATE: 2001-11-30
PRIOR APPLICATION NUMBER: 60/137,213
PRIOR FILING DATE: 1999-06-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JOURNAL: Cell
VOLUME: 70
PAGES: 1021-33
DATE: 1992
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TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                               JOURNAL: Infect. VOLUME: 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AUTHORS: Chatterjee, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AUTHORS: Cerami,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Plasmodium falciparum
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Pred. No. 1.6e+05;
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Pred. No. 0.0037;
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OTHER INFORMATION: consensus sequence US-09-858-068-6
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Matches 9
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Best Local Similarity
Matches 9; Conser
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LENGTH: 54
TYPE: PRT
ORGANISM: Artificial Sequence
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                                                                                                                                                             Sequence 9, Application US/10014070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR FILING DATE: 2000-05-15
PRIOR APPLICATION NUMBER: 60/204,160
PRIOR FILING DATE: 2000-05-15
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FastSEQ for Windows Version 4.0
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CURRENT APPLICATION NUMBER: US/09/858,081
CURRENT FILING DATE: 2001-05-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Kapeller-Libermann, Rosana
APPLICANT: Cook, William James
APPLICANT: Sitos-Santiago, Inmaculada
TITLE OF INVENTION: 33428, A NOVEL HUMAN METALLOPROTEASE
TITLE OF INVENTION: FAMILY MEMBER AND USES THEREOF
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APPLICANT: Bandaru, Rajasehkar
APPLICANT: Curtis, Rory A.J.
APPLICANT: Spurling, Heidi Lynn
APPLICANT: Millennium Pharmaceuticals, Inc.
APPLICANT: Millennium Pharmaceuticals, Inc.
TITLE OF INVENTION: 53014, A Human Metalloprotease Family
TITLE OF INVENTION: Member and Uses Therefor
FILE REFERENCE: MPI2000-523PIRCP1(M)
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PRIOR FILING DATE: 2000-05-15
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Pred. No. 0.0075;
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Pred. No. 0.0075;
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Best Local Similarity
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; OTHER INFORMATION: fragment/ analog of thrombospondin
US-09-197-770B-17
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Best Local S
Matches 9
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SEQ ID NO 17
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SEQ ID NO 9
LENCTH: 54
TYPE: PRT
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                                         APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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APPLICANT: Williams, Taffy
APPLICANT: Actor, Paul
TITLE OF INVENTION: RETROINVERSO POLYPEPTIDES THAT MIMIC OR INHIBIT
TITLE OF INVENTION: THROMBOSPONDIN ACTIVITY
FILE REFERENCE: 07206-0021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/10/014,070 CURRENT FILING DATE: 2001-11-13 PRIOR APPLICATION NUMBER: 60/258,373 PRIOR FILING DATE: 2000-12-22 NUMBER OF SEQ ID NOS: 11
APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/197,770B
CURRENT FILING DATE: 1998-11-23
NUMBER OF SEQ ID NOS: 38
                                                                                                                                            APPLICANT: Ashkenazi, Avi
                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Artificial Sequence FEATURE:
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les 9; Conser
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                                                      Filvaroff, Ellen
          Gao, Wei-Qiang
Gerber, Hanspeter
                                         Fong,
                                                                                                   Desnoyers, Luc
                                                                                                                 Botstein, David
                                                                                                                                 Baker Kevin P.
Gerritsen, Mary
                                                                                   Eaton, Dan
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APPLICANT:
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PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Secreted and Transmembrane Polypeptides TITLE OF INVENTION: Acids Encoding the Same FILE REFERENCE: P2630P1C7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066364
PRIOR FILING DATE: 1997-11-21
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CURRENT FILING DATE: 2001-10-15
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FILING DATE: 1998-03-27
APPLICATION NUMBER: 60/079728
FILING DATE: 1998-03-27
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APPLICATION NUMBER: 60/078910
FILING DATE: 1998-03-20
APPLICATION NUMBER: 60/078939
FILING DATE: 1998-03-20
                                                                                                                                      APPLICATION NUMBER: FILING DATE: 1998-03
                                                                                                                                                                                                                                                     APPLICATION NUMBER: 60/079664
FILING DATE: 1998-03-27
APPLICATION NUMBER: 60/079689
FILING DATE: 1998-03-27
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FILING DATE: 1998-03-11
                    APPLICATION NUMBER: 60/080105 FILING DATE: 1998-03-31
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                                                                                                                APPLICATION NUMBER: 60/079920
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FILING DATE: 1998-03-26
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FILING DATE: 1998-03-13
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APPLICATION NUMBER: 60/080107
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Shelton, David L.
Stewart, Timothy A.
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Hillan, Kenneth
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Grimaldi, J. Christopher
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OR FILING DATE: 1998-04-15
OR APPLICATION NUMBER: 60/082568
OR FILING DATE: 1998-04-21
OR APPLICATION NUMBER: 60/082569
OR FILING DATE: 1998-04-21
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DR APPLICATION NUMBER: 60/083495
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APPLICATION NUMBER: 60/081819
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APPLICATION NUMBER: 60/081952
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APPLICATION NUMBER: 60/082797
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APPLICATION NUMBER: 60/082700
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APPLICATION NUMBER: 60/083558
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Baker Kevin P
Botstein, David
          Gurney, Austin L.
Hillan, Kenneth J
Kljavin, Ivar J.
Kuo, Sophia S.
                                                                             Goddard, Audrey
Godowski, Paul J.
Grimaldi, J. Christopher
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Gao, Wei-Qiang
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Gerritsen, Mary E.
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OR APPLICATION NUMBER: 60/07
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Shelton, David L.
Stewart, Timothy
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FILING DATE: 1998-05-07
APPLICATION NUMBER: 60/084640

1998-05-07

APPLICATION NUMBER: 60/084598 FILING DATE: 1998-05-07

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US-09-978-697-301
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PRIOR APPLICATION NUMBER: 0.5-15

PRIOR FILING DATE: 1998-05-15

PRIOR APPLICATION NUMBER: 60/0

PRIOR APPLICATION NUMBER: 60/0
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FILING DATE: 1998-05-15
APPLICATION NUMBER: 60/085579
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APPLICATION NUMBER: 60/
FILING DATE: 1998-05-13
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FILING DATE: 1998-05-07
APPLICATION NUMBER: 60/085339
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FILING DATE: 1998-05-07
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APPLICATION NUMBER: 60/
FILING DATE: 1998-05-15
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APPLICATION NUMBER:
FILING DATE: 1998-0
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FILING DATE: 1998-05-15
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8; Conserv
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Baker Kevin P.
Botstein, David
                                                                                            Godowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J
Kljavin, Ivar J.
Kuo, Sophia S.
Kuo, Sophia S.
                                                                     Pan,
                                                                                                                                                                                Gerber, Hanspeter
Gerritsen, Mary E.
Goddard, Audrey
                                                                                                                                                                                                                                      Fong,
          Roy, Margaret Ann
Shelton, David L.
Stewart, Timothy A.
                                                                                                                                                                                                                           Gao,
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Filvaroff,
                                                                                                                                                                                                                                                                                  Eaton, Dan
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                                                                                 Napier, Mary A.
                                                        Paoni,
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                                                                     James;
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                                                         Nicholas F.
Daniel
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f, Ellen
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88.9%;
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PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR APPLICATION NUMBER: 60/065311
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066364
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/077450
PRIOR FILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 60/077632
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PRIOR APPLICATION NUMBER: 60/078910
PRIOR APPLICATION NUMBER: 60/078910
PRIOR APPLICATION NUMBER: 60/078939
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294
PRIOR APPLICATION NUMBER: 60/079656
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079656
PRIOR FILING DATE: 1998-03-26
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077641
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077649
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077791
PRIOR APPLICATION NUMBER: 60/0777791
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PRIOR APPLICATION NUMBER: 60/078004
PRIOR FILING DATE: 1998-03-13
PRIOR APPLICATION NUMBER: 60/078886
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PRIOR APPLICATION NUMBER: 60/078936
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OR APPLICATION NUMBER: 60/079663

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OR APPLICATION NUMBER: 60/079728
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BR FILLING DATE: 1998-03-30
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DR FILLING DATE: 1998-03-31
DR APPLICATION NUMBER: 60/080107
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FILING DATE: 1998-04-01
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FILING DATE: 1998-04-08
APPLICATION NUMBER: 60/081070
APPLICATION 1998-04-08
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FILING DATE: 1998-04-01
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APPLICATION NUMBER: 60/0
FILING DATE: 1998-05-07
APPLICATION NUMBER: 60/0
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FILING DATE: 1998-04-27
APPLICATION NUMBER: 60/083322
FILING DATE: 1998-04-28
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FILING DATE: 1998-04-21
APPLICATION NUMBER: 60/082569
                                                                                        FILING DATE: 1998-0 APPLICATION NUMBER:
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FILING DATE: 1998-04-29
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FILING DATE: 1998-04-29
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FILING DATE: 1998-04-09
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APPLICANT: Kuo, Sophia S.
APPLICANT: Napler, Mary A.
APPLICANT: Pan, James;
APPLICANT: Pani, Micholas F.
APPLICANT: Pani, Nicholas F.
APPLICANT: Shelton, David L.
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Pol
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630P1C14
CURRENT APPLICATION NUMBER: US/09/978,824
CURRENT FILING DATE: 2001-10-17
PRIOR APPLICATION NUMBER: 09/918585
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US-09-978-824-301
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445 WSPCTVTCG 453
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OR APPLICATION NUMBER: 60/085580
OR FILING DATE: 1998-05-15
OR APPLICATION NUMBER: 60/085573
OR FILING DATE: 1998-05-15
OR APPLICATION NUMBER: 60/085704
OR FILING DATE: 1998-05-15
OR APPLICATION NUMBER: 60/085697
OR FILING DATE: 1998-05-15
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DR APPLICATION NUMBER: 60/085700
DR FILING DATE: 1998-05-15
DR APPLICATION NUMBER: 60/085689
DR FILING DATE: 1998-05-15
DR APPLICATION NUMBER: 60/085579
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APPLICATION NUMBER: 60/085338
FILING DATE: 1998-05-13
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FILING DATE: 1998-05-07
APPLICATION NUMBER: 60/
FILING DATE: 1998-05-07
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8; Conserv
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Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J
Kljavin, Ivar J.
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Desnoyers, Luc
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Mismatches No ; 0 DB 5;

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PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR PELICATION NUMBER: 60/064249
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-03
PRIOR FILING DATE: 1997-11-13
PRIOR FILING DATE: 1997-11-21
PRIOR PELICATION NUMBER: 60/06364
PRIOR PELING DATE: 1997-11-21
PRIOR PELICATION NUMBER: 60/077450
PRIOR PELING DATE: 1998-03-10
PRIOR PELICATION NUMBER: 60/077632
PRIOR PELING DATE: 1998-03-11
PRIOR PELICATION NUMBER: 60/077641
PRIOR APPLICATION NUMBER: 60/077641
PRIOR APPLICATION NUMBER: 60/077649
PRIOR PELING DATE: 1998-03-11
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PRIOR PELICATION NUMBER: 60/07791
PRIOR PELICATION NUMBER: 60/07791
PRIOR PELICATION NUMBER: 60/078004
PRIOR REPLICATION NUMBER: 60/078004
PRIOR APPLICATION NUMBER: 60/078004
PRIOR APPLICATION NUMBER: 60/078004
PRIOR PELING DATE: 1998-03-12
PRIOR APPLICATION NUMBER: 60/078004
PRIOR PELING DATE: 1998-03-13
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PRIOR APPLICATION NUMBER: 60/078936
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078910
PRIOR APPLICATION NUMBER: 60/078939
PRIOR APPLICATION NUMBER: 60/079294
PRIOR APPLICATION NUMBER: 60/079294
PRIOR APPLICATION NUMBER: 60/079656
PRIOR APPLICATION NUMBER: 60/079664
PRIOR APPLICATION NUMBER: 60/079664
PRIOR APPLICATION NUMBER: 60/079669
PRIOR APPLICATION NUMBER: 60/079669
PRIOR PILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079786
PRIOR PILING DATE: 1998-03-37
PRIOR APPLICATION NUMBER: 60/079920
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PRIOR APPLICATION NUMBER: 60/080105
PRIOR APPLICATION NUMBER: 60/080105
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PRIOR APPLICATION NUMBER: 60/080107
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PRIOR APPLICATION NUMBER: 60/080107
PRIOR APPLICATION NUMBER: 60/080327
PRIOR PRILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080327
PRIOR APPLICATION NUMBER: 60/080327
PRIOR APPLICATION NUMBER: 60/080327
PRIOR APPLICATION NUMBER: 60/080327
PRIOR APPLICATION NUMBER: 60/080333
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/080334
PRIOR APPLICATION NUMBER: 60/080334
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PRIOR APPLICATION NUMBER: 60/080334
PRIOR APPLICATION NUMBER: 60/080329
PRIOR APPLICATION NUMBER: 60/080334
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APPLICATION NUMBER: 60/1

60/085323

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RESULT
US-09-970-966-186

Sequence 186, Application US/09970966

Sequence 186, Application US/09970966

GENERAL INFORMATION:
APPLICANT: Stolk, John A.

APPLICANT: Molesh, David Alan
APPLICANT: Molesh, David Alan
APPLICANT: Mulesh, David Alan
APPLICANT: Yu, Jiangchun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.484C6
CURRENT APPLICATION NUMBER: US/09/970,966
CURRENT APPLICATION NUMBER: US/09/970,966
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: SOFTWARE: FASTSEQ for Windows Version 4.0
: SEO ID NO 207
: LENGTH: 787
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-970-966-207
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Best Local
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Best Local
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APPLICANT: Xu, Jiangchun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
ETLE REFERENCE: 210121.484C6
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CURRENT FILING DATE: 2001-10-02
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PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085697
PRIOR FILING DATE: 1998-05-15
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7; Conserv
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8; Conserv
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Fling, Steven P.
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77.8%;
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Pred. No. 0.25;
2; Mismatches
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RESULT 15
US-09-197-770B-14
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                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
"hehes 7; Conservi
                                                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: Homo sapiens US-09-611-526-3833
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                                                                                                     Sequence 14, Application US/09197770B GENERAL INFORMATION:
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SOFTWARE: PatentIn Ver. 2.
SEQ ID NO 3833
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 186
LENGTH: 807
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Best Local Similarity 77.8
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: PRIMERS FOR SYNTHESIS OF FULL LENGTH cDNAS
TITLE OF INVENTION: AND THEIR USES
FILE REFERENCE: 08335/01/2
CURRENT APPLICATION NUMBER: US/09/611,526
CURRENT FILING DATE: 2000-07-07
PRIOR APPLICATION NUMBER: JP 1999-194486
PRIOR FILING DATE: 1999-07-08
PRIOR APPLICATION NUMBER: JP 2000-118774
PRIOR APPLICATION NUMBER: JP 2000-18774
PRIOR FILING DATE: 2000-01-11
PRIOR FILING DATE: 2000-01-11
PRIOR FILING DATE: 2000-01-10
PRIOR FILING DATE: 2000-01-10
PRIOR FILING DATE: 2000-05-02
PRIOR FILING DATE: 2000-05-02
            APPLICANT: Tuszynski, George
APPLICANT: Williams, Taffy
APPLICANT: Actor, Paul
APPLICANT: Actor, Paul
TITLE OF INVENTION: RETROINVERSO POLYPEPTIDES THAT MIMIC OR INHIBIT
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TYPE: PRT
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FILE REFERENCE: 07206-0021
                                                                                                                                                                                                             510 WSPCSISCG
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WAKAMATSU, AI
SUGIYAMA, TOMOYASU
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OTSUKI, TETSUJI
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HAYASHI, KOJI
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77.8%;
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Pred. No.
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Pred.
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0.25;
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CURRENT APPLICATION NUMBER: US/09/197,770B;
CURRENT FILING DATE: 1998-11-23
NUMBER OF SEQ ID NOS: 38
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 14
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: synthetic
OTHER INFORMATION: fragment/ analog of thrombospondin
US-09-197-770B-14

Query Match
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps
Oy 1 MSPCSVTC 8

Qy 1 MSPCSVTC 8
Search completed: January 29, 2002, 10:58:11
Job time: 2507 sec
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Database
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Minimum DB seq length: 0
Maximum DB seq length: 200000000
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10:
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109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3148936 seqs, 277657034 residues
          : //gn2_6/ptodata/2/paa/US083_COMB.pep: *
://gn2_6/ptodata/2/paa/US084_COMB.pep: *
://gn2_6/ptodata/2/paa/US085_COMB.pep: *
://gn2_6/ptodata/2/paa/US085_COMB.pep: *
://gn2_6/ptodata/2/paa/US085_COMB.pep: *
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Copyright (c) 1993 - 2000 Compugen Ltd
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /cgn2_6/ptodata/2/paa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/paa/US06_COMB.pep:*
/cgn2_6/ptodata/2/paa/US07_COMB.pep:*
/cgn2_6/ptodata/2/paa/US080_COMB.pep:*
/cgn2_6/ptodata/2/paa/US081_COMB.pep:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                        /cgn2_6/ptodata/2/paa/US082_COMB.pep:*
/cgn2_6/ptodata/2/paa/US60_COMB.pep:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3148936
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

	Result No.
987654321	m !
109 109 109 109 109 109	Score
100.0 100.0 100.0 100.0 100.0	Query Match
350 350 412 412 412 423 424	Query Match Length DB
21 22 3 3 13 13	DB B
21 US-09-763-397A-7 21 US-09-763-397A-2 22 US-09-820-843A-31 3 US-07-677-539B-6 3 US-07-727-636-6 13 US-08-948-885-18 13 US-08-948-929-1 13 US-08-948-932-929A-1 13 US-08-760-797-1	ID
Sequence 7, Appli Sequence 2, Appli Sequence 3, Appli Sequence 6, Appli Sequence 6, Appli Sequence 18, Appli Sequence 1, Appli Sequence 2, Appli Sequence 1, Appli	Description

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1 DIEKKICKMEKCSSVFNVVNS 21

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Ņ	Sequence 2, Appli	22			J	13,	41,	54,	20,	97,	34,	12,	93,	e 32,	48,	17,	32,	48	1042	97,	e 17,	e 78,	e 41,	48,	12,	27,	68	387	5, Appl	5,	ω `	ω	1, Appl	ω	۲	sequence 3, Appli

# ALIGNMENTS

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US-09-763-397A-7

Sequence 7, Application US/09763397A

GENERAL INFORMATION:
APPLICANT: The Government of the United States of America, as represented by the APPLICANT: Secretary of the Department of Health and Human Services, Centers for APPLICANT: Lal, Altaf A.
APPLICANT: Control and Prevention
APPLICANT: Lal, Altaf A.
APPLICANT: Hasnain, Seyed E.
TITLE OF INVENTION: Recombinant Multivalent Malarial Vaccine Against Plasmodium Fa
FILE REFERENCE: 6395-7049
CURRENT APPLICATION NUMBER: US/09/763,397A
CURRENT FILING DATE: 2001-02-16
PRIOR APPLICATION NUMBER: US 60/097,703
PRIOR APPLICATION NUMBER: PCT / US99/18869
PRIOR APPLICATION NUMBER: PCT / US99/18869
INVENTE: PATE: PATE: 1199-08-19
NUMBER OF SEQ ID NO 7
LENGTH: 21
TYPE: PRT
CORGANISM: Plasmodium falciparum
US-09-763-397A-7

Query Match
Best Local Similarity 100.0%; Score 109; DB 21; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.2e-09;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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                                    Qy
                                                                                                                                                                                 NAME/KEY: misc_feature;
OTHER INFORMATION: gi|4493889
US-09-820-843A-31
Ъ
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                                                                Query Match
Best Local Similarity 100.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 31, Application US/09820843A GENERAL INFORMATION:
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Best Local Similarity
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SEQ ID NO 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/763,397A CURRENT FILING DATE: 2001-02-16 PRIOR APPLICATION NUMBER: US 60/097,703 PRIOR FILING DATE: 1998-08-21 PRIOR APPLICATION NUMBER: PCT / US99/18869 PRIOR APPLICATION NUMBER: PCT / US99/18869 PRIOR FILING DATE: 1999-08-19 PRIOR FILING DATE: 1999-08-19 NUMBER OF SEQ ID NOS: 26
                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/820,843A
CURRENT FILING DATE: 2001-03-30
NUMBER OF SEQ ID NOS: 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Council of Scientific and Industrial Research TITLE OF INVENTION: A COMBUTATIONAL METHOD FOR THE IDENTIFICATION OF CANDIDATE PROTEITITE OF INVENTION: USEFUL AS ANTI-INFECTIVES FILE REFERENCE: Q63915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Ping Shi, Ya
APPLICANT: Hasnain, Seyed E.
TITLE OF INVENTION: Recombinant Multivalent Malarial Vaccine Against Plasmodium Falc:
FILE REFERENCE: 6395-57049
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: The Government of the United States of America, as represented by the APPLICANT: Secretary of the Department of Health and Human Services, Centers for Di APPLICANT: Control and Prevention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Plasmodium falciparum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
                                                                                                                                                                                                                                           NAME/KEY: misc_feature OTHER INFORMATION: Circumsporozoite (CS) protein
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                                                                                                                                                                                                                                                                                                                                                 ENGTH: 396
  362 DIEKKICKMEKCSSVFNVVNS 382
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                                        1 DIEKKICKMEKCSSVFNVVNS 21
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Pred. No. 6.6e-08;
Pred. No. 6.6e-08;
                                                                                 Score 109; DB 22; pred. No. 7.5e-08; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 350;
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                                                                                                                         Length 396;
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RESULT 4
US-07-677-539B-6
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                                                                                                                                                                                                                                                                                                     RESULT 5
US-07-727-636-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.
                                                                                                                                                                                                                                                                 Sequence 6, Application US/07727636 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEX: 6714627 CUSH INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: 26,581
REFERENCE/DOCKET NUMBER: 561
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-861-3067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: LAL, ALTAF A.
APPLICANT: GOLDMAN, IRA F.
TITLE OF INVENTION: CIRCUMSPOROZOITE PROTEIN OF PLASMODIUM
TITLE OF INVENTION: REICHENOWI AND VACCINE FOR HUMAN MALARIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: SCOTT, WATSON T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                APPLICANT: LAL, ALTAF A.
APPLICANT: GOLDMAN, IRA F.
TITLE OF INVENTION: REICHENOWI AND VACCINE FOR HUMAN MALARIA
TITLE OF INVENTION: REICHENOWI AND VACCINE FOR HUMAN MALARIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                          378 DIEKKICKMEKCSSVFNVVNS 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC
OPERATING SYSTEM:
SOFTWARE: Patentl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 1615 L S'
CITY: WASHINGTON
STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: FILING DATE: 199112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
                                                                                         STATE:
                                                                                                      STREET: 1615 L ST
CITY: WASHINGTON
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                                                                     COUNTRY:
                                                                                                                                            ADDRESSEE:
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Y: USA
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1615 L STREET, N.W.
                                                                                                                             E: CUSHMAN, DARBY & CUSHMAN 1615 L STREET, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             412 amino acids
                                                                        USA
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SYSTEM: PC-DOS/MS-DOS
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linear
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100.0%; Pred. No. 7.8e-08;
tive 0; Mismatches 0;
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; Sequence 18, Application US/08948885
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: SCOTT, WATSON T.

REGISTRATION NUMBER: 26,581
REFERENCE/DOCKET NUMBER: 5683,
TELECOMMUNICATION: INFORMATION:
TELEPHONE: 202-861-3067
TELEPAX: 202-822-0944
TELEEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity
Matches 21; Conserv
                                                                  INFORMATION FOR SEQ ID NO:
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APPLICATION NUMBER: US,
FILING DATE: 19910710
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                 FILING DATE: January 5, 1995
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 40028-A-PCT-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/313,288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS: sir
TOPOLOGY: linear
                                                                                                                                                                                                                                                                        FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: New York
STATE: New York
COUNTRY: USA
                                                                                                   TELEFAX: (212) 391-0526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM:
SOFTWARE: Patenti
   STRANDEDNESS:
                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
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                               LENGTH:
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                   amino
               412 amino acids
amino acid
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1185 Avenue of the Americas
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NVENTION: CLONING, EXPRESSION AND I
NOVEL SECRETED PROTEIN, I
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Pred. No. 7.8e-08;
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US-07-842-694-2
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                                                              RESULT
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GENERAL INFORMATION:
APPLICANT: De Wilde, Michel
APPLICANT: Cohen, Joseph
Sequence 2, Application US/07842694
GENERAL INFORMATION:
APPLICANT: Cohen, Joseph
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Best Local Similarity
Matches 21; Conserv
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Best Local S
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CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: 08/663,;
APPLICATION NUMBER: 13-JUNE-1996
                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 423 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATION SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/932,929A
APPLICATION NUMBER: US/08/932,929A
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER: 33,833
REFERENCE/DOCKET NUMBER: 84
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5096
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ATTORNEY/AGENT INFORMATION:
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ADDRESSEE: SmithKline
STREET: 709 Swedeland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: Hybrid Protein Between CS TITLE OF INVENTION: from Plasmodium and HBSAG NUMBER OF SEQUENCES: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          172 DIEKKICKMEKCSSVFNVVNS 192
                                                                                                                                                                                                                                                            STRANDEDNESS:
TOPOLOGY: li
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                                                                                                                         1 DIEKKICKMEKCSSVFNVVNS 21
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                                                                                                                                                                   100.0%; Score 109; DB 13; 100.0%; Pred. No. 8.1e-08; rive 0; Mismatches 0;
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Pred. No. 7.8e-08;
                                                                                                                                                                     Indels
                                                                                                                                                                                               Length 423;
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; ANTI-SENSE: NO US-07-842-694-2
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REGISTRATION NUMBER: 3115:
REFERENCE/DOCKET NUMBER: 1
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear MOLECULE TYPE: pro
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TITLE OF INVENTION: Ma
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/842,694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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LENGTH: 424 amino acid
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: US...
7TD: 19406-0939
                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: De Wilde, Michel APPLICANT: Cohen, Joseph
                                                                                                                                                                                                SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: HYBRID PROTEIN TITLE OF INVENTION: PLASMODIUM AND
                                                                  PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          173 DIEKKICKMEKCSSVFNVVNS 193
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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CITY: King of Prussia
STATE: Pennsylvania
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: SmithKline Beecham Corp./Corporate ADDRESSEE: Intellectual Property STREET: P.O. Box 1539 - UW2220
                                                                                                CLASSIFICATION:
                                                                                                                                 APPLICATION NUMBER: US/08/760,797 FILING DATE: 04-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 DIEKKICKMEKCSSVFNVVNS 21
APPLICATION NUMBER: 08/4 FILING DATE: 17-MAY-1995
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                                     08/442,612
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Pred. No. 8.1e-08;
0; Mismatches 0;
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HBSAG
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us-08-760-797-1
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US-08-760-797-3
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GENERAL INFORMATION:
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Best Local
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 424 amino acid:
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TELEPHONE: 610 270-5096
TELEFAX: 610 270-5090
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                               TELEFAX: 610 270-5090 INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA: 05/08/760,79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: HYBRID PROTEIN BETWEEN CS FROM TITLE OF INVENTION: PLASMODIUM AND HBSAG
                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Baumeister, Kirk
REGISTRATION NUMBER: 33,
                                                                                                                                                                                                                                               CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   169 DIEKKICKMEKCSSVFNVVNS 189
                                                               REFERENCE/DOCKET NUMBER: B4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610 270-5096
                                                                                                                                                              APPLICATION NUMBER: 08/442
FILING DATE: 17-MAY-1995
APPLICATION NUMBER: US 08
FILING DATE: 21-OCT-1994
CLASSIFICATION: 435
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Baumeister, Kirk REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: FILING DATE: 21-OCT
              SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: SmithKline Beecham Corp./Corporate ADDRESSEE: Intellectual Property STREET: P.O. Box 1539 - UW2220 CITY: King of Prussia STATE: Pennsylvania
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA
ZIP: 19406-0939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 DIEKKICKMEKCSSVFNVVNS 21
                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                   FILING DATE:
LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         amino acid
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424 amino acids
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Pred. No. 8.1e-08;
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                                                                                                                                    US-08-903-084-1
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US-08-903-084-1
                                                                         Query Match
Best Local :
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Best Local :
                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 424
PRIOR APPLICATION NUMBER: 08/741,575
FILING DATE: 30-OCT-1996
APPLICATION NUMBER: 08/303,542
FILING DATE: 09-SEP-1994
                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: B4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5024
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
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ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
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APPLICANT: Francotte, Myrian
APPLICANT: Kummert, Suzanne
APPLICANT: Slaoul, Moncef
APPLICANT: Wijendale, Frans
                                                                                                                                                MOLECULE TYPE:
                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: VACCINE FORMULATIONS CONTAINING
TITLE OF INVENTION: 3-O-DEACYLATED MONOPHOSPHORYL LIPID A AND A CARRIER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                169 DIEKKICKMEKCSSVFNVVNS 189
                                                                                                                                                                                                                                                      TELEPHONE: 610 - 5090
                                                                                                                                                                 TOPOLOGY:
                                                                                                                                                                            STRANDEDNESS:
                                                                                                                                                                                               TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/01 FILING DATE: 17-JUL-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM:
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                                                                        Local
                                                                                                                                                                                                          LENGTH:
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                          1 DIEKKICKMEKCSSVFNVVNS 21
                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19046
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                                                                                                                                                                                         : 424 amino acids
amino acid
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ilarity 100.0%;
Conservative (
                                                        100.0%;
conservative (
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                                                       Score 109; DB 13;
Pred. No. 8.1e-08;
0; Mismatches 0;
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Pred. No. 8.1e-08;
0: Mismatches 0;
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                                                                                    Length 424;
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Sequence 1, Application US/08932929
GENERAL INFORMATION:
APPLICANT: De Wilde, Michel
APPLICANT: Cohen, Joseph
TITLE OF INVENTION: HYBRID PROTEIN BE'
TITLE OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
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Best Local S
Matches 21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING CALL
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/74
APPLICATION NUMBER: 30-007-1196
CRA73(
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 30-OCT-1996
APPLICATION NUMBER: 08/36
FILING DATE: 09-SED-1994
ATTORNEY/AGENT INFORMATION:
NAME: Kerekes, Zoltan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
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MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Wijendale, Frans
TITLE OF INVENTION: VACCINE FORMULATIONS CONTAINING
TITLE OF INVENTION: 3-0-DEACYLATED MONOPHOSPHORYL LIPID A AND A CARRIER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Bruck, Claudine APPLICANT: Francotte, Myria
                                                                                                                                                                                                                                         169 DIEKKICKMEKCSSVENVVNS 189
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                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 610-270-5090
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Kerekes, Zoltan REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET:
                                                                                                                                                                                                                                                           1 DIEKKICKMEKCSSVFNVVNS 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 424 amino acids
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                                                                                                                                                                                                                                                                                                                           Similarity
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                                                                                                                                                                                                                                                                                                           100.0%; Score 109; ilarity 100.0%; Pred. No. 8 Conservative 0; Mismatches
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Slaoui, Moncef
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SmithKline Beecham Corp./Corporate Intellectual Property
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                                                                                   BETWEEN CS
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1.1e-08;
s 0;
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COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk

COUNTRY: USA ZIP: 19406-0939 STREET: P.O. Box 1539 - UW2220 CITY: King of Prussia

Pennsylvania

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; TOPOLOGY: li
; MOLECULE TYPE:
US-08-932-929-1
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US-08-932-929-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
APPLICATION NUMBER: US 08/244,085
FILING DATE: 21-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Baumeister, Kirk
NAME: Baumeister, Kirk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOSTWARE: PATENTIA RELEASE #1.0, VEISION #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: B4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610 270-5096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: De Wilde, Michel
APPLICANT: Cohen, Joseph
TITLE OF INVENTION: PLASMODIUM AND HBSAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
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               CLASSIFICATION: 435 PRIOR APPLICATION DATA:
                                                                                      SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   169 DIEKKICKMEKCSSVFNVVNS 189
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STRANDEDNESS: Si
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                                                                                                                                                                                                                                       STREET: P.O. Box 1539
CITY: King of Prussia
STATE: Pennsylvania
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                                                    FILING DATE:
                                                                     APPLICATION NUMBER: US/08/932,929
                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                             ADDRESSEE:
                                                                                                                                                                                                                                                                                                         ADDRESSEE: SmithKline Beecham Corp./Corporate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 DIEKKICKMEKCSSVFNVVNS 21
APPLICATION NUMBER:
                                                                                                                                                                                                      19406-0939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          424 amino acids
                                                                                                                                                                                                                                                                          E: Intellectual Property P.O. Box 1539 - UW2220
                                                                                                                                                                                                                        USA
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VENTION: HYBRID PROTEIN BETWEEN CS FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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                                                    18-SEP-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 109; DB 13; 100.0%; Pred. No. 8.1e-08; ive 0; Mismatches 0;
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 US/08/663,371
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; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-932-929-3
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; TOPOLOGY:
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Best Local Similarity
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INFORMATION FOR SEQ ID NO:
                                                                               INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 21-OCT-1994
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
TELEPHONE: 610 270-5096
                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/66:
FILING DATE: 13-JUNE-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: De Wilde, Michel
APPLICANT: Cohen, Joseph
TITLE OF INVENTION: Hybrid Protein Between CS
TITLE OF INVENTION: from Plasmodium and HBsAG
                                                                                                                                                  REFERENCE/DOCKET NUMBER: B4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5096
                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ELECUMENT STORM X: 610 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 33 REFERENCE/DOCKET NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 709 Swedeland CITY: King of Prussia STATE: PA
                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/932,929A FILING DATE: 18-SEPT-1997 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM CON OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 DIEKKICKMEKCSSVENVVNS 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH:
                                                                                                                                                                                                     NAME: Baumeister, Kirk REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                 TYPE: amino acid STRANDEDNESS: sir
                                                                                                                                    TELEFAX: 610-270-5090
                                                                 LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        19406
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                                                                 424 amino acids
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Search completed: January 29, 2002, 10:56:02 Job time: 2398 sec
                                                                                                                                                                   Query Match 100.0%; Score 109; DB 13; Length 424; Best Local Similarity 100.0%; Pred. No. 8.1e-08; Matches 21; Conservative 0; Mismatches 0; Indels 0;
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Minimum
Maximum
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No.
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Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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2222211154
2543210554
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Bd
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                                                                                                                                                                                                                                                                                                                                                                                            Score
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seg length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                         Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pending_Patents_AA_New:*

1: /cgn2_6/ptodata/2/paa/PCT_NEW_COMB.pep:*

2: /cgn2_6/ptodata/2/paa/US06_NEW_COMB.pep:*

3: /cgn2_6/ptodata/2/paa/US07_NEW_COMB.pep:*

4: /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep:*

5: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep:*

6: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep:*

7: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep:*
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Gapop 10.0 , Gapext 0.5
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    58
158
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 US-09-611-526-3845
US-09-708-427-35750
US-09-708-427-35750
US-09-620-111B-3030
US-09-620-111B-3039
US-09-894-018-121
US-09-894-018-121
US-09-708-427-22442
US-09-708-427-39156
US-09-708-427-39156
US-09-708-427-4855
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US-09-708-427-23776
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Sequence 3845, Ap Sequence 35760, A Sequence 3030, Ap Sequence 273, App Sequence 27442, A Sequence 27442, A Sequence 2663, Ap Sequence 2663, Ap Sequence 26073, App Sequence 26073, Ap Sequence 290, App Sequence 290, App Sequence 23776, A Sequence 23776, A Sequence 23776, A Sequence 23776, A Sequence 23706, A Sequence 23706, A Sequence 23705, A Sequence 23704, A
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Db BB	US-S	
Query Ma Best Loo Matches	US-09-611-526 Sequence 38 Sequence 38 GEMERAL INFE APPLICANT: APPL	4444443330333227 44444433376322127
Match Local Similarity es 7; Conserv 4 KKICKMEKCSSVFN :	ON TO	
larity 50 Conservativ KCSSVFN 17	-3845 45, Applicati ORMATION: OTA, TOSHIO NISHIKAWA, ISOGAI TAK HAYASHI, KO ISHII, SHIZ KAWAI, YURI WAKAMATSU, SUGIYAMA, TI NAGAI, KEII KOJIMA, SHI OTSUKI, TET KOGA, HISAS NYENTION: PRI OTSUKI, TET KOGA, HISAS NYENTION: PRI OTSUKI, TET KOGA, HISAS NYENTION: PRI CATION NUMBE ENCE: 08335/0 PLICATION NUMBE LING DATE: 2000 LING DATE: 2000 ICATION NUMBE NG DATE: 2000 SEQ ID NOS: 4 PATENTIN VET: 845 HOMO SAPIENS -3845	######################################
40. 50. ative 17	26-3845 26-3845, Application US/0 MFORMATION: T: OTA, TOSHIO T: ISCAL, TAKAO TT: SUGITAMA, TOMOVASU TT: WAKAMATSU, AI TT: WAKAMATSU, AI TT: WAKAMATSU, AI TT: KOGA, HISASHI TT: LINGATION UNBERS FO INVENTION: AND THEIR THENCE: 0835/0122 APPLICATION NUMBER: JP 1 LING DATE: 2000-01-11 LING DATE: 2000-01-11 LING DATE: 2000-05-02 TP SEQ ID NOS: 4484 T: PATENTIN VET. 2.1 3845 167 RT RT RT RT THOMO SAPIENS 26-3845	1221 317 366 382 464 452 120 270 270 272 272 376 376 377
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Score 44; DB 5; Length Pred. No. 13; 2; Mismatches 5; Ind	611526 SYNTHESIS OF FULL USES 09/611,526 7 99-194486 00-118774	US-09-919-891-2 US-09-985-153-54 US-10-006-867-116 US-09-708-427-33001 US-09-708-427-33001 US-09-708-427-64932 US-09-708-427-64932 US-09-708-427-24404 US-09-708-427-24404 US-09-708-427-24404 US-09-708-427-24403 US-09-708-427-2498-1047 US-09-708-427-21985 US-09-708-427-9857 US-09-708-427-21983 US-09-708-427-21983 US-09-708-427-21983 US-09-708-427-21983
gth 167; Indels 0;	LENGTH CDNAS	Sequence
Gaps		2, Appli 116, Appl 33000, A 33000, A 232999, A 23299, A 24932, A 1049, Appl 1048, Appl 1048, Ap 244404, A 11047, Ap 9857, Ap 99857, Ap 21981, A 21981, A
0		44 b4 44 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4

RESULT 2
US-09-708-427-35760
; Sequence 35760, Application US/09708427
; GENERAL INFORMATION:

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RESULT 3
US-09-708-427-35758
; Sequence 35758, Applic
; GENERAL INFORMATION:
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                                                                 RESULT 4
US-09-620-111B-3030
Sequence 3030, Application US/09620111B
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: Ceres Seq. US-09-708-427-35758
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TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: THEREBY
FILE REFERENCE: 2750-1243P
CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: Patentin version 3.1
SEQ ID NO 35760
LENGTH: 115
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Matches 6
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APPLICANT: N. ALEXANDROV et al.

TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES

TITLE OF INVENTION: THEREBY

FILE REFERENCE: 2750-1243P
CURRENT ETILING DATE: 2000-11-09

NUMBER OF SEQ ID NOS: 85364
SOFTWARE: PATCHIN VETSION 3.1

SEQ ID NO 33758
LENGTH: 117
APPLICANT: N. ALEXANDROV et al. TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides TITLE OF INVENTION: Thereby
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                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc_feature
LOCATION: 1..117
OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc_feature
LOCATION: 1..117
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6; Conserva
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Pred. No.
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NAME/KEY: misc_feature
; LOCATION: 1..58
; OTHER INFORMATION: Xaa is any am
; NAME/KEY: misc_feature
; LOCATION: 1..58
; OTHER INFORMATION: Ceres Seq. ID
US-09-620-111B-3030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; LOCATION: 1..68
; OTHER INFORMATION: Xaa is ; NAME/KEY: misc_feature
; NAME/KEY: 1..68
; LOCATION: 1..68
; OTHER INFORMATION: Ceres Sous-09-620-111B-3029
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Best Local Similarity
"-+ches 9; Conserv?
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                                                                                                                                                                                                                                                                                    US-09-894-018-273; Sequence 273, Application US/09894018
                                                                                                                                                                                                                                                                                                                                                           RESULT
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CURRENT APPLICATION NUMBER: US/09/620,111B
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 9298
SEQ ID NO 3030
LENGTH: 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptid TITLE OF INVENTION: Thereby FILE REFERENCE: 2750-1070P FILE REFERENCE: 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 3029, Application US/09620111B GENERAL INFORMATION:
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Best Local
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                              APPLICANT:
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TITLE OF INVENTION: METODS AND SYSTEM FOR OPTIMIZING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 68
TYPE: PRT
ORGANISM: Arabidopsis thaliana
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9; Conserv
                              Newman, Mark
Brown, David
                                                                   Baker, Denisw
Newman, Mark
                                                                                                                                Livingston, Brian
                                                                                                                                                                 Chestnut, Robert
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34.6%;
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Pred. No. 9.1;
7; Mismatches
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Pred. No. 7
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TITLE OF INVENTION:

MINIGENES AND PEPTIDES THEREBY

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PRIOR APPLICATION NUMBER: PCT/US00/35568
PRIOR FILING DATE: 2000-12-28
PRIOR APPLICATION NUMBER: US 60/173,390
PRIOR FILING DATE: 1999-12-28
PRIOR APPLICATION NUMBER: US 60/284,221
PRIOR FILING DATE: 2001-04-16
NUMBER OF SEQ ID NOS: 368
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 273
                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: PCT/US00/35568
PRIOR FILING DATE: 2000-12-28
PRIOR FILING DATE: 1999-12-28
PRIOR FILING DATE: 1999-12-28
PRIOR APPLICATION NUMBER: US 60/284,221
PRIOR FILING DATE: 2001-04-16
NUMBER OF SEQ ID NOS: 368
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 141
ENGTH: 276
RESULT 8
US-09-708-427-22442
; Sequence 22442, Application US/09708427
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Best Local :
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APPLICANT: Baker, Denisw
APPLICANT: Newman, Mark
APPLICANT: Newman, Mark
APPLICANT: Brown, David
TITLE OF INVENTION: METODS AND SYSTEM FOR OPTIMIZING
FILE REFERENCE: 39963-20033.00
FILE REFERENCE: 39963-20033.00
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CURRENT APPLICATION NUMBER: US/09/894,018
CURRENT FILING DATE: 2001-06-27
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CURRENT FILING DATE: 2001-06-27
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TYPE: PRT
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                                                                                                                                                                                                                                                                                                      ORGANISM: Artificial Sequence
                                                                                                102
                                                                                              13 SSVFNVVNS 21
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|102 SSVFNVVNS 110
                                                                                                                                                                  Local Similarity
les 9; Conser
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9; Conservative
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                                                                                                                                                                   Conservative
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Pred. No.
                                                                                                                                                                  Mismatches
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Query Match
Best Local Similarity
Thes B; Conserv
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; NAME/KEY: misc_feature
; LOCATION: 1.372
; OTHER INFORMATION: Ceres Seq. ID 1840904
US-09-708-427-22442
US-09-894-018-121 ; Sequence 121, Application US/09894018
                                                                                                                                                                                                                                                 ; LOCATION: 1..374
; OTHER INFORMATION: Xaa is any
; NAME/KEY: misc_feature
; LOCATION: 1..374
; OTHER INFORMATION: Ceres Seq.
US-09-620-394B-5663
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                                                                                                                                  Query Match
Best Local Similarity 5/...
Thes 8; Conservative
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CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 9131
SEQ ID NO 5663
LENGTH: 374
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CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: Patentin version 3.1
SEQ ID NO 22442
LENGTH: 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 5663, Application US/09620394B
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai
APPLICANT: BROVER, Vyacheslav
TITLE OF INVENTION: Thereby
FILE REFERENCE: 2750-1067P
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APPLICANT: N. ALEXANDROV et al
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                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Arabidopsis thaliana
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57.1%;
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57.1%;
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Pred. No. 55;
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GENERAL INFORMATION:

APPLICANT: EPIMMUNE, APPLICANT: Sette, A

APPLICANT:

Chestnut, Robe Livingston, Baker, Denisw

Robert

Brian

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; FEATURE:
; OTHER INFORMATION: PfCTL/HTL(N)
US-09-894-018-121
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LOCATION: 1..150
OTHER INFORMATION: Ceres Seq. ID 1852376
US-09-708-427-39156
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RESULT 12
US-09-708-427-26073
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 121
                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: PatentIn version 3.1
SEQ ID NO 39156
LENGTH: 150
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Best Local (
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APPLICANT: N. ALEXANDROV et al.
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CURRENT FILING DATE: 2001-06-27
PRIOR APPLICATION NUMBER: PCT/US00/35568
PRIOR FILING DATE: 2000-12-28
PRIOR APPLICATION NUMBER: US 60/173,390
PRIOR APPLICATION NUMBER: US 60/284,221
PRIOR APPLICATION NUMBER: US 60/284,221
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TITLE OF INVENTION: METODS AND SYSTEM FOR OPTIMIZING
TITLE OF INVENTION: MINIGENES AND PEPTIDES THEREBY
FILE REFERENCE: 39963-20033.00
                                                                                                                                             Matches
                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES TITLE OF INVENTION: THEREBY FILE REFERENCE: 2750-1243P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
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                                                                                                                                                                                                                                                                                             NAME/KEY: misc_feature
LOCATION: 1..150
OTHER INFORMATION: Xaa is any amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH:
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                                                                                                                                                                                                                                                                                                                                                FEATURE:
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nes 9; Conserv
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21 SSVFNVVNS 29
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                                                                             84 DLEKKFCKFGRVTS 97
                                                                                             1 DIEKKICKMEKCSS 14
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Brown, David
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100.0%; Pred. No.
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67;
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RESULT 14 US-09-708-427-4856

Sequence 4856, Application US/09708427 GENERAL INFORMATION: APPLICANT: N. ALEXANDROV et al.

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NAME/KEY: misc_feature
LOCATION: 1..238
OTHER INFORMATION: Ceres Seq. ID 1815731
US-09-708-427-26073
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CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: Patentin version 3.1
SEQ ID NO 26073
LENGTH: 238
TURNEL STATE OF THE PATENTIAL STATE OF THE PA
                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Corynebacterium glutamicum US-09-605-703B-292
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                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 60/152,318
PRIOR FILING DATE: 1999-09-03
NUMBER OF SEQ ID NOS: 2934
SEQ ID NO 292
LENGTH: 239
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Best Local Similarity 45.6
Matches 9; Conservative
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TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID
TITLE OF INVENTION: THEREBY
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                                                                                                                                             Query Match
Best Local Similarity
Matches 5; Conserv
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APPLICANT: Haborhauer, Gregor

TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING NOVEL

TITLE OF INVENTION: PROTEINS

FILE REFERENCE: BGI-129CP
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APPLICANT:
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LOCATION: 1..238
OTHER INFORMATION: Xaa is any amino acid
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210 NVETRHCKRERCAAI 224
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                                                                      1 DIEKKICKMEKCSSV 15
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Pred. No.
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Pred. No. 51;
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: TYPE: PRT
: ORGANISM: Arabidopsis thaliana
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: 1.256
: OTHER INFORMATION: Xaa is any amino acid
: NAME/KEY: misc_feature
: LOCATION: 1.256
: OTHER INFORMATION: Ceres Seq. ID 1813256
US-09-708-427-4855
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ORCANISM: Arabidopsis thaliana
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1..241
OTHER INFORMATION: xaa is any amino acid
NAME/KEY: misc_feature
LOCATION: 1..241
OTHER INFORMATION: Ceres Seq. ID 1813257
US-09-708-427-4856
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Search completed: January 29, 2002, 10:58:10 Job time: 2506 sec
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Best Local Similarity 38.3
Thes 7; Conservative
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GENERAL INFORMATION:
APPLICANT: N. ALEXANDROV et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: THEREBY
FILE REFERENCE: 2750-1243P
CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: Patentin version 3.1
SEQ ID NO 4855
LENGTH: 256
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Best Local Similarity 38.3
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CURRENT FILING DATE: 2000-11-09
NUMBER OF SEG ID NOS: 85364
SOFTWARE: PatentIn version 3.1
SEQ ID NO 4856
LENGTH: 241
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                                                                                    4 KKICKMEKCSSVFNVVNS 21
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36 KVLCDVNACAVVYNPFNS 53
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Pred. No. 51;
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Pred. No. 54;
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Post-processing: Minimum Match 0%
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2: /cgn2_6/ptodata/2/paa/US07_COMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

Match Length DB ID  100.0 23 21 US-09-763-397A-6 100.0 24 3 US-07-610-222-3 100.0 24 8 US-08-480-512-55 100.0 350 21 US-09-763-397A-2		Score Match Length DB ID	100.0 23 21 US-09-763-397A-6	100.0 24 3 US-07-610-222-33	100.0 24 8 US-08-480-512-55	100.0 350 21 US-09-763-397A-2	100 0 110 3 116-07-677-6300-6	100.0 412 3 05-0/-5338-0	Result NO. 1 2 3 4	Score 127 127 127 127	Query Match 100.0 100.0 100.0	Length 23 24 24 350	21 21 21 21	ID US-09-763-397A-6 US-07-610-222-33 US-08-480-512-55 US-09-763-397A-2	Description Sequence 6, Appli Sequence 33, Appl Sequence 55, Appl Sequence 2, Appli
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US-09-763-197A-5

Sequence 6, Application US/09763397A

Sequence 6, Application US/09763397A

Sequence 6, Application US/09763397A

Sequence 6, Application US/09763397A

Sequence 7, Applicam; The Government of the United States of America, as represented by the Applicam; Control and Prevention

APPLICAMT: Secretary of the Department of Health and Human Services, Centers for Applicam; Control and Prevention

APPLICAMT: Lal, Altaf A.

APPLICAMT: Lal, Altaf A.

APPLICAMT: Hasnain, Seyed E.

TITLE OF INVENTION: Recombinant Multivalent Malarial Vaccine Against Plasmodium Fa FILE REFERENCE: 6395-57049

CURRENT PAPLICATION NUMBER: US/09/763,397A

CURRENT PAPLICATION NUMBER: US/09/763,397A

CURRENT PAPLICATION NUMBER: US 60/097,703

PRIOR APPLICATION NUMBER: US 60/097,703

PRIOR FILING DATE: 1999-08-19

NUMBER OF SEQ ID NO.

SEQ ID NO.

SEQ ID NO.

SEQ ID NO.

LENGTH: 23

TYPE: PAT

ORGANISM: Plasmodium falciparum

US-09-763-397A-6

Ouery Match

Best Local Similarity 100.0%; Score 127: DB 21: Length 23:
Best Local Similarity 100.0%; Pred. No. 2.5e-11:
Best L
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RESULT 2
US-07-610-222-33
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; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: LAVIN Jr., Lawrence M.
REGISTRATION NUMBER: 30,768
REFERENCE/DOCKET NUMBER: 2481.1003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
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TITLE OF INVENTION: Induction of Cytotoxic
NUMBER OF SEQUENCES: 36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Deres, Karl
APPLICANT: Wiesmuller, Karl-Heinz
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APPLICANT:
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FILING DATE: 19901108
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Rammensee, Hans-Georg
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                                                                                                   Jung, Gunther
              Buhring, Hans-Jorg
Becker, Gerhard
Bessler, Wolfgang
                                                                Metzger, Jorg
                                                                                  Wiesmuller, Karl-Heinz
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TELEFAX: 202-408-4400 [NFORMATION FOR SEQ ID NO:
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APPLICANT: Deres, Karl
TITLE OF INVENTION: Conjugate, Its Preparation and its Uses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 20-APR-PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 08-NOV-
PRIOR APPLICATION DATA:
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APPLICATION NUMBER:
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SEQUENCE CHARACTERISTICS:
LENGTH: 24 amino acids
                                                                                       TELECOMMUNICATION INFORMATION:
                                                                                                                                                            FILING DATE: 10-NOV-1989 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                FILING DATE: 22-APR-PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                    FILING DATE: 24-JUN-
PRIOR APPLICATION DATA:
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APPLICATION NUMBER: US 07
APPLICATION 27-SEP-1990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
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CLASSIFICATION: 424
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20005-3315
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Schild, HansJorg
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                                                                        202-408-4000
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20-APR-1989
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20-JUN-1986
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24-JUN-1985
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26-OCT-1992
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MOLECULE TYPE:

TOPOLOGY:

linear

peptide

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Best Local
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Best Local
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PRIOR FILING DATE: 1998-08-21
PRIOR APPLICATION NUMBER: PCT / US99/18869
PRIOR FILING DATE: 1999-08-19
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Lal, Altaf A.
APPLICANT: Ping Shi, Ya
APPLICANT: Hasnain, Seyed E.
TITLE OF INVENTION: Recombinant Multivalent Malarial Vaccine Against Plasmodium Falci
FILE REFERENCE: 6395-57049
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: The Government of the United States of America, as represented by the APPLICANT: Secretary of the Department of Health and Human Services, Centers for Dis APPLICANT: Control and Prevention APPLICANT: Lal, Altaf A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/763,397A CURRENT FILING DATE: 2001-02-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
                MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 350
                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN, DARBY & CUSHMAN
STREET: 1615 L STREET, N.W.
                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                         TITLE OF INVENTION: CIRCUMSPOROZOITE PROTEIN OF PLASMODIUM TITLE OF INVENTION: REICHENOWI AND VACCINE FOR HUMAN MALARIA NUMBER OF SEQUENCES: 54
                                                                                                                                                                                                                                                                                                                            APPLICANT: LAL, ALTAF A.
APPLICANT: GOLDMAN, IRA F.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            51 KPKDELDYENDIEKKICKMEKCS 73
                                                                                                                                                                          STATE: D.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
  APPLICATION NUMBER:
                                                                                                                                       ZIP: 20036
                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 KPKDELDYENDIEKKICKMEKCS 23
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                                                                                                                                                                                            WASHINGTON
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  US/07/677,539B
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Query Match
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RESULT 6
US-07-727-636-6
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GENERAL INFORMATION:
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                                                                                                                          TELEX: 6714627 CUSH INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                              APPLICATION NUMBER: US/07/
FILING DATE: 19910710
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: SCOTT, WATSON T.
REGISTRATION NUMBER: 26,58
REFERENCE/DOCKET NUMBER: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEX: 6714627 CUSH INFORMATION FOR SEQ ID NO:
TOPOLOGY: 1i
MOLECULE TYPE:
17-727-636-6
                                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                             TELECOMMUNICATION INFORMATION: TELEPHONE: 202-861-3067
                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: LAL, ALTAF A.
APPLICANT: GOLDMAN. CIRCUMSPOROZOITE PROTEIN OF PLASMODIUM
TITLE OF INVENTION: REICHENOWI AND VACCINE FOR HUMAN MALARIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS
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TELEFAX: 202-822-0944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: SCOTT, WATSON T.
REGISTRATION NUMBER: 26,'
REFERENCE/DOCKET NUMBER:
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                                                                        LENGTH:
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TYPE: AMINO ACID
STRANDEDNESS: single
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CLASSIFICATION:
                                                                                                                                                        TELEFAX:
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                                                  STRANDEDNESS:
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                                                                    AMINO ACID
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1615 L STREET, N.W.
                                                                                     412 amino acids
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US-08-948-885-18
; Sequence 18, Application US/08948885
; GENERAL INFORMATION:
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US-08-932-929A-1
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TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-948-885-18
                                                                                                                      Sequence 1, Application US/08932929A GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO:
                              APPLICANT: De Wilde, Michel
APPLICANT: Cohen, Joseph
TITLE OF INVENTION: Hybrid Protein Between CS
TITLE OF INVENTION: from Plasmodium and HBsAG
NUMBER OF SEQUENCES: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: White, John P.
REGIZENTON NUMBER: 28,678
REFERENCETON NUMBER: 40028-A-PCT-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIJUM TYPE: Floppy disk
COMPUTER: IBM CC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Jessell, TITLE OF INVENTION: TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 412 amino acid
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APPLICATION NUMBER: US 08/313,288
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                   CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                             368 KPKDELDYENDIEKKICKMEKCS 390
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/948,885 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
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   ADDRESSEE:
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SmithKline Beecham Corporation
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                                                                                                                                                                                                                                                                                                                                 412;
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US-07-842-694-2
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Best Local S
Matches 23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 423 amino acid
                   REFERENCE/DOCKET NUMBER: INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 33,833
REFERENCE/DOCKET NUMBER: B45015-1FWC2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/663,371
FILING DATE: 13-JUNE-1996.
ATTORNEY/AGENT INFORMATION:
NAME: BAUNCHISTER, KIR
                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Cohen, Joseph
APPLICANT: De Wilde, Michel
TITLE OF INVENTION: Malaria Vaccine Antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: FastSEQ for CURRENT APPLICATION DATA:
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                                                                   APPLICATION NUMBER: US/0:
FILING DATE: 1920227
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Canter, Carol G.
                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             162 KPKDELDYENDIEKKICKMEKCS 184
                                                                                                                                                                                                                                                                                                                             ADDRESSEE: SIII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 18 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                         STREET: P.O. Box 1539
CITY: King of Prussia
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les 23; Conserv
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                                                    NAME: Canter, Carol G. REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 KPKDELDYENDIEKKICKMEKCS 23
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King of Prussia
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RESULT 11
US-07-727-636-5
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Best Local (
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GENERAL INFORMATION:
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                                                                                                                     Matches
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TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 388 amino acids
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TOPOLOGY: lin
MOLECULE TYPE:
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TELEFAX: 202-822-0944
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: SCOTT, WATSON T.
REGISTRATION NUMBER: 26,5
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                      STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: peptide
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CORRESPONDENCE ADDRESS:
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APPLICANT: GOLDMAN, IRA F.
TITLE OF INVENTION: CIRCUMSPOROZOITE PROTEIN OF PLASMODIUM
TITLE OF INVENTION: REICHENOWI AND VACCINE FOR HUMAN MALARIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HYPOTHETICAL:
                                                       163 KPKDELDYENDIEKKICKMEKCS 185
                                                                                                                   Local Similarity 91.3 hes 21; Conservative
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FILING DATE: 19911205
CLASSIFICATION: 424
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nes 23; Conserv
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91.3%;
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                                                                                                                Score 122; DB 3; Pred. No. 4.3e-09; National Ches 0;
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Pred. No. 8.8e-10;
                                                                                                                                             DB 3; Length 388;
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US-09-820-843A-31
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; OTHER INFORMATION: g1|4493889
US-09-820-843A-31
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                                                                                                               CURRENT APPLICATION NUMBER: US/09/820,843A
CURRENT FILING DATE: 2001-03-30
NUMBER OF SEQ ID NOS: 118
SOFTWARE: PATENTIN version 3.0
SEQ ID NO 31
LENGTH: 396
TYPE: PAT
ORGANISM: Plasmodium falciparum
                                                                                                                                                                                                                                                                              Sequence 31, Application US/09820843A
GENERAL INFORMATION:
APPLICANT: Council of Scientific and Industrial Research
TITLE OF INVENTION: A COMPUTATIONAL METHOD FOR THE IDENTI
TITLE OF INVENTION: USEFUL AS ANTI-INFECTIVES
FILE REFERENCE: 063915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-861-3067
TELEPAX: 202-82-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEO ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 388 amino acids
TYPE: AMINO ACID
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Best Local
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FILING DATE: 19910710
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: SCOTT, WATSON T.
REGISTRATION UNMBER: 26,58
REFERENCE/DOCKET NUMBER: 5
                                  NAME/KEY: misc_feature
OTHER INFORMATION: Circumsporozoite (CS) protein
NAME/KEY: misc_feature
                                                                                                  FEATURE:
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APPLICANT: LAL, ALTAF A.

APPLICANT: GOLDMAN, IRA F.

APPLICANT: GOLDMAN, IRA F.

TITLE OF INVENTION: CIRCUMSPOROZOITE PROTEIN OF PLASMODIUM
TITLE OF INVENTION: REICHENOWI AND VACCINE FOR HUMAN MALARIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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CITY: WASHINGTON
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Similarity 91.3%;
21; Conservative
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linear
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Pred. No. 4.3e-09;
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                                        RESULT 14
US-08-760-797-3
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US-08-760-797-1
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                Sequence 3, Applicati
GENERAL INFORMATION:
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Best Local Similarity
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                         TELEFAX: 610 270-5090
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 19405 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: SYSTEM: PC DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER: 33,833
REFERENCE/DOCKET NUMBER: B4
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Baumeister, Kirk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: De Wilde, Michel
APPLICANT: Cohen, Joseph
                                                                                                                                                                                                                                                  MOLECULE TYPE: protein -760-797-1
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                                                                                                            159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 08/4.
FILING DATE: 17-MAY-1995
APPLICATION NUMBER: US
FILING DATE: 21-OCT-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08 FILING DATE: 04-DEC-1996
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                                                                                                                          1 KPKDELDYENDIEKKICKMEKCS 23
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                                                                                                                                                                                                                                                                                                              amino acid
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                           Application US/08760797
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De Wilde, Michel
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95.7%;
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PLASMODIUM AND HBSAG
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95.7%;
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Pred. No. 6.1e-09;
                                                                                                                                                                                    Score 121; DB 11;
Pred. No. 6.6e-09;
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                                                                                                                                                                                                 Length 424;
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/760,797 FILING DATE: 04-DEC-1996 CLASSIFICATION: 435 PRIOR APPLICATION DATA: 08/442,612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION: TELEPHONE: 610 270-5096
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: HYBRID PROTEIN BETWEEN CS FROM TITLE OF INVENTION: PLASMODIUM AND HBSAG
                                                                                                                                                                      APPLICANT: Francotte, Myriam
APPLICANT: Kummert, Suzanne
APPLICANT: Slaoui, Moncef
APPLICANT: Wijendale, Frans
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ATTORNEY/AGENT INFORMATION:
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                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein
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                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                     TITLE OF INVENTION: VACCINE FORMULATIONS CONTAINING TITLE OF INVENTION: 3-0-DEACYLATED MONOPHOSPHORYL L
                                                                                                                                                                                                                                                                                                                                                                     159 KPKDELDYANDIEKKICKMEKCS 181
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FILING DATE: 17-MAY-1995
APPLICATION NUMBER: US 0
FILING DATE: 21-OCT-1994
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                                  STATE:
                                            CITY: King of Prussia
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           COUNTRY:
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                U.S.A.
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SYSTEM: PC-DOS/MS-DOS
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O. Box 1539 - UW2220
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Pred. No. 6.
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5.6e-09;
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COMPUTER READABLE FORM:

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COMPUTER: IDENCOMPATIBLE
COMPUTER: IDEN COMPATIBLE
COMPUTER: IDEN COMPATIBLE
COMPATING SYSTEM: DOS
CORRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/903,084
FILING DATE: 17-JUL1997
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/741,575
FILING DATE: 30-OCT-1996
APPLICATION NUMBER: 09/741,575
FILING DATE: 09-SEP-1994
ATTORNEY/AGENT INFORMATION:
APPLICATION NUMBER: 30-OCT-1996
ATTORNEY/AGENT INFORMATION:
TELEFORMATION NUMBER: 38,938
REGISTRATION NUMBER: 38,938
REGISTRATION NUMBER: 38,938
REGISTRATION NUMBER: 38,938
REGISTRATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 424 andino acids
TTELEFAX: 610-720-5024
TTELEFAX: 610-720-7202
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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Perfect score:
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       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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length: 2000000000
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Match
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1: /cgn2_6/ptodata/2/paa/PCT_NEW_COMB.pep:*

2: /cgn2_6/ptodata/2/paa/US06_NEW_COMB.pep:*

3: /cgn2_6/ptodata/2/paa/US07_NEW_COMB.pep:*

4: /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep:*

5: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep:*

6: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep:*

7: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep:*
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US-09-708-427-5052
US-09-708-427-5051
US-09-897-516-6570
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US-09-708-427-19153
US-09-708-427-19153
US-09-708-427-19151
US-09-708-427-19151
US-09-708-427-19151
US-09-708-427-19151
US-09-708-427-113369
US-09-708-427-14304
US-09-708-427-14304
US-09-708-427-14304
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sequence
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                 7357, Ap
19153, Ap
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19379, A
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US-09-708-427-5053
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32.3	32.3	32.3	32.3	32.3	32.3	32.3	32.3	32.7	32.7	32.7	33.1	33.1	33.1	33.1	33.1	33.9	33.9
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US-09-708-427-5892	US-09-708-427-5893	US-09-620-394B-1047	US-09-620-394B-1048	US-09-620-394B-1049	US-09-815-242-12569	US-09-815-242-11666	US-09-815-242-5560	US-09-708-427-11573	US-09-708-427-11574	US-09-708-427-11575	US-09-611-526-3265	US-09-815-242-11461	US-09-620-394B-5279	US-09-708-427-39156	US-60-323-991-30	US-09-708-427-56475	US-09-708-427-56476
Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Seguence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence
5892, Ap	5893, Ap	1047, Ap	1048, Ap	1049, Ap	12569, A	11666, A	5560, Ap	11573, A	11574, A	ζ.	3265, Ap	11461, A	5279, Ap	39156, A	30, Appl	56475, A	56476, A

ALIGNMENTS

## US-09-708-427-5052 Sequence 5052, Application US/09708427 GENERAL INFORMATION: APPLICANT: N. ALEXANDROV et al. TITLE OF INVENTION: SEQUENCE-DETERMINED DNA TITLE OF INVENTION: THEREBY FILE REFERENCE: 2750-1243P CURRENT APPLICATION NUMBER: US/09/708,427 CURRENT APPLICATION NUMBER: US/09/708,427 CURRENT FILING DATE: 2000-11-09 NUMBER OF SEQ ID NOS: 85364 SOPTMARE: Patentin version 3.1 SEQ ID NO 5052 LENGTH: 872 FEATURE: NAME/KEY: misc\_feature LOCATION: 1.867 OTHER INFORMATION: Xaa is any an NAME/KEY: misc\_feature LOCATION: 1.867 OTHER INFORMATION: Ceres Seq. II US-09-708-427-5053 FILE REFERENCE: 2750-1243P CURRENT APPLICATION NUMBER: US/09/708,427 CURRENT FILING DATE: 2000-11-09 NUMBER OF SEQ ID NOS: 85364 SOFTWARE: PatentIn version 3.1 SEQ ID NO. 5053 LENGTH: 867 TYPE: PRT ORGANISM: Arabidopsis thaliana Sequence 5053, Application US/09708427 GENERAL INFORMATION: APPLICART: N. ALEXANDROV et al. TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID TITLE OF INVENTION: THEREBY Query Match Best Local Similarity Matches 9; Conserv 816 RDTDSYINDIEKCLCSQE 833 3 KDELDYENDIEKKICKME 20 Conservative 36.2%; any amino <u>ب</u> Score 46; | Pred. No. 1 ID 1813621 Mismatches acid DNA FRAGMENTS DB 5; ув ..2e+02; 7; Length 867 AND CORRESPONDING 0; Gaps POLYPEPTID 0

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APPLICANT: N. ALEXANDROY et al.
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SEQ ID NO 5051
LENGTH: 920
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Best Local
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APPLICANT:
APPLICANT:
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Matches 9; Conserv
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CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES TITLE OF INVENTION: THEREBY FILE REFERENCE: 2750-1243P
           APPLICANT: Malvar, Thomas M.
APPLICANT: Slater, Steven C.
APPLICANT: Spiridonov, Sergei
TITLE OF INVENTION: Xenorhabdus sp. Genome
FILE REFERENCE: 38-21(51847)B
CURRENT APPLICATION NUMBER: US/09/897,516
CURRENT FILING DATE: 2001-06-29
                                                                                                                                                                                                     APPLICANT:
                                                                                                                                                                                                                   APPLICANT: Corbin, David R.
 PRIOR
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LOCATION: 1..920
OTHER INFORMATION: Ceres Seq.
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LOCATION: 1..920
OTHER INFORMATION: Xaa is
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                                                                                                                                                                                                                                                                                                                                               869 RDTDSYINDIEKCLCSQE 886
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                                                                                                                                                                                                                                                                                                                                                                                    3 KDELDYENDIEKKICKME 20
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KDELDYENDIEKKICKME 20
                                                                                                                                                                                                                                        INFORMATION:
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                                                                                                                                            Goldman, Barry S.
Hinkle, Gregory J.
Huesing, Joseph E.
Krasomil-Osterfeld, Karina C.
                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     36.2%;
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US 60/215, 161
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Pred. No. 1.3e+02;
2; Mismatches 7;
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                                                                      And Uses Thereof
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RESULT 5
US-10-018-105-4
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US-09-708-427-7358
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NUMBER OF SEQ ID NOS: 8409
SEQ ID NO 6570
LENGTH: 1124
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Best Local Similarity 50.0%;
                                                                                                                                    SEQ ID NO 7358
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: BUSSEY, Howard
APPLICANT: DAVISON, John
TITLE OF INVENTION: DISCIPLICATION OF CANDIDA ALBICANS ESSENTIAL FUNGAL
TITLE OF INVENTION: SPECIFIC GENES AND USE THEREOF IN ANTIFUNGAL DRUG
TITLE OF INVENTION: DISCOVERY
FILE REFERENCE: 10182-015
CURRENT APPLICATION NUMBER: US/10/018,105
CURRENT FILING DATE: 2001-11-05
PRIOR APPLICATION NUMBER: PCT/CA00/00533
PRIOR FILING DATE: 2000-05-05
PRIOR APPLICATION NUMBER: 60/132,878
PRIOR FILING DATE: 1999-05-05
PRIOR FILING DATE: 1999-05-05
                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEO ID NOS: 85364
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID TITLE OF INVENTION: THEREBY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 6 SOFTWARE: PatentIn Ver. 2.1
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                                                                                                                                                                                                                               FILE REFERENCE: 2750-1243P
                                                                                                                                                                                                                                                                                          APPLICANT: N. ALEXANDROV et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Candida albicans
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                                                      ORGANISM: Arabidopsis thaliana FEATURE:
                                                                                               TYPE: PRT
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                NAME/KEY: misc_feature LOCATION: 1..416
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OTHER INFORMATION: Xaa is
                                                                                                               LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 36.8 nes 7; Conservative
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Pred. No. 1.8e+02;
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Best Local Similarity
""Thes 8; Conserve
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: LCCATION: 1..533
: OTHER INFORMATION: Ceres Seq.
US-09-708-427-7357
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: LOCATION: 1..416
: OTHER INFORMATION: Ceres
US-09-708-427-7358
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US-09-708-427-19153
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                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 19153
LENGTH: 550
TYPE: PRT
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CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: PatentIn version 3.1
SEQ ID NO 7357
LENGTH: 533
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Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                       APPLICANT: N. ALEXANDROV et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: THEREBY
FILE REFERENCE: 2750-1243P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILE REFERENCE: 2750-1243P
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                                FEATURE: misc_feature .
LOCATION: 1..550
OTHER INFORMATION: Xaa is any amino acid
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LOCATION: 1..533
OTHER INFORMATION: Xaa is any amino acid
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                   NAME/KEY: misc_feature LOCATION: 1..550
OTHER INFORMATION: Ceres Seq. ID 1835494
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Pred. No. 1.4e+02;
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Pred. No. 1.1e+02;
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US-09-708-427-19152
US-09-708-427-19152, Application US/09708427

GENERAL INFORMATION:

APPLICANT: N. ALEXANDROV et al.

TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID FILTE OF INVENTION: THEREBY

FILE REFERENCE: 2750-1243P

CURRENT APPLICATION NUMBER: US/09/708,427

CURRENT APPLICATION NUMBER: US/09/708,427

CURRENT FILING DATE: 2000-11-09

NUMBER OF SEQ ID NOS: 85364

SOTWARE: Patentin version 3.1

SEQ ID NO 19152

LENGTH: 558

TYPE: PRT
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; LCCATION: 1..553
; OTHER INFORMATION: Ceres Seq. ID 1816973
US-09-708-427-7356
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Best Local Similarity
"hehes 8; Conserv:
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Best Local Similarity
Watches 10; Conserva
; OTHER INFORMATION: Ceres Seq. US-09-708-427-19152
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GENERAL INFORMATION:
APPLICANT: N. ALEXANDROV et al
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SEQ ID NO 7356
LENCTH: 553
TYPE: PRT
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CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
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                                                              NAME/KEY: misc_feature
LOCATION: 1..558
OTHER INFORMATION: Xaa is any amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
NAME/KEY: misc_feature
LOCATION: 1..553
OTHER INFORMATION: Xaa
                                  NAME/KEY: misc_feature LOCATION: 1..558
                                                                                                                                          ORGANISM: Arabidopsis thaliana
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47.6%;
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Pred. No.
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Pred. No. 1.4e+02;
                  ID 1835493
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GENERAL INFORMATION:
APPLICANT: N. ALEXANDROV et al.
APPLICANT: N. ALEXANDROV et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: THEREBY
FILE REFERENCE: 2750-1243P
CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOCTWARE: Patentin version 3.1
SEQ ID NO 19151
LENGTH: 577
                                                            PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILLING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
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Best Local Similarity
Matches 10; Conserv
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                              APPLICANT: Xu, H: Howard
TITLE OF INVENTION: Identification of Essential
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Haselbeck, Robert
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc_feature
LOCATION: 1..577
OTHER INFORMATION: Ceres Seq. ID 1835492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc_feature
LOCATION: 1..577
OTHER INFORMATION: Xaa is any amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   267 KPKKELDLDQDKAAKVNGEEK 287
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Yamamoto, Robert T.
                                                                                                                                                                                                                                                                                                                                                                                                           Wall, Daniel
Trawick, John D.
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Pred. No. 1.5e+02;
Pred. No. 1.5e+02;
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Pred. No. 1.5e+02;
"'Amatches 9;
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g
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LENGTH: 607
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Best Local
                                                                     Query Match
Best Local Similarity
Matches 8; Conserv
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APPLICANT:
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CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Identification TITLE OF INVENTION: Prokaryotes FILE REFERENCE: ELITRA.011A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Haselbeck, Robert APPLICANT: Ohlsen, Kari L.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: 60/269,308 PRIOR FILING DATE: 2001-02-16
                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 60/242,578 PRIOR FILING DATE: 2000-10-23 PRIOR APPLICATION NUMBER: 60/253,625 PRIOR FILING DATE: 2000-11-27
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PRIOR FILING DATE: 2000-05-26
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                                                                                                                                                                                                                           LENGTH: 607
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498 KRKEEVDLRNEVDQAIFATEK 518
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Local Similarity 38.1%; Pred. No.
hes 8; Conservative 6; Mismatch
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                                   1 KPKDELDYENDIEKKICKMEK 21
                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 60/257,931 FILING DATE: 2000-12-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Xu, H. Howard
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                                                                         Conservative
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                                                                                             Score 44;
Pred. No. 1
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                                                                                             DB 5;
1.6e+02;
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RESULT 14
US-09-708-427-14304
S-09-08-427-14304
Sequence 14304, Application US/09708427
GENERAL INFORMATION:

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LENGTH: 803

TYPE: PRT

ORGANISM: Arabidopsis thaliana
FEATURE:
NAME/KEY: misc feature
LOCATION: 1.803
OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc_feature
LOCATION: 1.803
OTHER INFORMATION: Ceres Seq. ID 1827596
US-09-708-427-14303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Arabidopsis thaliana
FEARTURE:
NAME/KEY: misc_feature
LOCATION: 1.772
OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc_feature
LOCATION: 1.772
LOCATION: 1.772
OTHER INFORMATION: Ceres Seq. ID 1827597
US-09-708-427-14304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-708-427-14303
US-09-708-427-14303
Sequence 14303, Application US/09708427
GENERAL INFORMATION:
APPLICANT: IN ALEXANDROV et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: THEREBY
FILE REFERENCE: 2750-12439
CURRENT-APPLICATION NUMBER: US/09/708,427
CURRENT-APPLICATION NUMBER: US/09/708,427
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: PAtentin version 3.1
SEQ ID NO 14303
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Search completed: January 29, 2002, 10:58:09 Job time: 2505 sec
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TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES

TITLE OF INVENTION: THEREBY

FILE REFERENCE: 2750-1243P

CURRENT APPLICATION NUMBER: US/09/708,427

CURRENT FILING DATE: 2000-11-09

NUMBER OF SEQ ID NOS: 85364

SOFTWARE: Patentin version 3.1

SEQ ID NO 14304

LENGTH: 772

TYPE: PRT
                                                                                                                                                                              Query Match 34.6%;
Best Local Similarity 44.4%;
Matches 8; Conservative
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Best Local Similarity 44.4%;
Matches 8; Conservative
                                                                                              647 DDPDLQNTFFYKLCKVEK 664
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                                                                                                                          4 DELDYENDIEKKICKMEK 21
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Pred. No. 2e+02;
4; Mismatches
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Pred. No. 2.1e+02;
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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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          Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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75
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/cgn2_6/ptodata/2/paa/US081_COMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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69	69	69	69	75	75	75	75	75	Score
92.0	92.0	92.0	92.0	100.0	100.0	100.0	100.0	100.0	Query Match
396	20	20	20	412	412	412	350	13	Query Match Length DB
22	G	5	w	13	w	w	21	21	DB:
2 US-09-820-843A-31	US-08-119-694B-21	US-08-119-694-21	US-07-947-033-21	US-08-948-885-18	US-07-727-636-6	US-07-677-539B-6	US-09-763-397A-2	US-09-763-397A-5	ID
Sequence 31, Appl	Sequence 21, Appl	Sequence 21, Appl	Sequence 21, Appl	Sequence 18, Appl	Sequence 6, Appli	Sequence 6, Appli	Sequence 2, Appli	Sequence 5, Appli	Description

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US-60-324-109-18985	9-	-60-324-10	-628-359-38	5-161-45	97-873-176	-09-834-366-17	-169-340-70	-09-732-210-	-08-905-135-4	æ	73	•	-US01-08631-	-60-128-476	-713		-09-540-236-	-248-796-1	-60-207-583-6	-09-485-	-09-485-421-	-700-408-	-09-757-026-	-US01-14826-	-60-222-039-	-60-197-873-	0-197-873-	US-09-834-366-24566	834-366-	-90	PCT-US99-09970-2	PCT-US01-23861-2	PCT-US01-14826-223	-636-5	100
Sequence 1			Sequence 3					Sequence 7	Sequence 4		Sequence 2	Sequence 2	Sequence 39	Sequence 3	Sequence 2	Sequence 2	Sequence 2	Sequence 1	a	Sequence 2			ര	σ		ര		.,		o N		Sequence 2,	N	տ	
18985, A	37, Appl	19086, A	38, Appl	1572, Ap	17600, A	17600, A	707, App	707, App	~	1239, Ap	21504, A	21504, A	9492, A	3431, Ap	2331, Ap	2326, Ap	e 2919, Ap	16171, A	02, Ap	-	`	~	55,	'n	2, Appli	•	-	24566, A			Appli	Appli			1

## ALIGNMENTS

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RESULT 1
US-09-763-397A-5
Sequence 5, Application US/09763397A
Sequence 5, Application US/09763397A
Sequence 5, Application US/09763397A
Sequence 5, Application US/09763397A
Septence 5, Application US/09763397A
Septence 5, Application US/09763397A
APPLICANT: Secretary of the United States of America, as represented by the Applicant: Secretary of the Department of Health and Human Services, Centers for Applicant: Control and Prevention
APPLICANT: Hasnain, Seyed E.
APPLICANT: Ping Shi, Ya
APPLICANT: Ping Shi, Ya
APPLICANT: Ping Shi, Ya
APPLICANT: Ping Shi, Ya
CURENT FILLAGION NUMBER: US/09/763,397A
CURRENT FILING DATE: 2001-02-16
CURRENT FILING DATE: 2001-02-16
PRIOR APPLICATION NUMBER: US/097,703
PRIOR FILING DATE: 1998-08-19
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patentin version 3:1
SEQ ID NO 5
SEQ ID NO 5
SEQ ID NO 5
LENGTH: 13
TYPE: PRT
CORGANISM: Plasmodium falciparum
US-09-763-397A-5

Query Match
Best Local Similarity 100.0%; Pred. No. 4.6e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 6, Applicati
GENERAL INFORMATION:
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT FILING DATE: 2001-02-16
PRIOR APPLICATION NUMBER: US 60/097,703
PRIOR FILING DATE: 1998-08-21
PRIOR APPLICATION NUMBER: PCT / US99/18869
PRIOR FILING DATE: 1999-08-19
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILE REFERENCE: 6395-57049
CURRENT APPLICATION NUMBER: US/09/763,397A
CURRENT FILING DATE: 2001-02-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Ping Shi, Ya
APPLICANT: Hasnain, Seyed E.
TITLE OF INVENTION: Recombinant Multivalent Malarial Vaccine Against Plasmodium Falc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: The Government of the United States of America, as represented by the APPLICANT: Secretary of the Department of Health and Human Services, Centers for APPLICANT: Control and Prevention
ATTORNEY/AGENT INFORMATION:
NAME: SCOTT, WATSON T.
REGISTRATION NUMBER: 26,581
REFERENCE/DOCKET NUMBER: 5683
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-861-3067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 35
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Artificial Sequence
                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: GOLDMAN, IRA F.
TITLE OF INVENTION: CIRCUMSPOROZOITE PROTEIN OF PLASMODIUM
TITLE OF INVENTION: REICHENOWI AND VACCINE FOR HUMAN MALARIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: LAL, ALTAF A.
APPLICANT: GOLDMAN, IRA
                                                                                                                           APPLICATION NUMBER: US
FILING DATE: 19911205
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                       COUNTRY:
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1615 L STREET, N.W.
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Pred. No. 0.0021;
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US-07-727-636-6
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Best Local
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Best Local Similarity
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TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                          TELEFAX: 202-822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: SCOTT, WATSON T.
REGISTRATION NUMBER: 26,
                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: CIRCUMSPOROZOITE PROTEIN OF PLASMODIUM TITLE OF INVENTION: REICHENOWI AND VACCINE FOR HUMAN MALARIA
                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION: TELEPHONE: 202-861-3067
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109 KHKKLKQPGDGNP 121
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FILING DATE: 19910710
                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM:
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TOPOLOGY: 11
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                 1 KHKKLKQPGDGNP 13
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13; Conserv
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AMINO ACID
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                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                          IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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Pred. No.
                                                                   Score 75;
Pred. No.
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                                                       Mismatches
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; MOLECULE TYPE: peptide US-08-948-885-18
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Best Local Similarity
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PRIOR APPLICATION NUMBER: US 08/:
APPLICATION NUMBER: US 08/:
FILING DATE: JANUARY 5, 19/
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: White, John P. 8,678
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 40028-A-PCT-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                               APPLICANT: Cerami, Carla
APPLICANT: Frevert, Ute
APPLICANT: Sinnis, Photini
APPLICANT: Nussenzweig, Victor
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR INHIBITING
TITLE OF INVENTION: HEPATOCYTE INVASION BY MALARIAL SPOROZOITES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Jessell, Thomas M. and Avihu Klar
TITLE OF INVENTION: CLONING, EXPRESSION AND USES OF A
TITLE OF INVENTION: NOVEL SECRETED PROTEIN, F-SPONDIN
NUMBER OF SEQUENCES: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
COMPUTER READABLE FORM:
                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                    109 KHKKLKQPGDGNP 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/948,885 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: New York
STATE: New Yor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (212) 391-0526
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                                                                         New York
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                                                       New York
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1185 Avenue of the Americas
                                                                                           805 Third Avenue
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                                 United States of America
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Y 5, 1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 92.0
Best Local Similarity 92.0
Matches 12; Conservative
                                                                                                APPLICATION UNMBER: US/08/119,694
FILING DATE: 10-Sept-1993
ATTORNEY/AGENT INFORMATION:
NAME: Adda C. Gogoris, Esq.
REGISTRATION NUMBER: 29,714
REGISTRATION NUMBER: 5986/17607-US1
REFERENCE/DOCKET NUMBER: 5986/17607-US1
TELECOMMUNICATION 1870-7700
TELEPHONE: (212) 527-7700
TELEFAX: (212) 753-6237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Adda C. Gogoris, Esq.
REGISTRATION NUMBER: 29,714
REFERENCE/DOCKET NUMBER: 5980
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 527-7700
TELEFAX: (212) 753-6237
                                                                       TELEFAX: (212) 753-623
TELEX: 236687
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                             COMPUTER: AST Premium II 386/33
OPERATING SYSTEM: DOS 3.3
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Frevert, Ute
APPLICANT: Sinnis, Photini
APPLICANT: Nussenzweig, Victor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
                                 SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR INHIBITING TITLE OF INVENTION: HEPATOCYTE INVASION BY MALARIAL TITLE OF INVENTION: SPOROZOITES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (22 TELEFAX: 236687
                                                                                                                                                                                                                                                                                                                                                                                                               STATE: N
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 20 amino TYPE: 'AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/07/947,033 FILING DATE: 19920917 CLASSIFICATION: 530
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COMPUTER: A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 KHKKLKQPADGNP 15
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                                                                                                                                                                                                                                                                                                                                                                                                 10022
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New York
The Control of America
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       805 Third Avenue
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            unknown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E: Diskette, 5, inch, 1.2 MB storage AST Premium II 386/33
SYSTEM: DOS 3.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Darby & Darby, P.C.
                                                                                                                                                                                                                                                                                                                                                            Diskette,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 92.0%;
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                                                                                                                                                                                                                                                                                                                                                            5, inch, 1.2 MB storage
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Pred. No. 0.00071;
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RESULT 9
US-09-820-843A-31
; Sequence 31, Application US/09820843A
; Sequence 31, Application US/09820843A
; GENERAL INFORMATION:
; APPLICANT: Council of Scientific and Industrial Research
; TITLE OF INVENTION: A COMPUTATIONAL METHOD FOR THE IDENTIFICATION OF CANDIDATE PROTEI
; TITLE OF INVENTION: USEFUL AS ANTI-INFECTIVES
; FILE REFERENCE: Q63915
                                                                                                                                                                                                                                     Ş
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                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                          Query Match
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APPLICANT: Frevert, Ute
APPLICANT: Sinnis, Photini
APPLICANT: Nussenzweig, Victor
TITLE OF INVENTION: COMPOSITIONS
TITLE OF INVENTION: INHIBITING H
                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Adda C. Gogoris, Esq.
REGISTRATION NUMBER: 29,714
REFERENCE/DOCKET NUMBER: 5986/17607-US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 527-7700
TELEPAX: (212) 753-6237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/119,694B
FILING DATE: 10-Sept-1993
ATTORNEY/AGENT INFORMATION:
NAME: Adda C. Gogoris, Esq.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5, inch, 30
COMPUTER: COMPAQ PROLINEA MT 4/66
OPERATING SYSTEM: DOS 3.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Word Perfect CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION:
                                                                                                                                                                                                                                                                        Local Similarity hes 12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 805 This
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 10022
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                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH:
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                                                                                                                                                                                                                                   1 KHKKLKQPGDGNP 13
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                                                                                                                                                                                                                                                                                                                                                                                                                     20 amino acids
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                                                                                                                                                                                                                                                                                        92.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     92.0%;
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Pred. No. 0.00071;
                                                                                                                                                                                                                                                                          Mismatches
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                                                                                                                                                                                                                                                                                         .00071;
                                                                                                                                                                                                                                                                        1; Indels
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Query Match
Best Local Similarity
""" 9; Conserv
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; OTHER INFORMATION: Circumsporozoite (CS) protein
; NAME/KEY: misc_feature
; OTHER INFORMATION: g1|4493889
US-09-820-843A-31
γQ
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                                                                                                                    US-07-677-539B-5
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US-07-677-539B-5
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LENGTH: 396
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                TELEPHONE: 202-861-301
TELEFAX: 202-822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT FILING DATE: 2001-03-30 NUMBER OF SEQ ID NOS: 118 SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/07/
FILING DATE: 19911205
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: SCOTT, WATSON T.
REGISTRATION UNMBER: 26,58
REFERENCE/DOCKET NUMBER: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 396
TYPE: PRT
ORGANISM: Plasmodium falciparum
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: LEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                TOPOLOGY: 1
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION: TELEPHONE: 202-861-3067
                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: LAL, ALTAF A.
APPLICANT: GOLDMAN, IRA F.
TITLE OF INVENTION: CIRCUMSPOROZOITE PROTEIN OF PLASMODIUM
TITLE OF INVENTION: REICHENOWI AND VACCINE FOR HUMAN MALARIA
                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                 STRANDEDNESS:
                                                                                                                                                                  LENGTH: 300 ...
TYDE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
ZIP: 20036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 1615 L S
CITY: WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                89 KHKKLKQPADGNP 101
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 1 KHKKLKQPGDGN 12
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                                                                                                                                                                                               388 amino acids
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                                Conservative
                                                                                                                                                 linear
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                                                                                                                                peptide
                                                                                                                                                               single
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92.3%;
                                                 68.0%;
75.0%;
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                                                                                                                                                                                                                                                                                                                                26,581
                                1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                 Score 51; DB Pred. No. 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. 0.023;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
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                                                                 Length 388;
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                                  Indels
                                0;
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                                  Gaps
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109 KHNKLKQPGNDN 120

US-07-727-636-5

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GENERAL INFORMATION:

APPLICANT: Hyseq, Inc
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
FILE REFERENCE: 21272-103
CURRENT FILING DATE: 2001-05-16
CURRENT FILING DATE: 2001-05-16
PRIOR APPLICATION NUMBER: 09/577, 408
PRIOR FILING DATE: 2000-05-18
PRIOR APPLICATION NUMBER: 09/695, 781<51> 2000-09-22
PRIOR APPLICATION NUMBER: 09/715,889<151> 2000-10-24
PRIOR APPLICATION NUMBER: 09/775,330<151> 2000-11-17
PRIOR APPLICATION NUMBER: 09/775,330<151> 2001-02-01
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 202-822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
LENGTH: 388 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/07/727,636
FILING DATE: 19910710
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: SCOTT, WATSON T.
REGISTRATION NUMBER: 26,581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 5, Application US/07727636 GENERAL INFORMATION:
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                NUMBER OF SEQ ID NOS: 864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 56
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-861-3067
TELEPHAX: 202-822-0944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF EQUIENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN, DARBY & CUSHMAN
STREET: 1615 L STREET, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: GOLDMAN, IRA F.
TITLE OF INVENTION: CIRCUMSPOROZOITE PROTEIN OF PLASMODIUM
TITLE OF INVENTION: REICHENOWI AND VACCINE FOR HUMAN MALARIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: LAL, APPLICANT: GOLDM
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Custom
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PCT-US01-23861-2
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CURRENT APPLICATION NUMBER: PCT/US99/09970
CURRENT FILING DATE: 1999-05-07
NUMBER OF SEQ ID NOS: 180
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
LENGTH: 102
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Applicat GENERAL INFORMATION:
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Best Local Similarity
Matches 8; Conserv
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CURRENT APPLICATION NUMBER: PCT/US01/238
CURRENT FILING DATE: 2001-07-31
PRIOR APPLICATION NUMBER: US 60/222,039
PRIOR FILING DATE: 2000-07-31
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Munger, William E. APPLICANT: Kulkarni, Prakash APPLICANT: Kulkarni, Prakash APPLICANT: Getzenberg, Robert R. TITLE OF INVENTION: Expression of a GAGE/PAGE-like Protein in Benign Prostatic TITLE OF INVENTION: Hyperplasia
                                                                                                                                                                                                                                                                                                                                  APPLICANT: McCoy, John M.
APPLICANT: LaVallie, Edward R.
APPLICANT: Collins-Racie, Lisa
                                                                                                                             APPLICANT: Genetics institute, Inc.
TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING
FILE REFERENCE: GI 6069-74A
                                                                                                                                                                                   APPLICANT: Bowman, Michael R.
APPLICANT: DiBlasio-Smith, Elizabeth
APPLICANT: Widom, Angela
                                                                                                                                                                                                                                                                              APPLICANT: Merberg, David APPLICANT: Treacy, Maurice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 10
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Jacobs, Kenneth
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TYPE: PRT
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APPLICANT: Jacobs, Kenneth
APPLICANT: LaVallie, Edward R.
APPLICANT: Collins-Racie, Lisa A.
APPLICANT: Collins-Racie, Lisa A.
APPLICANT: Collins-Racie, Lisa A.
APPLICANT: Werberg, David
APPLICANT: Merberg, David
APPLICANT: Steininger II, Robert J.
APPLICANT: Steininger II, Robert J.
APPLICANT: Bowman, Michael R.
APPLICANT: Bowman, Michael R.
APPLICANT: Bowman, Michael R.
APPLICANT: Genetics Institute, Inc.
APPLICANT: Genetics Institute, Inc.
TITLE OF INVENTION SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
FILE REFERENCE: GI 6069-74A
CURRENT APPLICATION NUMBER: US/09/306,111
Search completed: January 29, 2002, 10:56:01 Job time: 2397 sec
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US-09-306-111-2
                                                                                                                                                                                                                                                                                Query Match 62.7%;
Best Local Similarity 61.5%;
Matches 8; Conservative
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Best Local Similarity 61.5%;
Matches 8; Conservative
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90 KHAKTKEAGDGQP 102
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90 KHAKTKEAGDGQP 102
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              Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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3: /cgn2_6/ptodata/2/paa/U

4: /cgn2_6/ptodata/2/paa/U

5: /cgn2_6/ptodata/2/paa/U

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Query Match
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Sequence 11247, Application US/09708427; GENERAL INFORMATION:
APPLICANT: N. ALEXANDROV et al.
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                                                   FILE REFERENCE: 2750-1243P
CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: Patentin version 3.1
SEQ ID NO 11246
                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: N. ALEXANDROV et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: THEREBY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES TITLE OF INVENTION: THEREBY FILE REFERENCE: 2750-1243P CURRENT APPLICATION NUMBER: US/09/708,427 CURRENT FILING DATE: 2000-11-09 NUMBER OF SEQ ID NOS: 85364 SOFTWARE: Patentin version 3.1 SEQ ID NO 11247 LENGTH: 628
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc_feature
LOCATION: 1..628
O'HER INFORMATION: Xaa is any amino acid
NAME/KEY: misc_feature
LOCATION: 1..628
O'HER INFORMATION: Ceres Seq. ID 1822796
i-09-708-427-11247
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                    TYPE: PRT
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ORGANISM: Arabidopsis thaliana
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                                      LENGTH: 633
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Pred. No. 42;
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NAME/KEY: misc_feature
; LOCATION: 1. 633
; LOCHER INFORMATION: Ceres Seq.
US-09-708-427-11246
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; Sequence 6245, Application US/09708427
; GENERAL INFORMATION:
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US-09-708-427-6246
; Sequence 6246, Application US/09708427
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APPLICANT: N. ALEXANDROV et al.
APPLICANT: N. ALEXANDROV et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID
TITLE OF INVENTION: THEREBY
FILE REFERENCE: 2750-1243P
                                                                                                                  CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: PatentIn version 3.1
SEQ ID NO 6245
LENGTH: 454
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SEQ ID NO 6246
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Best Local Similarity 58.3%;
Matches 7; Conservative
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Best Local Similarity 66.7%;
Matches 8; Conservative
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CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
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LOCATION: 1..425
OTHER INFORMATION: Ceres Seq.
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TYPE: PRT
ORGANISM: Arabidopsis thaliana
                        NAME/KEY: misc_feature LOCATION: 1..454
                                                                                ORGANISM: Arabidopsis thaliana
                                                                                                      TYPE: PRT
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OTHER INFORMATION: Xaa
                                                                FEATURE:
OTHER INFORMATION: Xaa is any amino acid
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Pred. No. 45;
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Query Match
Best Local Similarity
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LOCATION: 1.558
; OTHER INFORMATION: Xaa is any amino
NAME/KEY: misc_feature
; LOCATION: 1.558
; OTHER INFORMATION: Ceres Seq. ID 181
US-09-708-427-6244
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; LOCATION: 1. 454
; OTHER INFORMATION: Ceres Seq.
US-09-708-427-6245
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Sequence 43901, Application US/09708427
GENERAL INFORMATION:
APPLICANT: N. ALEXANDROV et al.
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GENERAL INFORMATION:
APPLICANT: N. ALEXANDROV et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: THEREBY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: PatentIn version 3.1
SEQ ID NO 6244
LENGTH: 558
                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: PatentIn version 3.1
SEQ ID NO 43901
LENGTH: 122
                                                                                                                                                                                                                                                                           TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES TITLE OF INVENTION: THEREBY FILE REFERENCE: 2750-1243P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE: 2750-1243P
                 NAME/KEY: misc_feature
LOCATION: 1..122
OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc_feature
LOCATION: 1..122
                                                                                                            FEATURE:
                                                                                                                            ORGANISM: Zea mays subsp. mays
                                                                                                                                                   TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Arabidopsis thaliana
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OTHER INFORMATION: Ceres Seq. ID 1848537
                                                                                                                                                                                                                                                                                                                                                                                                                                                             227 KEKALKEKGEGN 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               123 KEKALKEKGEGN 134
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58.3%;
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58.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ID 1815596
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Pred. No. 47;
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LOCATION: 1..126
; OPHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc_feature
LOCATION: 1..126
; OPHER INFORMATION: Ceres Seq. ID 1848536
US-09-708-427-43900
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                                                                                                                                              APPLICANT: N. ALEXANDROV et al.

TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID

TITLE OF INVENTION: THEREBY

FILE REFERENCE: 2750-124 3P

CURRENT PLICATION NUMBER: US/09/708,427

CURRENT PILING DATE: 2000-11-09

NUMBER OF SEQ ID NOS: 85364

SOFTWARE: Patentin version 3.1

SEQ ID NO 43899

LENGTH: 152

TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                     Sequence 43899, Application US/09708427 GENERAL INFORMATION:
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Best Local Similarity
Matches 7; Conserv
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LENGTH: 126
TYPE: PRT
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Best Local Similarity 77.8
Matches 7; Conservative
             FEATURE:

NAME/KEY: misc_feature

LOCATION: 1..152

OTHER INFORMATION: Xaa i.

NAME/KEY: misc_feature

LOCATION: 1..152

CTUED INFORMATION: COVOR
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CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: N. ALEXANDROV et al. TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID TITLE OF INVENTION: THEREBY FILE REFERENCE: 2750-1243P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn version 3.1
OTHER INFORMATION: Ceres Seq. ID 1848535
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                                                                                                                                 ORGANISM:
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38 KRLKQSGDG
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                                                                                                                                 Zea mays subsp.
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77.8%;
                                                       is any amino acid
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    Mismatches

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Pred. No. 19;
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Pred. No. 18;
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APPLICANT: Bower, Stanley G.

APPLICANT: Hinkle, Gregory J.

APPLICANT: Slater, Steven C.

TITLE OF INVENTION: Sphingomonas elodea genome sequences and use:
FILE REFERENCE: 38-10(15806)B

CURRENT APPLICATION NUMBER: US/10/015,127

CURRENT FILING DATE: 2001-10-29

PRIOR APPLICATION NUMBER: US 60/252,455

PRIOR APPLICATION NUMBER: US 60/252,455

PRIOR FILING DATE: 2000-11-22

NUMBER OF SEQ ID NOS: 14357

SEQ ID NO 13035

LENGTH: 252

TUDNIBER OF SEQ ID NOS: 14357
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US-10-015-127-13035
; Sequence 13035, Application US/10015127
; GENERAL INFORMATION:
                                                                                                                                                              ; OTHER INFORMATION: Ceres US-09-708-427-32720
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US-09-708-427-32720
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                                                                                                                                                                                                                                                                                                                                            Sequence 32720, Application US/09708427
GENERAL INFORMATION:
APPLICANT: N. ALEXANDROV et al.
TITLE OF INVENTION: SEQUENCE DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: THEREBY
FILE REFERENCE: 2750-1143P
CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: Patentin version 3.1
SEQ ID NO 32720
LENGTH: 287
                                                                Query Match
Best Local Similarity
Matches 7; Conserv
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Best Local Similarity 45.5%;
Matches 5; Conservative
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TYPE: PRT
                                                                                                                                                                                                                                 NAME/KEY: misc_feature
LOCATION: 1..287
OTHER INFORMATION: Xaa is any
                                                                                                                                                                                                NAME/KEY: misc_feature LOCATION: 1..287
                                                                                                                                                                                                                                                                                            FEATURE:
                                                                                                                                                                                                                                                                                                         ORGANISM: Arabidopsis thaliana
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241 QHRKIAEPGSG 251
46 KVKEVEQEGDGN 57
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                                  1 KHKKLKQPGDGN 12
                                                                      Conservative
                                                                                     50.7%;
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77.8%;
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                                                                                   Score 38; DB
Pred. No. 44;
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Pred. No. 23;
                                                                                                                                                                                 ID 1834864
                                                                      Mismatches
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RESULT 13
US-09-708-427-32719
US-09-708-427-32719
Sequence 32719, Application US/09708427
GENERAL INFORMATION:
APPLICANT: N. ALEXANDROV et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID
TITLE OF INVENTION: THEREBY
FILE REFERENCE: 2750-1243P
CURRENT APPLICATION UMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: Patentin version 3.1
SEQ ID NO 32719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 14
US-09-708-427-32718
; Sequence 32718, Application US/09708427
; GENERAL INFORMATION:
; APPLICANT: N. ALEXANDROV et al.
                                                       Query Match
Best Local Similarity
7; Conserve
                                                                                                                                                                      ; NAME/KEY: misc_feature
; LOCATION: 1..435
; OTHER INFORMATION: Ceres Seq. ID 1834862
US-09-708-427-32718
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; LCCATION: 1..342
; OTHER INFORMATION: Ceres Seq. ID 1834863
US-09-708-427-32719
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CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: Patentin version 3.1
SEQ ID NO 32718
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID TITLE OF INVENTION: THEREBY FILE REFERENCE: 2750-1243P
                                                                                                                                                                                                                                         ORGANISM: Arabidopsis thaliana
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1..435
OTHER INFORMATION: Xaa is any amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Arabidopsis thaliana FEATURE:
NAME/KEY: misc_feature
LOCATION: 1..342
OTHER INFORMATION: Xaa is any amino acid
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TYPE: PRT
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TYPE: PRT
194 KVKEVEQEGDGN 205
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                                   1 KHKKLKQPGDGN 12
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                                                                       Conservative
                                                                                           50.7%;
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58.3%;
                                                                                         Score 38; DB
Pred. No. 67;
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                                                                         Mismatches
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                                                                                                              Length 435;
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RESULT 15 US-60-337-358-600

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Anfei
Yang, Chunzhi
Zeng, Xiaoping
APPLICANT: Zhao, Yajuan
APPLICANT: Zhao, Yajuan
APPLICANT: Zhao, Yajuan
APPLICANT: Zhao, Yajuan
FILE REFERENCE: 38-15(52796)A
CURRENT APPLICATION NUMBER: US/60/337,358
CURRENT FILING DATE: 2001-12-04
NUMBER OF SEQ ID NOS: 745
SEQ ID NO 600
LENGTH: 856
TYPE: PAT
ORGANISM: Zea mays
US-60-337-358-600
Search completed: January 29, 2002, 10:58:09 Job time: 2505 sec
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APPLICANT: Ahrens, Jeffrey E.
APPLICANT: Ball, James A.
APPLICANT: Banu, G.
APPLICANT: Bell, Erin
APPLICANT: Beddupalli, Raghava
APPLICANT: Chomet, Paul S.
APPLICANT: Daly, Mackenzie
                                                                                                                        Query Match
Best Local Similarity
Matches 8; Conserv
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APPLICANT:
APPLICANT:
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APPLICANT:
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                                                                  1 KHKKLKQPG--DG 11
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539 KHKLLREPGQPDG 551
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Dong, Jinzhuo
Duff, Stephen M.
Edgerton, Michael D
Galligan, Meghan M.
Hinchey, Brenda S.
Huang, Shihshieh
Johnson, Richard G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Madson, Linda L.
Malloy, Kathleen A.
McKiel, Christine L.
Miller, Philip W.
Padmathi, Machikanti
Parnell, Laurence D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lee, Gary
Lin, Jie-Yi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sheridan, Paul
Sherman, Paul L.
Start, William G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kretzmer, Keith A.
Laccetti, Lucille B.
Lai, Chao-Qiang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Jung, Vincent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Deikman, Jill
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lu, Bin
Luethy, Michael M.
Lund, Adrian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    iu, Jingdong
                                                                                                                           Conservative
                                                                                                                                        50.7%;
                                                                                                                        Score 38; DB 7; Length 856
Pred. No. 1.3e+02;
2; Mismatches 1; Indels
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                                                                                                                         Gaps
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Result
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Scoring table:
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Sequence:
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                                                                                                                                                                                                                                                                      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB seq length: 0
DB seq length: 2000000000
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         protein search, using sw model
       100.0
100.0
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69
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1.893 Million cell updates/sec
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    /cgn2_6/ptodata/2/paa/PCTUS_COMB.pep:*
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(cgn2_6/ptodata/2/paa/US086_COMB.pep: *
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(cgn2_6/ptodata/2/paa/US089_COMB.pep: *
(cgn2_6/ptodata/2/paa/US090_COMB.pep: *
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NANPNANPNANP 12
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/cgn2_6/ptodata/2/paa/US07_COMB.pep:*
/cgn2_6/ptodata/2/paa/US080_COMB.pep:*
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/cgn2_6/ptodata/2/paa/US084_COMB.pep:*
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/cgn2_6/ptodata/2/paa/US082_COMB.pep:*
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13
14
 PCT-US99-03055-105
US-07-958-321-9
US-07-958-321-11
US-08-387-932-4
1 US-08-773-675-8
1 US-08-998-335-1
3 US-08-998-335-1
4 US-09-060-450-1
4 US-09-074-410-34
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Sequence 105, Appli
Sequence 9, Appli
Sequence 11, Appli
Sequence 4, Appli
Sequence 8, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 34, Appli
                                                                                                                                                                                Description
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## ALIGNMENTS

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APPLICANT: Birkett, Ashley J.

TITLE OF INVENTION: Strategically modified Hepatitis B Core Proteins and TITLE OF INVENTION: their Derivatives

FILE REFERENCE: Syn-101 4564/69529

CURRENT APPLICATION NUMBER: PCT/US99/03055

CURRENT FILING DATE: 1999-02-11

EARLIER APPLICATION NUMBER: 60/074537

EARLIER FILING DATE: 1998-02-12

NUMBER OF SEQ ID NOS: 113

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 105

LENGTH: 12

TYPE: PRT

ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 1

PCT-US99-03055-105

; Sequence 105, Application PC/TUS9903055

; GENERAL INFORMATION:
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Query Match
Best Local Similarity
Matches 12; Conserv
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JOURNAL: Science
VOLUME: 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                           PAGES: 1436-1440
DATE: 1985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: Description of Artificial Sequence: Cytochrome OTHER INFORMATION: P-450 fragment
100.0%; silarity 100.0%; silarity 100.0%; sometime of the conservative of the conserva
Score 69; DB 1; 1
Pred. No. 0.00064;
); Mismatches 0;
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Gaps

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US-07-958-321-11
; Sequence 11, Application US/07958321
; GENERAL INFORMATION:
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US-07-958-321-9
                                                                                                                                                                                                  RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 435

PRIOR APPLICATION NUMBER: GB 9022190.4

FILING DATE: 12-CCT-1990

PRIOR APPLICATION NUMBER: PCT/GB91/01785

FILING DATE: 14-CCT-1991

ATTORNEY/AGENT INFORMATION:

NAME: MacLean, Kurt A.

REGISTRATION NUMBER: 31,118

REGISTRATION NUMBER: 31,118
                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 714-263-8260 INFORMATION FOR SEQ ID NO:
APPLICANT: Perham, nacural APPLICANT: Willis, Anne E.
APPLICANT: Willis, Anne E.
APPLICANT: Greenwood, Juddith
TITLE OF INVENTION: ENGINEERED BACTERIOPHAGES AND VACCINES
TITLE OF INVENTION: CONTAINING THEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 89
TELECOMMUNICATION INFORMATION:
TELEPHONE: 714-263-8250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Willis,
                                                                                                                                                                                                                                                                                                                                            Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: UZIP: 90067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: POMS, SMITH, LANDE & ROSE STREET: 2121 Avenue of the Stars CITY: Los Angles
                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US
FILING DATE: 19921222
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                                                                                                                                                                                                                                                                                                                                            100.0%; Score 69; DB 3; 100.0%; Pred. No. 0.00064;
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TELEPAX: 714-263-8260
TELEFAX: 714-263-8260
INFORMATION FOR SEQ ID NO: 11
SEQUENCE CHARACTERISTICS:
FENGTH: 12 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 4, Application:
                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Vers. #1.25
CURRENT APPLICATION DATA:
                                                                                                                                    ZIP: 19477

COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: MacLean, Kurt A.
REGISTION NUMBER: 31,118
REFERENCE/DOCKET NUMBER: 89
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: PCT/GB91/01785 FILING DATE: 14-OCT-1991 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9022190.4
FILING DATE: 12-OCT-1990
PRIOR APPLICATION DATA:
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STREET: LOS Angles
CITY: LOS Angles
CTATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                            APPLICANT: FISCHER, PETER
APPLICANT: TYLER, MARGARET I
TITLE OF INVENTION: Retro-, Inverso-, and Retro-Inverso
TITLE OF INVENTION: Synthetic Peptide Analogues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein
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CLASSIFICATION:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                   STREET: Spring House Corporate Cntr., P.O. Box 457 CITY: Spring House
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CLASSIFICATION: 424
                   FILING DATE:
                                  APPLICATION NUMBER:
                                                                                                                         MEDIUM TYPE:
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United States of America
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                                    US/08/387,932
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PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT// FILING DATE: 27-AUG-1993

PCT/AU93/00441

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Best Local :
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                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ANTI-SCHAPEL
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
ORGANISM: Plasmodium falciparum
ORGANISM: Plasmodium falciparum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PUBLICATION INFORMATION:
DOCUMENT NUMBER: AU PL4374
FILING DATE: 27-AUG-1992
                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/604,958
FILING DATE: 03-JUN-1996
ATTORNEY/ACENT INFORMATION:
NAME: MITCHARD, LEONARD C.
                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-540-9200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear MOLECULE TYPE: pept
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 27-AUG-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: PERHAM, RICHARD N. APPLICANT: WILLIS, ANNE APPLICANT: GREENWOOD, JUDITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HYPOTHETICAL:
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                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: ENGINEERED BACTERIOPHAGES AND VACCINES TITLE OF INVENTION: CONTAINING THEM
                                                                                                      FILING DATE: 24 CLASSIFICATION:
                                                                                                                                                                                                                                                            COUNTRY: U.S.A. ZIP: 22201-4714
                                                                                                                                                                                                                                                                                              CITY: ARLINGTON
STATE: VIRGINIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Match 100.0%;
Local Similarity 100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 31,215
                                                                                                                                      APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 215-540-5818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 NANPNANPNANP 12
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                MITCHARD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Application US/08773675
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                  NUMBER: US/08/773,675
24-DEC-1996
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LEONARD C.
BER: 29,009
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Pred. No. 0.00064;
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; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-773-675-8
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US-08-998-335-1
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; ORGANISM: P. falciparum US-08-998-335-1
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                                                                                                                                                                                                                                                                                                                                                                RESULT
                                                                   APPLICANT: NUSSENZWEIG, RUTH S.
APPLICANT: NUSSENZWEIG, RUTH S.
APPLICANT: ROSE, Keith
TITLE OF INVENTION: POLYOXIME-BASED ANTI-MALARIAL VACCINES
FILE REFERENCE: 5986/IC599-US1
CURRENT FILING DATE: 1997-12-24
EARLIER APPLICATION NUMBER: 60/034,506
EARLIER APPLICATION NUMBER: 60/034,506
EARLIER APPLICATION NUMBER: 60/034,506
EARLIER FILING DATE: 1996-12-24
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local S
Matches 12
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EARLIER FILING DATE: 1996-12-24
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1
LENGTH: 12
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Best Local Similarity
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CURRENT APPLICATION NUMBER: US/08/998,335
CURRENT FILING DATE: 1997-12-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Nussenzweig, Ruth S.
APPLICANT: Rose, Keith
TITLE OF INVENTION: POLYOXIME-BASED ANTI-MALARIAL VACCINES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (703) 816-410 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                  APPLICANT: Nardin, Elizabeth
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                                     TYPE: PRT
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                                                     LENGTH: 12
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LENGTH: 12 amino acids
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TELECOMMUNICATION INFORMATION:
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703) 816-4100
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Pred. No. 0.00064;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-060-450-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1, Application US/09060450 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 1
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Nardin, Elizabeth
APPLICANT: Moreno, Alberto
TITLE OF INVENTION: UNIVERSAL T-CELL EPITOPES FOR ANTI-MALARIAL VACCINES
FILE REFERENCE: 5986/18615-US1
CURRENT APPLICATION NUMBER: US/09/060,450
CURRENT FILING DATE: 1998-01-21
EARLIER APPLICATION UMMER: 60/033,916
EARLIER FILING DATE: 1997-01-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 12
                                 CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 60/045,949
FILING DATE: 08-MAY-1997
                                                                                                         SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION UNMER: US/09/074,410 FILING DATE: 08-MAY-1998
                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY & LARDNER
STREET: 3000 K Street, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: REDDISH, MAIK A.

APPLICANT: LONGENECKER, B. Michael
TITLE OF INVENTION: METHOD FOR GENERATING ACTIVATED T-CELLS
TITLE OF INVENTION: AND ANTIGEN-PULSED ANTIGEN-PRESENTING CELLS
NUMBER OF SEQUENCES: 34
ATTORNEY/AGENT INFORMATION: NAME: Saxe, Bernhard D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: AGRAWAL, Babita
APPLICANT: KRANTZ, Mark J
                                                                                                                                                                                                                                                                    STATE: D.C. COUNTRY: U.S.A. ZIP: 20007-5109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
nes 12; Conserv
                                                                                                                                                                                                                                                                                                                       CITY: Washington
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Pred. No. 0.00064;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 69;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
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FEATURE:
COTHER INFORMATION: Description of Artificial Sequence: synthetic
COTHER INFORMATION: peptide
US-09-300-959-39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-300-959-39
; Sequence 39, Applica
; GENERAL INFORMATION:
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Best Local Similarity
Watches 12; Conserve
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                                                                                                                                                                                                                                                                            US-09-763-397A-4
                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.
12; Conservative
                                                                                                                                                                                                                                    Sequence 4, Application US/09763397A GENERAL INFORMATION:
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SEQ ID NO 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 04
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
TELEPHAX: (202) 672-5399
INFORMATION FOR SEQ ID NO: 34:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/300,959
CURRENT FILING DATE: 1999-04-27
PRIOR APPLICATION NUMBER: US 60/083,154
PRIOR FILING DATE: 1998-04-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Zanetti, Maurizio
TITLE OF INVENTION: Somatic FILE REFERENCE: P-ZA 3519
                                                 APPLICANT: Control and Prevention
APPLICANT: Lal, Altaf A.
APPLICANT: Lal, Altaf A.
APPLICANT: Ping Shi, Ya
APPLICANT: Hasnain, Seyed E.
TITLE OF INVENTION: Recombinant Multivalent Malarial Vaccine Against Plasmodium
FILE REFERENCE: 6395-57049
CURRENT APPLICATION NUMBER: US/09/763,397A
CURRENT FILING DATE: 2001-62-16
                                                                                                                                                                                                APPLICANT: The Government of the United States of America, as represented by the APPLICANT: Secretary of the Department of Health and Human Services, Centers for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS:
               PRIOR FILING DATE: 1998-08-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 12
TYPE: PRT
ORGANISM: Artificial Sequence
PRIOR APPLICATION NUMBER: PCT / US99/18869
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
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TOPOLOGY: li
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     peptide
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100.0%; ;
ative 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 69; 100.0%; Pred. No.
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Pred. No.
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thes 0;
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US-07-958-321-13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 13, Application US/07958321 GENERAL INFORMATION:
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR FILING DATE: 1999-08-19
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                      TELEPHONE: 714-263-829
TELEFAX: 714-263-8260
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 12
TYPE: PRT
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/G
FILING DATE: 14-OCT-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9022190.4
FILING DATE: 12-OCT-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Perham, Richard N. APPLICANT: Willis, Anne E. APPLICANT: Greenwood, Judith
                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION: TELEPHONE: 714-263-8250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: ENTITLE OF INVENTION: CC NUMBER OF SEQUENCES: 2 CORRESPONDENCE ADDRESS:
              NAME/KEY: Peptide LOCATION: 1..13 OTHER INFORMATION: OTHER INFORMATION:
                                                                                                                                     WOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                           NAME: MacLean, Kurt A.
REGISTRATION NUMBER: 31,118
REFERENCE/DOCKET NUMBER: 89-208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: U: FILING DATE: 19921222
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CITY: Los Angles
                                                                                                   ORGANISM:
                                                                                                                                                                       TOPOLOGY:
   OTHER INFORMATION:
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                                                                                                                                                                                     amino acid
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                                                                                                                     SOURCE:
                                                                                                                                                                                                    13 amino acids
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                                                                                                                                                                       linear
                                                                                                     P. falciparum
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/note= "Chemically synthesized
peptide used to check reactivity of antibodies
raised against fdMal."
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Pred. No.
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RESULT 13
US-08-138-514-8
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                                                                   US-08-138-514-8
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Best Local Similarity
Matches 12; Conserv
            Query Match
Best Local 9
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                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-3901
TELEFAX: (908) 594-4720
INFORMATION FOR SEQ ID NO: 8:
                                                                                                                                                                                                                                                                        MOLECULL NU
HYPOTHETICAL: NU
TRNSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/138,514
FILING DATE: 15-OCT-1993
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS LENGTH: 13 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                         FEATURE
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                              FRAGMENT TYPE:
                                                                                          NAME/KEY:
LOCATION:
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OPERATING SYSTEM:
SOFTWARE: PatentI
                                                                                OTHER INFORMATION: /label- amide
                                                                                                                                     LOCATION:
                                                                                                                                                   NAME/KEY:
                                                                                                                                                                                                                     LOCATION:
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ch 100.0%; Score 69; Similarity 100.0%; Pred. No. 12; Conservative 0; Mismatcl
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                                                                                                                                                                                                                                                                                                                               amino acid
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                                                                                                                                                                                                                                                                                                                                              13 amino acids
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10..12
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2..4
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                                                                                                                                                                                                                                                                                                                   linear
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                                                                                                         Modified-site
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NO
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, Gerard H
35,746
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Pred. No. 0.0007;
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            0.0007;
                            DB 5;
                        Length 13;
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Matches

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; FILING DATE: US-08-387-932-3
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GENERAL INFORMATION:
Query Match
Best Local Similarity
Matches 12; Conserv
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PRIOR APPLICATION DATA:
APPLICATION UMBER: PCT/AU93/
FILING DATE: 27-AUG-1993
PRIOR APPLICATION UMBER: AU 4374
APPLICATION NUMBER: AU 4374
FILING DATE: 27-AUG-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO:
                                                                               LOCATION: 1..2
LOCATION: 1..2
COTHER INFORMATION: /label= A
OTHER INFORMATION: /note= "RESIDUE 1 IS AN EXTRA CYSTEINE
OTHER INFORMATION: RESIDUE ADDED TO THE N-TERMINUS OF THE
OTHER INFORMATION: PEPTIDE"
PUBLICATION INFORMATION:
DOCUMENT NUMBER: AU PL4374
FILING DATE: 27-AUG-1992
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APPLICANT: FISCHER, PETER
APPLICANT: TYLER, MARGARET I
APPLICANT: TYLER, MARGARET I
TITLE OF INVENTION: Retro-, Inverso-, and Retro-Inverso
TITLE OF INVENTION: Synthetic Peptide Analogues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Vers. #1.25
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                    HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
ORIGINAL FRAGMENT TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: GH
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-540-9200
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                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: pe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: Spring House Corporate Cntr., P.O. Box 457 CITY: Spring House
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 31,215
                                                                                                                                                                                                                                                                                                          ORGANISM: Plasmodium falciparum DEVELOPMENTAL STAGE: SPOROZOITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 215-540-5818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE:
                                                                                                                                                                                                                                                                  NAME/KEY: Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                         amino acid
GY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bak, Mary E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pennsylvania
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     Conservative
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                 100.0%;
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   0;
                   Score 69;
Pred. No.
   Mismatches
                   DB 7;
0.0007;
                                       Length 13;
   Indels
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RESULT 15
US-08-773-675-11
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search completed: January 29, 2002, 10:56:00
Job time: 2396 sec
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GENERAL INFORMATION:
APPLICANT: PERHAM, RICHARD N.
                                                                                                                                                                Query Match
Best Local
                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                              TELEFAX: (703) 816-41 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 24-DEC-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08,
FILING DATE: 03-JUN-1996
ATTORNEY/AGENT INFORMATION:
ATTECRATED IFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION: TELEPHONE: (703) 816-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: ENGINEERED BACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: WILLIS, ANNE APPLICANT: GREENWOOD, JUDITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                               STRANDEDNESS:
TOPOLOGY: li
                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: MITCHARD, LEONARD C
REGISTRATION NUMBER: 29,0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/0 FILING DATE: 24-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: ARLINGTON STATE: VIRGINIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET:
                                                                                                                                                              Local
                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER:
                                                                                 1 NANPNANPNANP
                                                                                                1 NANPNANPNANP 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 NANPNANPNANP 13
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                                                                                                                                               l Similarity
12; Conserv
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                                                                                                                                                                                                                                                                                              amino acid
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ilarity 100.0%;
Conservative 0
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NO: 11:
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Pred. No. 0.0007
; Mismatches
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                                                                                                                                                                                Length 13;
                                                                                                                                                    Indels
                                                                                                                                                    0;
                                                                                                                                                    Gaps
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Sequence 13, Appl
Sequence 11, Appli
Sequence 6, Appli
Sequence 6, Appli
Sequence 2, Appli
Sequence 26410, A
Sequence 26410, A
Sequence 78694, A
Sequence 78694, A
Sequence 3416, A
Sequence 3417, Ap
Sequence 2211, Ap
Sequence 12005, A
Sequence 12005, A
Sequence 12005, A
Sequence 2211, Ap
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                                                                    ; Search time 120.95 Seconds
(without alignments)
3.631 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Description
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Sequence 3
Sequence 3
Sequence 1
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(g012_6/ptodata/2/paa/USO6_NEW_COMB.pep:*
(g012_6/ptodata/2/paa/USO6_NEW_COMB.pep:*
(g012_6/ptodata/2/paa/USO7_NEW_COMB.pep:*
(g012_6/ptodata/2/paa/USO9_NEW_COMB.pep:*
(g012_6/ptodata/2/paa/USO9_NEW_COMB.pep:*
(g012_6/ptodata/2/paa/USO0_NEW_COMB.pep:*
(g012_6/ptodata/2/paa/USO0_NEW_COMB.pep:*
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-938-406-5
US-09-843-696B-23
US-09-842-500-1
US-09-482-500-1
US-09-482-500-1
US-09-643-696B-6
US-09-708-427-26419
US-09-708-427-26419
US-09-708-427-78694
US-09-708-427-78694
US-09-708-427-78694
US-09-708-427-3418
                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                    173191 seqs, 36597120 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUMMARIES
                                                                    January 29, 2002, 10:58:07
                                                                                                                                                                                                                                                                                  Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                               sw model
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Gapop 10.0 , Gapext 0.5
                                               - protein search, using
                                                                                                                                         1 NANPNANPNANP 12
                                                                                                                                                                                                                                                 seq length: 0 seq length: 2000000000
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Match Length
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Perfect score:
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Maximum DB
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53326, A
2222, A
2222, A
1187, AP
1104, AP
77, AP
77, AP
11902, AP
11906, AP
11996, AP
11996, AP
11996, AP
12109, AP
2109, AP
                                                                                                                                                   Sequence 4718, A Sequence 7, Appl Sequence 1896, A Sequence 1895, A Sequence 1895, A Sequence 1894, A Sequence 19136, Sequence 2109, A Sequenc
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APPLICANT: Travis, James
APPLICANT: Travis, James
APPLICANT: Genco, Caroline A.
APPLICANT: Genco, Caroline A.
TITLE OF INVENTION: GINGIVALIS PEPTIDES AND METHODS
TITLE OF INVENTION: GINGIVALIS PEPTIDES AND METHODS
FILE REFERENCE: 235.00120120
CURRENT APPLICATION NUMBER: 08/09/543,696B
PRIOR APPLICATION NUMBER: 08/822,324
                                                                                      Sequence
Sequence
Sequence
                       Sequence
                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 5, Application US/09938406

GENERAL INFORMATION:
APPLICANT: LOWell, George
APPLICANT: LOWell, George
APPLICANT: Vancott, Thomas
APPLICANT: Howell, George
APPLICANT: PLIX, Deborah
TITLE OF INVENTION: PROTEIN AND PEPTIDE VACCINES FOR
TITLE OF INVENTION: INDOCING MUCOSAL IMMUNITY
FILE REFERENCE: 40646-20002.10
CURRENT APPLICATION NUMBER: US/09/938,406
CURRENT FILING DATE: 2001-08-21
PRIOR APPLICATION NUMBER: US 09/214,701
PRIOR APPLICATION NUMBER: US 09/214,701
PRIOR APPLICATION NUMBER: US 60/021,687
PRIOR FILING DATE: 1999-09-30
PRIOR FILING DATE: 1996-07-10
PRIOR FILING DATE: 1996-07-10
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5
LENGTH: 68
                  S-09-708-427-53325
S-09-706-446A-2229
S-09-760-446A-1187
S-09-646-673A-104
S-09-788-427-1204
S-09-788-427-1204
S-09-981-353-7
S-09-708-427-4189
S-09-708-427-4189
S-09-708-427-4116
S-09-708-427-4116
S-09-708-427-4116
S-09-708-427-11936
S-09-708-427-11936
S-09-708-427-11936
S-09-708-427-11936
S-09-708-427-1109
S-09-708-427-1109
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llarity 100.0%; Pred. No. 0.00016;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 23, Application US/09543696B GENERAL INFORMATION:
236
303
303
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309
309
402
431
451
465
571
1333
446
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CORGANISM: P. falciparum
US-09-938-406-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NANPNANPNANP 12
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Best Local Similarity
Matches 12; Conserv
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us-09-763-397a-4.rapn

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1 NANPNANPNANP 12
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                           LENGTH: 1477
                                                                                                                                                                                                                                                                                                                                                     US-09-482-500A-1
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LENGTH: 1704
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
    SEQ ID NO 1
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APPLICANT: POCHEMPA, Jan
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CONTROL OF BLOOD COAGULATION
FILE REPERENCE: 235.00160101
CURRENT APPLICATION NUMBER: US/09/482,500
CURRENT FILING DATE: 2000-01-13
PRIOR APPLICATION NUMBER: US 60/115,869
PRIOR FILING DATE: 1999-01-13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Corbin, David R.
APPLICANT: Coldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hacsing, Joseph B.
APPLICANT: Malvar, Thomas M.
APPLICANT: Salete, Steven C.
APPLICANT: Spiridonov, Sergei
TITLE OF INVENTION: Xenorhabdus sp. Genome Sequences And Uses Thereof
FILE REFERENCE: 38-21(51847)a
CURRENT APPLICATION NUMBER: US/09/897,516
CURRENT FILING DATE: 2000-06-39
PRIOR FILING DATE: 2000-06-30
NUMBER OF SEQ ID NOS: 8409
SEQ ID NO 5117
LENGTH: 818
                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                      ; OTHER INFORMATION: Description of Artificial Sequence:Peptide US-09-543-696B-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 818;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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Pred. No. 0.012;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 5;
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0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 5117, Application US/09897516 GENERAL INFORMATION:
PRIOR FILING DATE: 1997-03-21
PRIOR APPLICATION NUMBER: 60/013,945
PRIOR FILING DATE: 1996-03-22
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 23
LENGTH: 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1, Application US/09482500
GENERAL INFORMATION:
APPLICANT: Travis, James
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       71.0%;
80.0%;
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75.0%;
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PatentIn version 3.0
                                                                                                                                                                  ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 75.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 80.0
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: PRT
; ORGANISM: Xenorhabdus sp.
US-09-897-516-5117
                                                                                                                                                                                                                                                                                                                                                                      1 NANPNANPNANP 12
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10 NPNPNPNPNP 21
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681 NPNPNPNP 690
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 3
US-09-897-516-5117
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                                                                                                                                               TYPE: PRT
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SOFTWARE:
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APPLICANT: Travis, James
APPLICANT: Travis, James
APPLICANT: Imamura, Takahisa
APPLICANT: Imamura, Takahisa
APPLICANT: Dotempa. Jan
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CONTROL OF BLOOD COAGULATION
FILE REFERENCE: 235.00160101
CURRENT APPLICATION NUMBER: US/09/482,500A
CURRENT FILING DATE: 2001-12-17
PRIOR FILING DATE: 1999-01-13
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Sequence 6, Application US/09543696B

Sequence 6, Application US/09543696B

GENERAL INFORMATION:
APPLICANT: Potempa, Jan S.
APPLICANT: Travis, James
APPLICANT: Genco, Caroline A.
ATILE OF INVENTION: GINGIVALIS PEPTIDES AND METHODS
FILE REFERENCE: 235.00120120
CURRENT APPLICATION NUMBER: US/09/543,696B

CURRENT FILING DATE: 1000-04-05
PRIOR FILING DATE: 1997-03-21
PRIOR FILING DATE: 1997-03-21
PRIOR FILING DATE: 1997-03-22

NUMBER OF SEQ ID NOS: 30

SOFTWARE: PatentIn Ver. 2.1
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                                                                                                       Length 1477;
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                                                                                                       Score 49; DB 5;
Pred. No. 4.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 5;
                                                                                                                                Pred. No. 4.4;
0; Mismatches
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Pred. No. 4
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; TYPE: PRT
; ORGANISM: Porphyromonas gingivalis
US-09-482-500-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Porphyromonas gingivalis
US-09-543-6968-6
                                                                                                                                                                                                                                                                                                                                         ; Sequence 1, Application US/09482500A; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: Porphyromonas gingivalis US-09-482-500A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    71.0%;
66.7%;
                                                                                                          71.0%;
66.7%;
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SOFTWARE: Patentin version 3.0
SEQ ID NO 1
                                                                                                       Query Match 71.0
Best Local Similarity 66.7
Matches 8; Conservative
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Best Local Similarity 66.7
Matches 8; Conservative
                                                                                                                                                                                                                        720 NGTPNPNPNPNP 731
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Sequence 26419, Application US/09708427
GENERAL INFORMATION:
APPLICANT: N. ALEXANDROV et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID
TITLE OF INVENTION: THEREBY
FILE REFERENCE: 2750-1243P
CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOGTWARE: Patentin version 3.1
SEQ ID NO 26419
LENGTH: 953
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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID
TITLE OF INVENTION: THEREBY
TITLE OF INVENTION: THEREBY
CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
SEQ ID NOS: 85364
SEQ ID NO 78695
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Pred. No. 7.9;
0; Mismatches
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Pred. No. 4.9;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc_feature

LOCATION: 1.953

OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc_feature

LOCATION: 1.953

OTHER INFORMATION: Ceres Seq. ID 1818047
US-09-708-427-26419
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1.0.424
COTION: 1..424
COTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc_feature
1.0.CATION: 1..424
COTHER INFORMATION: Ceres Seq. ID 1963464
US-09-708-427-78695
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Best Local Similarity 66.7%;
Matches 8; Conservative (
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Best Local Similarity 80.0%;
Matches 8; Conservative
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                                                              US-09-708-427-26419
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GENERAL INFORMATION:
GENERAL INFORMATION:
TAPLICANT: N. ALEXANDROW et al.
TITLE OF INVENTION: THEREBY
TITLE OF INVENTION: THEREBY
TITLE OF INVENTION: THEREBY
CURRENT APPLICATION UNMBER: US/09/708,427
CURRENT APPLICATION UNMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: Patentin version 3.1
SEQ ID NO 26420
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Pred. No. 6.3;
0; Mismatches
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Pred. No. 2.1;
    Pred. No. 5.1;
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: VOGANATHAN, THILLAINATHAN
APPLICANT: VOGANATHAN, THILLAINATHAN
TITLE OF INVENTION: SGK2 AND ITS USES
FILE REFERENCE: KINE025CIP
CURRENT APPLICATION NUMBER: US/09/971,118
CURRENT FILING DATE: 2001-10-03
PRIOR APPLICATION NUMBER: PCT/US01/21479
PRIOR APPLICATION NUMBER: 60/237,419
STORMARE: PSSC ID NOS: 8
SOFTWARE: PSSC ID NOS: 8
LENGTH: 367
                    0; Mismatches
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: LOCATION: 1..757
: COTHER INFORMATION: Xaa is any amino acid
: NAME/KEY: misc_feature
: LOCATION: 1..757
: COTHER INFORMATION: Ceres Seq. ID 1818048
US-09-708-427-26420
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66.78;
  66.78;
Best Local Similarity 66.7
Matches 8; Conservative
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Matches 8; Conservative
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Matches 8; Conservative
                                                                                   | || || || || || 947 NGTPNPNPNPNP 958
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ORGANISM: Homp sapiens
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21 NLGPSANPNAQP 32
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US-09-708-427-26420
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US-09-971-118-2
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APPLICANT: N. ALEXANDROV et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYBEPTID
TITLE OF INVENTION: THEREBY
FILE REFERENCE: 2750-1243P
CURRENT PEPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 3418
LENGTH: 343
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; GENERAL INFORMATION:
; APPLICANT: N. ALEXANDROV et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID
; TITLE OF INVENTION: THEREBY
          TITLE OF INVENTION: SEQUENCE-DEFERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID TITLE OF INVENTION: THEREBY CURRENT APPLICATION NUMBER: 05/09/708,427

CURRENT APPLICATION NUMBER: 2000-11-09

NUMBER OF SEQ ID NOS: 85364

SOFTWARE: Patentin version 3.1
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Pred. No. 7.8;
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; OTHER INFORMATION: Ceres Seq. ID 1810473
US-09-708-427-3418
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ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                  ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                        NAME/KEY: misc_feature
LOCATION: 1..342
COTHER INFORMATION: Ceres Seq.
US-09-708-427-3419
  APPLICANT: N. ALEXANDROV et al
                                                                                                                                                                                                                                                                             LOCATION: 1..342
OTHER INFORMATION: Xaa is any
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Best Local Similarity 34.00
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Best Local Similarity 34.0
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                                                                                                                                                        SEQ ID NO 3419
LENGTH: 342
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      Sequence 78694, Application US/09708427
GENERAL INFORMATION:
APPLICANT: N. ALEXANDROV et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES TITLE OF INVENTION: THEREBY FILE REFERENCE: 2750-1243P
FULE REFERENCE: 2750-1243P
CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: Patentin Version 3.1
SEQ ID NO 78694
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TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: THEREBY
FILE REFERENCE: 2750-1248
FILE REFERENCE: 2750-1248
CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: PATCHIN VERSION 3.1
SEQ ID NO 31468
LENGTH: 346
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                                                                                                                                                                                                                                                                                                            NAME/KEY: misc_feature
1.521
LOCATION: 1.521
COTHER THORMATION: Xaa is any amino acid
NAME/KEY: misc_feature
LOCATION: 1.521
COTHER INFORMATION: Ceres Seq. ID 1963463
US-09-708-427-78694
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CTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc_feature
LOCATION: 1.346
USTHER INFORMATION: Ceres Seq. ID 1832153
US-09-708-427-31468
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2-09-708-427-3419
; Sequence 3419, Application US/09708427
; GENERAL INFORMATION:
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ORGANISM: Arabidopsis thaliana
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70.0%;
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80.0%;
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Best Local Similarity 80.0
Matches 8; Conservative
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5 DPNPNPNPNP 14
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US-09-708-427-78694
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FILE REFERENCE: 2750-1243P
CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
WUBER OF SEQ ID NOS: 85364
SOFTWARE: Patentin version 3.1
SEQ ID NO 3417
FEROTH: 356
TYPE: PRT
ORGANISM: Arabidopsis thaliana
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1.356
COTHER INFORMATION: Xaa is any amino acid
MAME/KEY: misc_feature
LOCATION: 1.356
COTHER INFORMATION: Ceres Seq. ID 1810472
US-09-708-427-3417
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Search completed: January 29, 2002, 10:58:08 Job time: 2504 sec

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